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(54) **RECOMBINANT ATTENUATED DENGUE VIRUSES COMPRISING A DELETION IN THE 3' UNTRANSLATED REGION AND ADDITIONAL ATTENUATING MUTATIONS INDUCED BY CHEMICAL MUTAGENESIS**

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Filed: **Mar. 2, 2009**

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(60) Continuation of application No. 11/446,050, filed on Jun. 2, 2006, now Pat. No. 7,560,118, which is a division of application No. 10/719,547, filed on Nov. 21, 2003, now Pat. No. 7,226,602, which is a continuation of application No. PCT/US02/16308, filed on May 22, 2002.

(60) Provisional application No. 60/293,049, filed on May 22, 2001.

(51) **Int. Cl.**
A61K 39/12 (2006.01)
C12N 7/04 (2006.01)

(52) **U.S. Cl.**
USPC **424/218.1; 435/236**

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

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(57) **ABSTRACT**

The invention provides compositions featuring an attenuated dengue virus mutant or an attenuated chimeric dengue virus mutant.

10 Claims, 12 Drawing Sheets

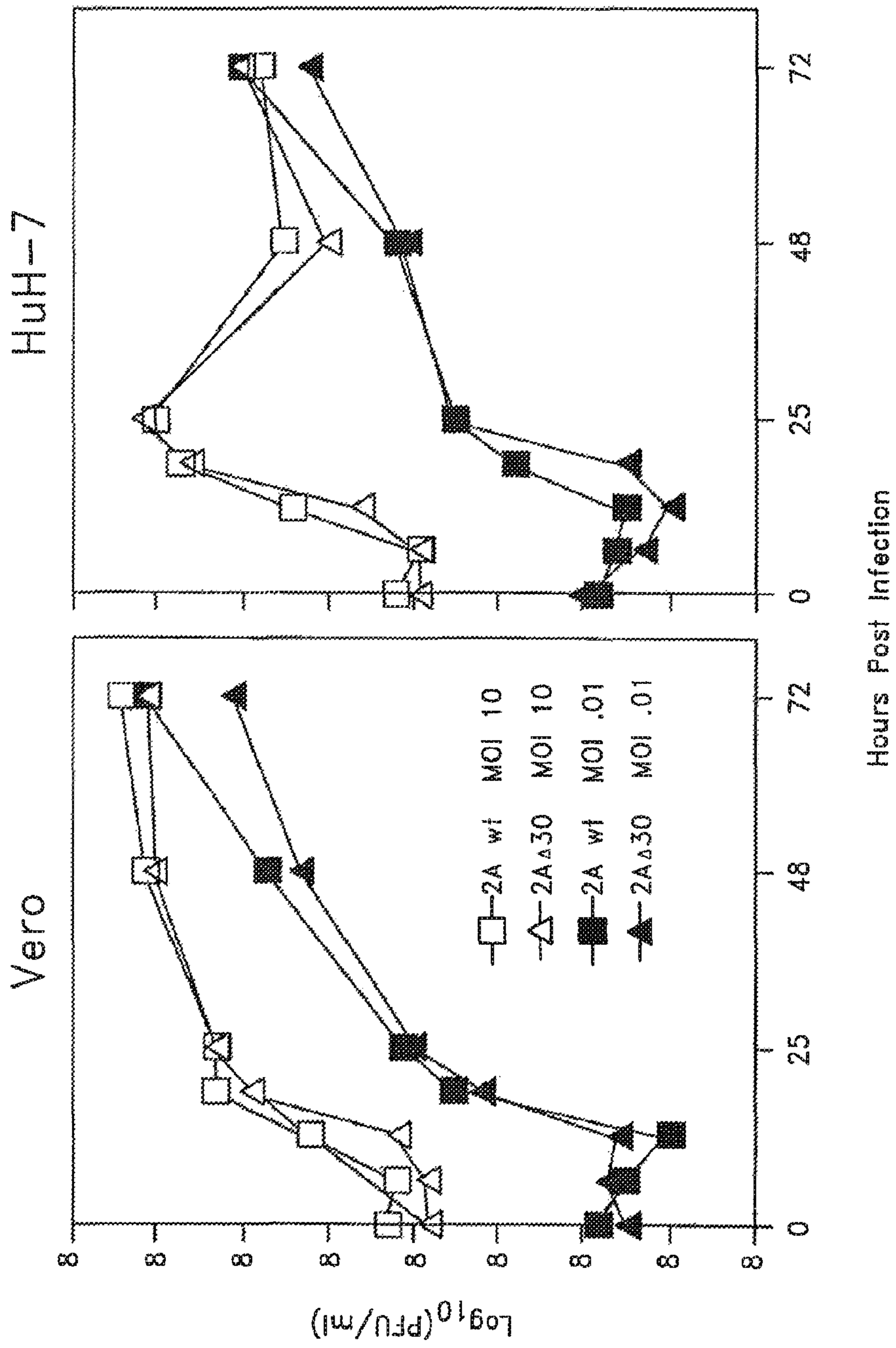


FIG. 1

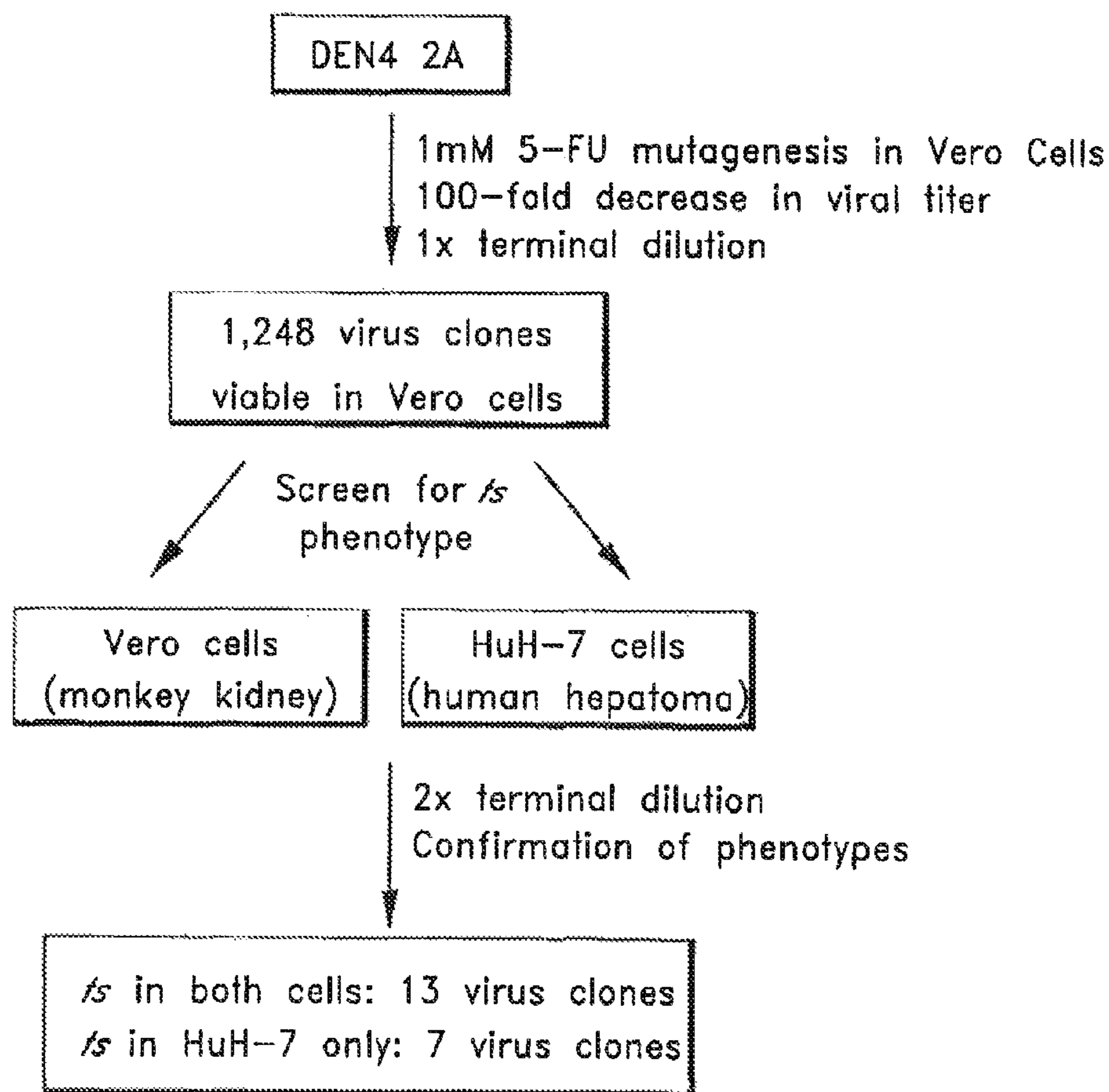


FIG. 2

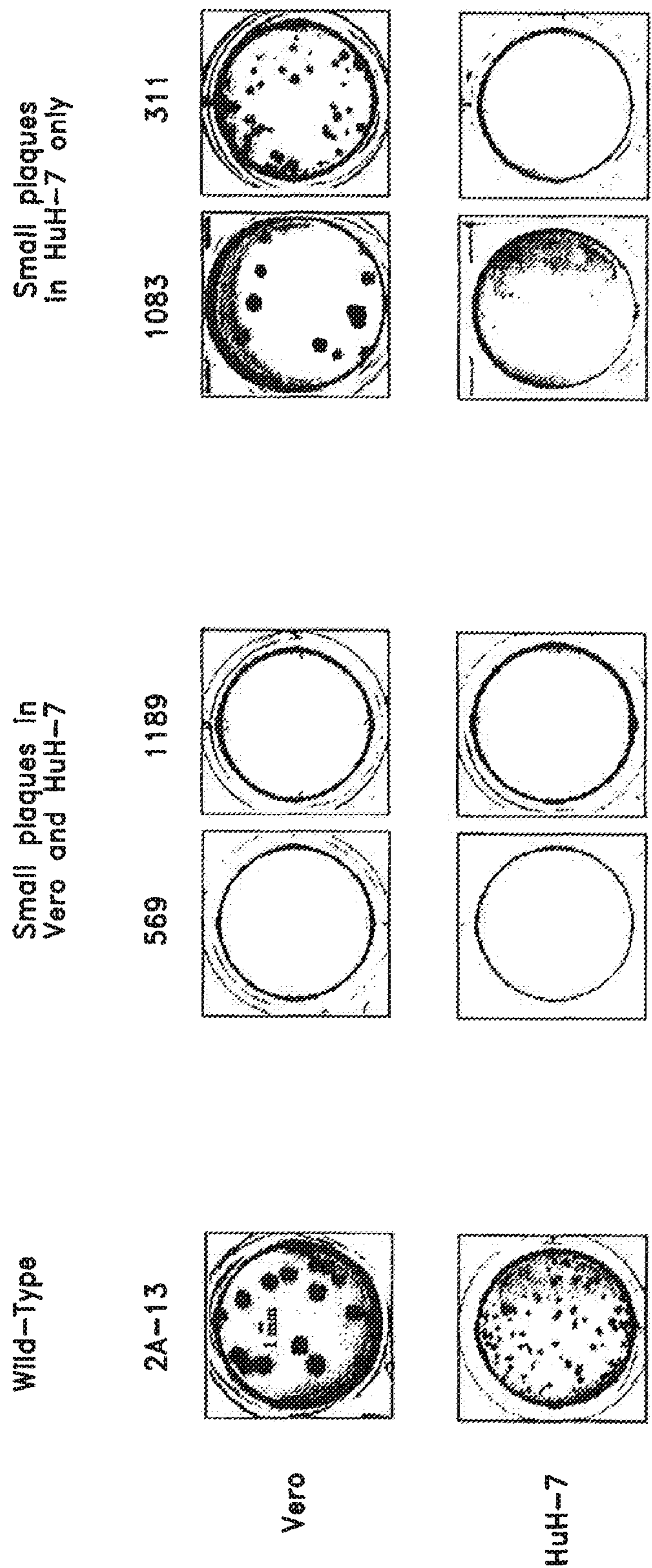


FIG. 3A

FIG. 3B

FIG. 3C

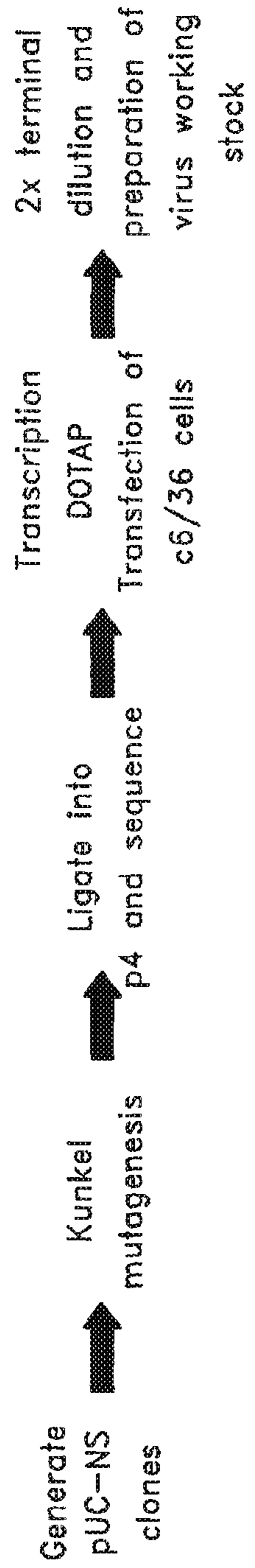
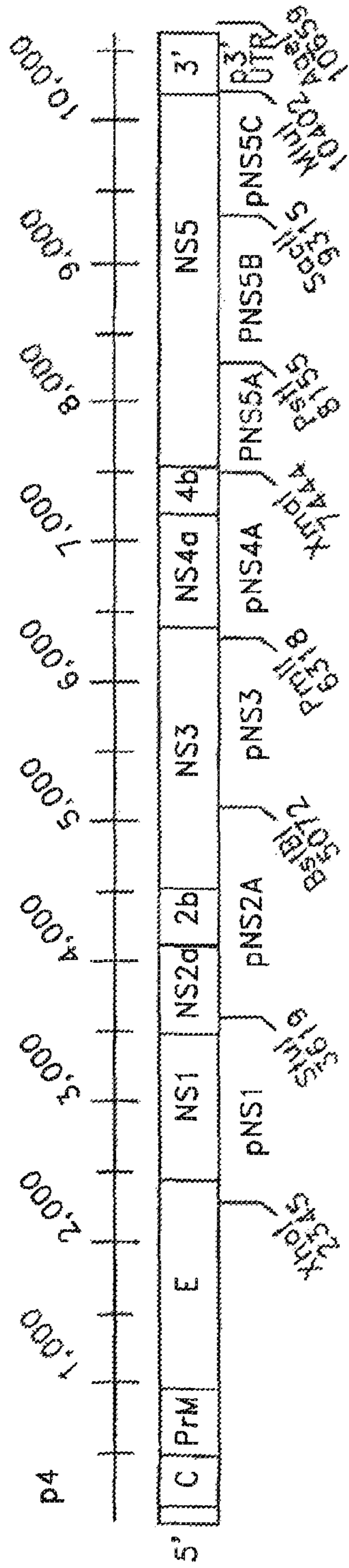


FIG. 4

1	GTGTTGETLG EKWKRLNSL <u>DRKEFEYKR</u> SGILEVDRTE AKSALKDQSK	SAM
51	<u>IKHAVSRGSS</u> KIRWIVERGM VKPKGKVVDL GCGRGGWSYY MATLKNVTBY	
101	KGYTKGGPGH <u>EEPIPMATYG</u> WNLVKLHSGV DVFYKPTQV DTLLCPDSES	
151	SSNPTIEEGR TLRVLKMVEP WLSSKPEFCI KVLNPYMPTV IEELEKLQRK	
201	HGGNLVRCPL SRNSTHEMYW VSGASGNIVS SVNTTSKMLL NRFTTRHRKP	
251	TYEKDVDLGA GTRSVSTETE <u>KPDMTIIGRR</u> LQRLQEEHKE TWHYDQENPY	
301	RTWAYHGSYE <u>APSTGSASSM</u> VNGVVKLLTK PWDVIPMVTQ LAMTDITPFG	Importin - binding + NLS
351	<u>QQRVENEKVD</u> TRTPQPKPGT RMVMTTANW LWALLGKKKN PRLCTREEFI	
401	SKVRSMAAIG AVFQEEQGT SASEAVNDSR FWELVDKERA LHQEGKCESC	
451	VYNNMGKREK <u>KLGEFGRAG</u> SRAIWYMWLG ARFLEFEALG FLNEDHWFGK	
501	ENSWSGVEGE GLHRLGYILE <u>EIDKKDGLM</u> YADDTAGWDT RITEDDLQNE	
551	ELITEQMAPH <u>HKILAKAIFK</u> LTYQNKVVKV LRPTPRGAVM DIISRKDQRG	
601	SGQVGTYGLN TFTNMEVQLI RQMEAEGVIT <u>QDDMONPKGL</u> <u>KERVEKWLKE</u>	Polymerase
651	CGVDRLKRNA ISGDDCVVKP <u>LDERFGTSL</u> FLNDMGKVRK DIPQWEPSKG	
701	WKNWQEVVFC <u>SHHFHKIFMK</u> DGRSLVVPCR NQDELIGRAR ISQGAGWSLR	
751	ETACLKAYA QMWSLMYFHR <u>RDLRLASMAI</u> CSAVPTIEWFP TSRTTWSIHA	
801	HHQWMTEDM LKVWNRVWIE <u>DNPNTDKTP</u> VHSWEDIFYL GKREDLWCGS	
851	LIGLSSRATW AKNIHTAITQ VRNLIGKEEY VDYPVMKRY SAPSESEGL	

FIG. 5

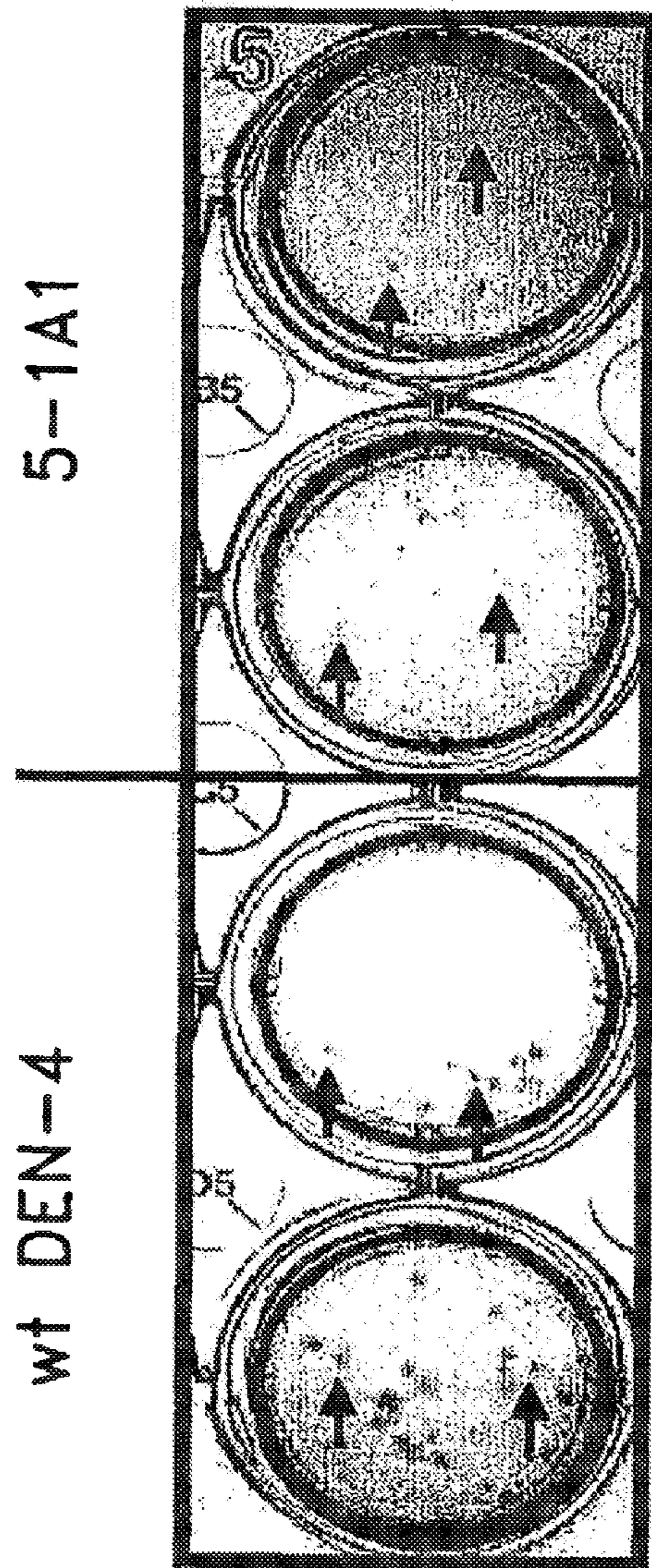


FIG. 6

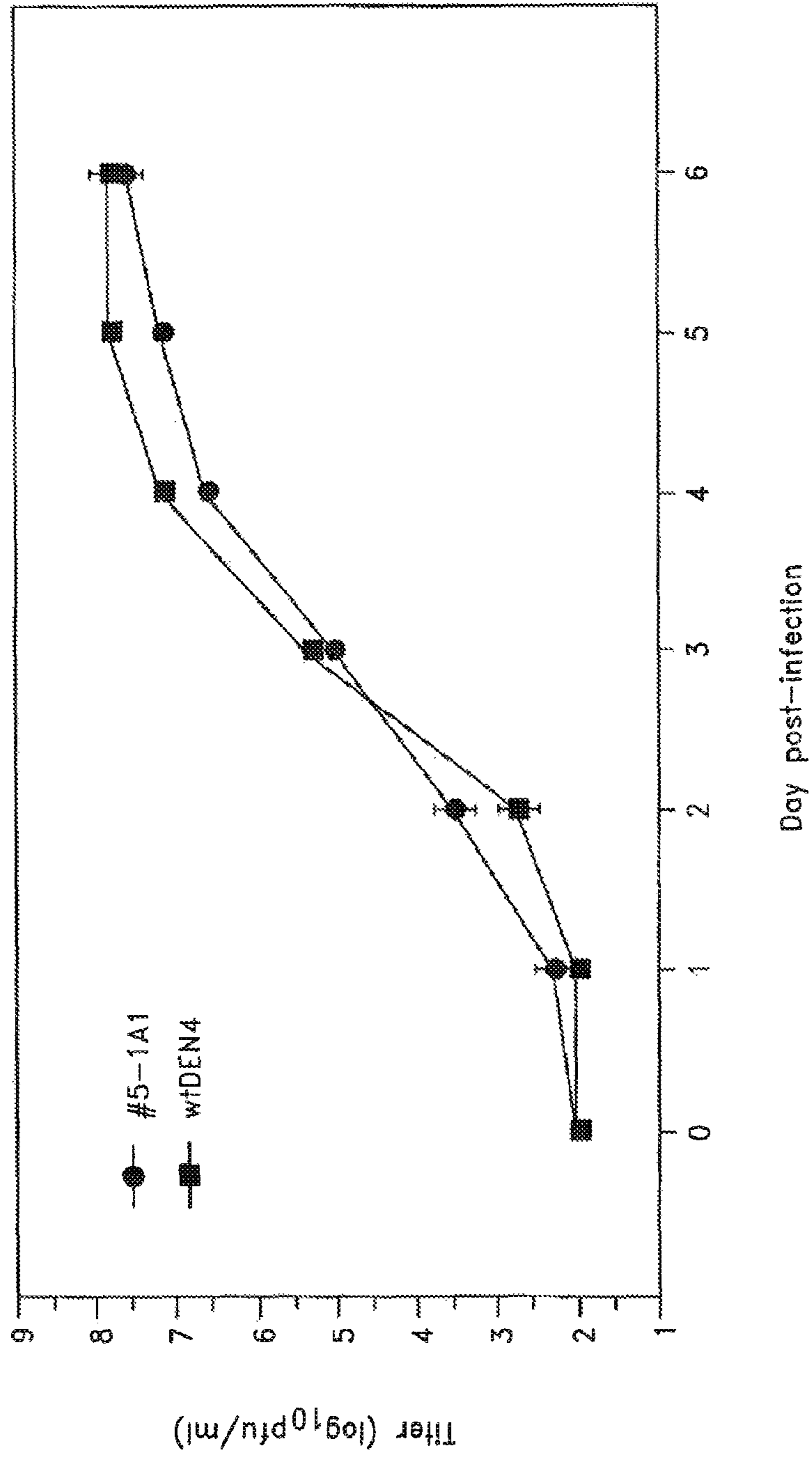


FIG. 7

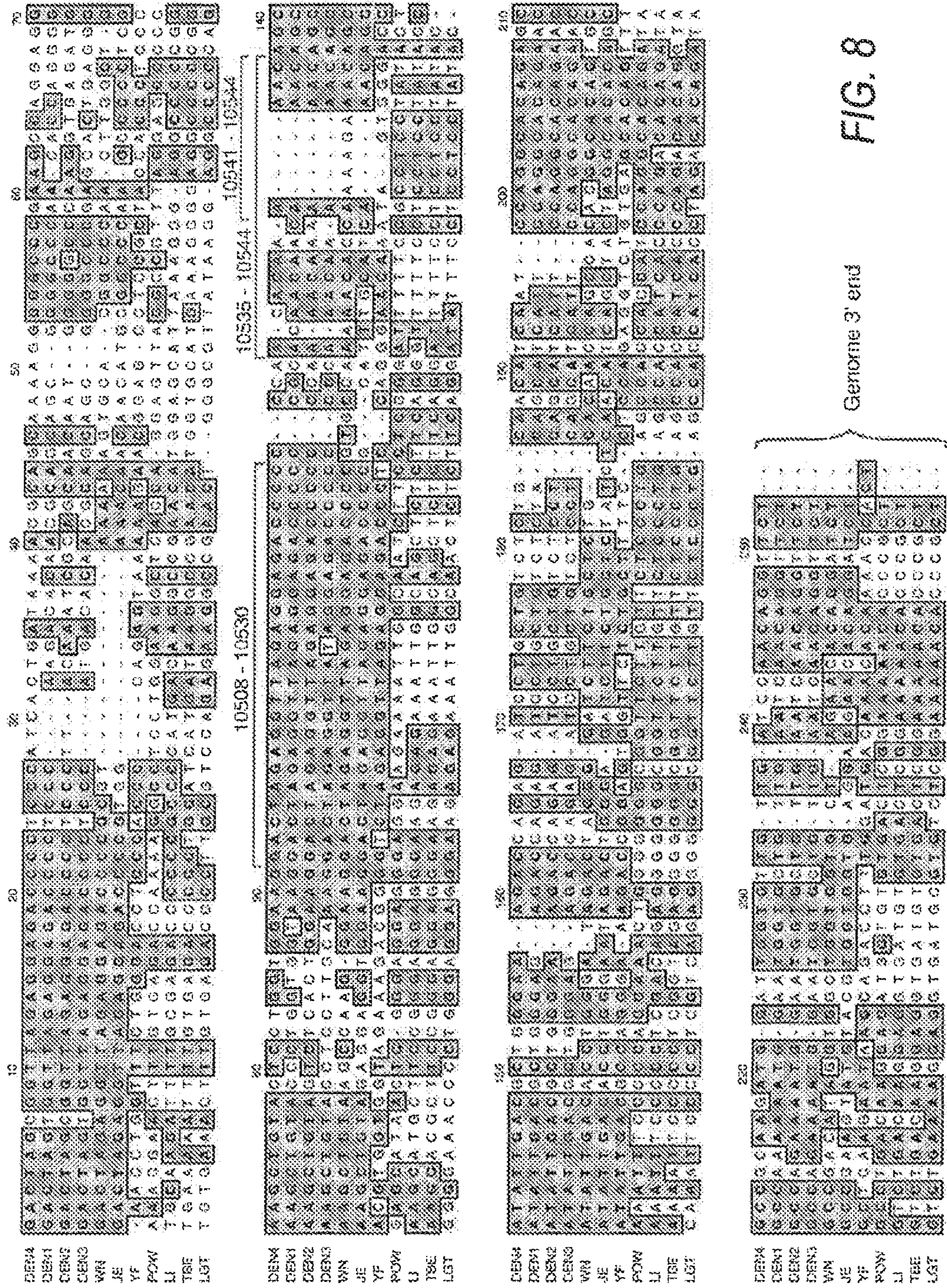


FIG. 8

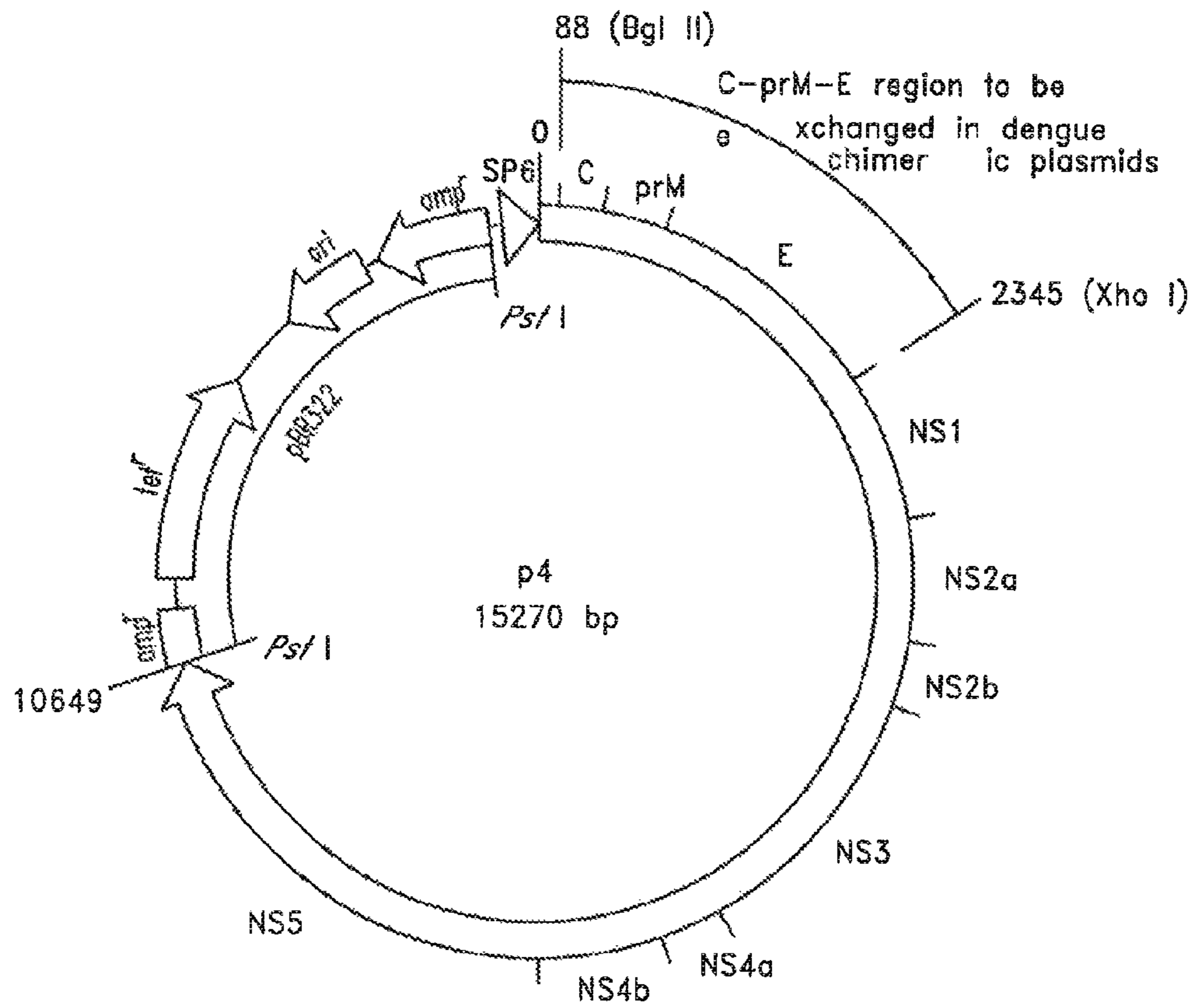


FIG. 9

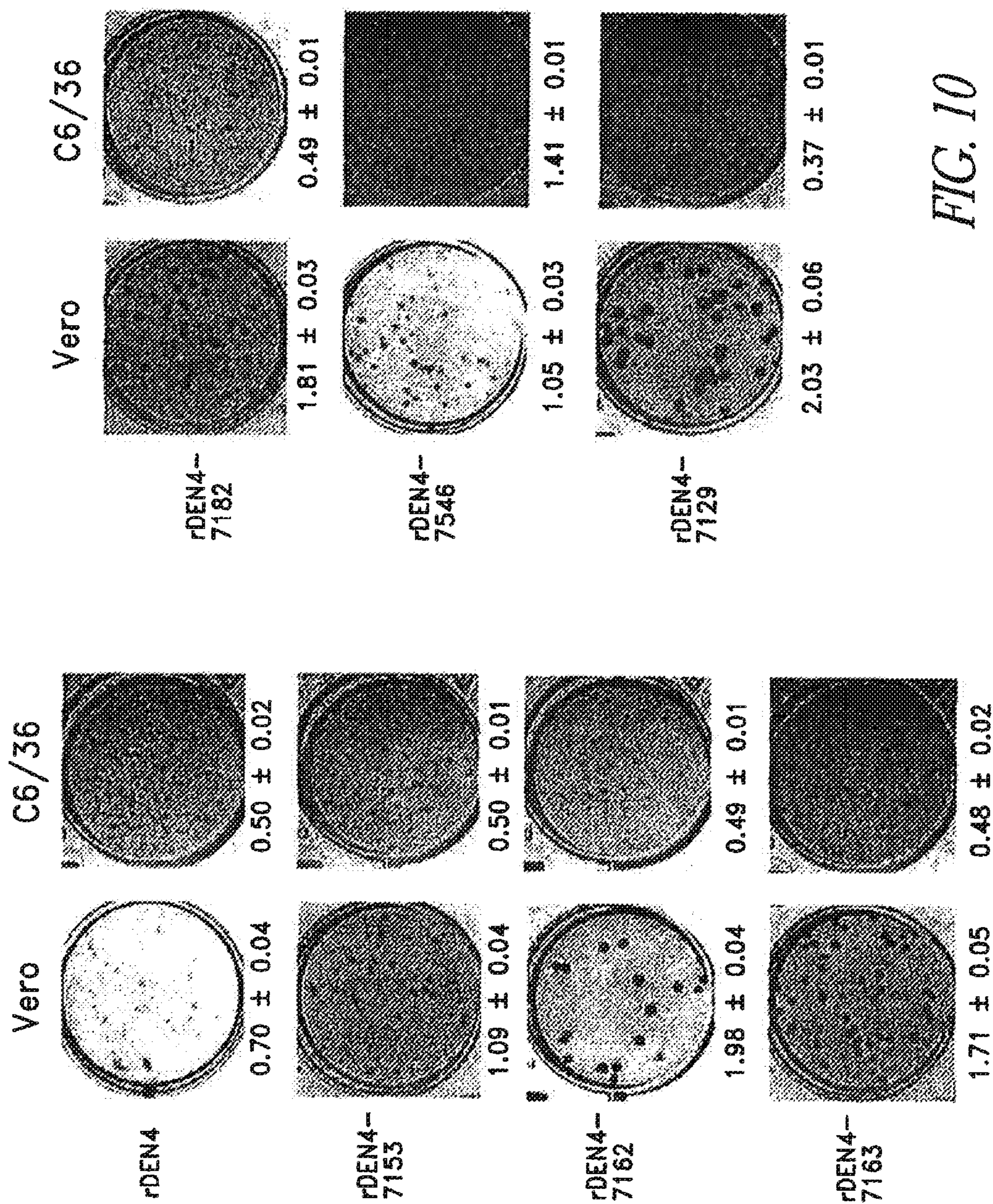


FIG. 10

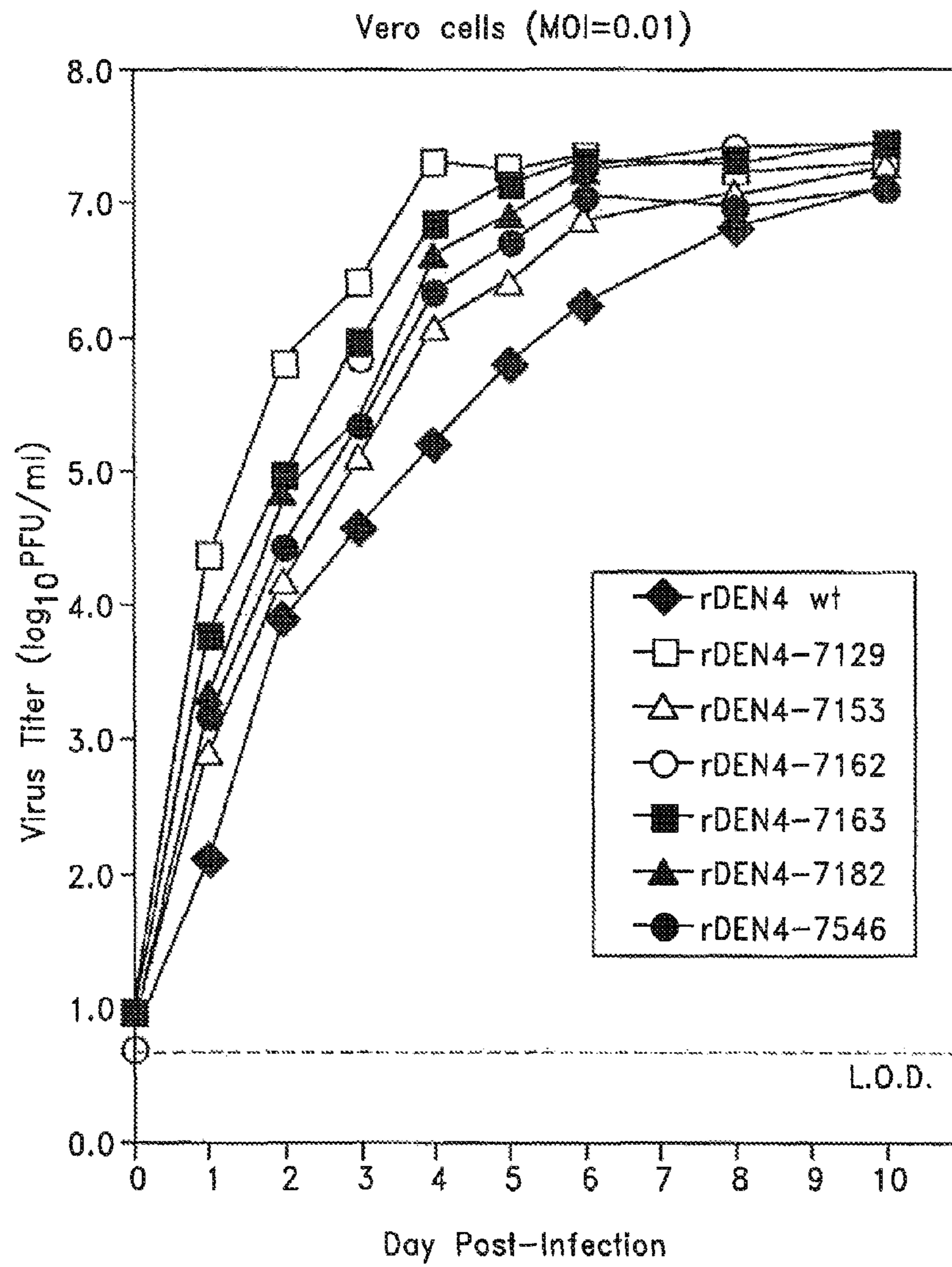


FIG. 11

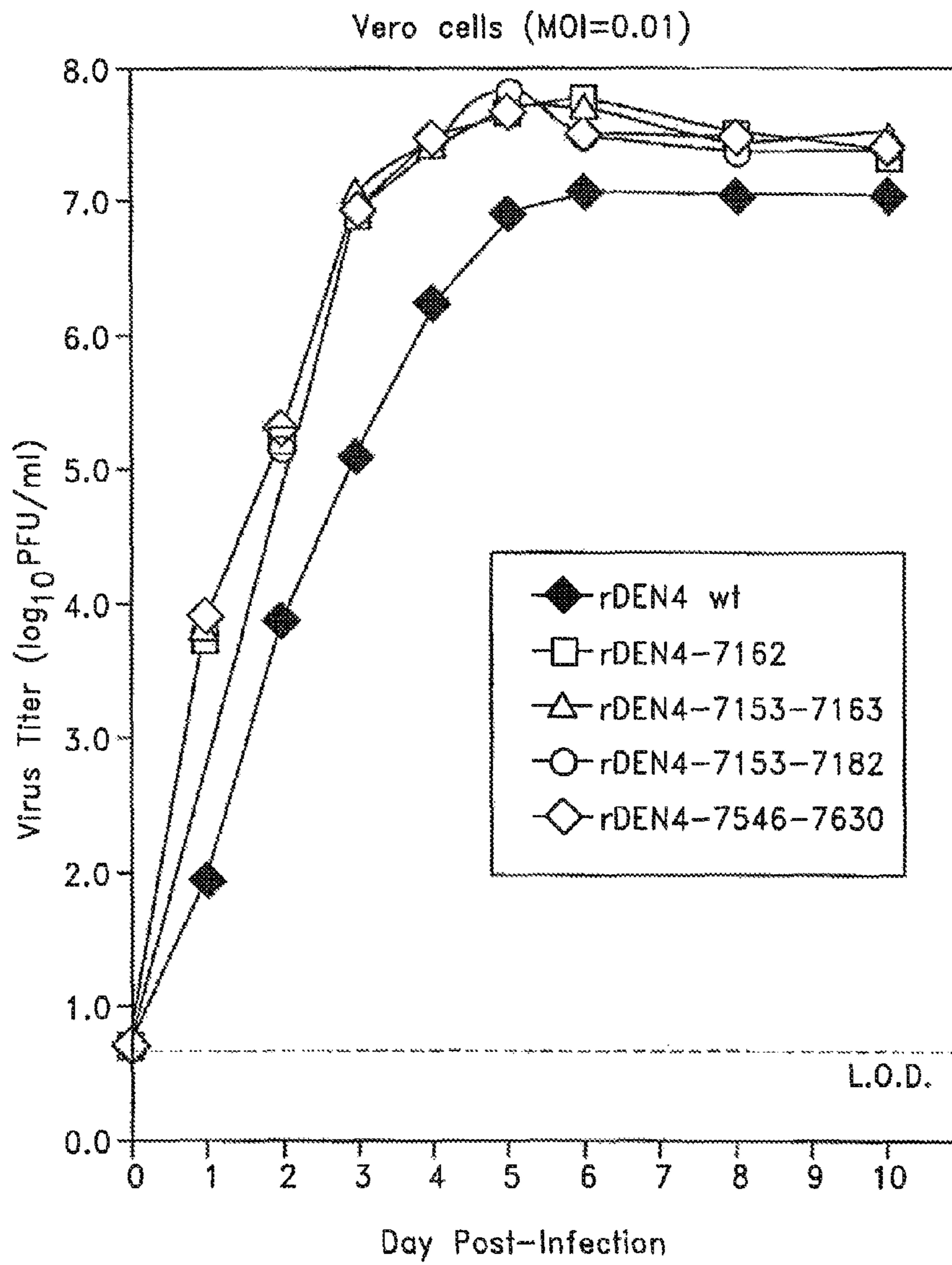


FIG. 12

**RECOMBINANT ATTENUATED DENGUE
VIRUSES COMPRISING A DELETION IN THE
3' UNTRANSLATED REGION AND
ADDITIONAL ATTENUATING MUTATIONS
INDUCED BY CHEMICAL MUTAGENESIS**

Matter enclosed in heavy brackets [] appears in the original patent but forms no part of this reissue specification; matter printed in italics indicates the additions made by reissue.

RELATED APPLICATIONS

This application is a continuation of U.S. application Ser. No. 11/446,050, filed Jun. 2, 2006, now U.S. Pat. No. 7,560,118, which is a divisional of U.S. application Ser. No. 10/719,547, filed Nov. 21, 2003, now U.S. Pat. No. 7,226,602, which is a continuation and claims the benefit of priority of International Application No. PCT/US02/16308 filed May 22, 2002, designating the United States of America and published in English as WO 02/095075 on Nov. 28, 2002, which claims the benefit of priority of U.S. Provisional Application No. 60/293,049, filed May 22, 2001, all of which are hereby expressly incorporated by reference in their entirety.

SEQUENCE LISTING

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled NIH214-1CDV1C1_Sequence Listing.TXT, created Feb. 20, 2009, which is 249 Kb in size. The information in the electronic format of the Sequence Listing is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

A menu of mutations was developed that is useful in fine-tuning the attenuation and growth characteristics of dengue virus vaccines.

BACKGROUND OF THE INVENTION

Dengue virus is a positive-sense RNA virus belonging to the Flavivirus genus of the family Flaviviridae. Dengue virus is widely distributed throughout the tropical and semitropical regions of the world and is transmitted to humans by mosquito vectors. Dengue virus is a leading cause of hospitalization and death in children in at least eight tropical Asian countries (WHO, 1997. *Dengue haemorrhagic fever: diagnosis, treatment prevention and control*—2nd ed. Geneva: WHO). There are four serotypes of dengue virus (DEN-1, DEN-2, DEN-3, and DEN-4) which annually cause an estimated 50-100 million cases of dengue fever and 500,000 cases of the more severe form of dengue virus infection, dengue hemorrhagic fever/dengue shock syndrome (DHF/DSS) (Gubler, D. J. & Meltzer, M. 1999 *Adv Virus Res* 53:35-70). DHF/DSS is seen predominately in children and adults experiencing a second dengue virus infection with a serotype different than that of their first dengue virus infection and in primary infection of infants who still have circulating dengue-specific maternal antibody (Burke, D. S. et al. 1988 *Am J Trop Med Hyg* 38:172-80; Halstead, S. B. et al. 1969 *Am J Trop Med Hyg* 18:997-1021; Thein S. et al. 1997 *Am J Trop Med Hyg* 56:566-72). A vaccine is needed to lessen the disease burden caused by dengue virus, but none is licensed. Because of the association of more severe disease

with secondary dengue virus infection, a successful vaccine must induce immunity to all four serotypes. Immunity is primarily mediated by neutralizing antibody directed against the envelope E glycoprotein, a virion structural protein. Infection with one serotype induces long-lived homotypic immunity and a short-lived heterotypic immunity (Sabin, A. 1955 *Amer J Trop Med Hyg* 4:198-207). Therefore, the goal of immunization is to induce a long-lived neutralizing antibody response against DEN-1, DEN-2, DEN-3, and DEN-4, which can best be achieved economically using live attenuated virus vaccines. This is a reasonable goal since a live attenuated vaccine has already been developed for the related yellow fever virus, another mosquito-borne flavivirus present in tropical and semitropical regions of the world (Monath, T. P. & Heinz, F. X. 1996 in: Fields B. N. et al. eds. *Fields Virology* Philadelphia: Lippincott-Ravan Publishers, 961-1034).

Several live attenuated dengue vaccine candidates have been developed and evaluated in humans or non-human primates. The first live attenuated dengue vaccine candidates were host range mutants developed by serial passage of wild type dengue viruses in the brains of mice and selection of mutants attenuated for humans (Kimura, R. & Hotta, S. 1944 *Japanese J Bacteriology* 1:96-99; Sabin, A. B. & Schlesinger, R. W. 1945 *Science* 101:640; Wisseman, C. L. Jr. et al. 1963 *Am J Trop Med* 12:620-623). Although these candidate vaccine viruses were immunogenic in humans, their poor growth in cell culture discouraged further development. Additional live attenuated DEN-1, DEN-2, DEN-3, and DEN-4 vaccine candidates have been developed by serial passage in tissue culture (Angsubhakorn, S. et al. 1994 *Southeast Asian J Trop Med Public Health* 25:554-9; Bancroft, W. H. et al. 1981 *Infect Immun* 31:698-703; Bhamarapavati, N. et al. 1987 *Bull World Health Organ* 65:189-95; Eckels, K. H. et al. 1984 *Am J Trop Med Hyg* 33:684-9; Hoke, C. H. Jr. et al. 1990 *Am J Trop Med Hyg* 43:219-26; Kanesa-thasan, N. et al. 2001 *Vaccine* 19:3179-88) or by chemical mutagenesis (McKee, K. T. Jr. et al. 1987 *Am J Trop Med Hyg* 36:435-42). It has proven very difficult to achieve a satisfactory balance between attenuation and immunogenicity for each of the four serotypes of dengue virus using these approaches and to formulate a tetravalent vaccine that is safe and satisfactorily immunogenic against each of the four dengue viruses (Kanesa-thasan, N. et al. 2001 *Vaccine* 19:3179-88; Bhamarapavati, N. & Sutee, Y. 2000 *Vaccine* 18 Suppl 2: 44-7).

Two major advances utilizing recombinant DNA technology have recently made it possible to develop additional promising live attenuated dengue virus vaccine candidates. First, methods have been developed to recover infectious dengue virus from cells transfected with RNA transcripts derived from a full-length cDNA clone of the dengue virus genome, thus making it possible to derive infectious viruses bearing attenuating mutations which have been introduced into the cDNA clone by site-directed mutagenesis (Lai, C. J. et al. 1991 *PNAS USA* 88:5139-43). Second, it is possible to produce antigenic chimeric viruses in which the structural protein coding region of the full-length cDNA clone of dengue virus is replaced by that of a different dengue virus serotype or from a more divergent flavivirus (Bray, M. & Lai, C. J. 1991 *PNAS USA* 88: 10342-6; Chen, W. et al. 1995 *J Virol* 69:5186-90; Huang, C. Y et al. 2000 *J Virol* 74:3020-8; Pletnev, A. G. & Men, R. 1998 *PNAS USA* 95:1746-51). These techniques have been used to construct intertypic chimeric dengue viruses which have been shown to be effective in protecting monkeys against homologous dengue virus challenge (Bray, M. et al. 1996 *J Virol* 70:4162-6). Despite these advances, there is a need to develop attenuated antigenic

dengue virus vaccines that specify a satisfactory balance between attenuation and immunogenicity for humans.

SUMMARY OF THE INVENTION

The invention provides mutations that confer temperature sensitivity in Vero cells or human liver cells, host-cell restriction in mosquito or human liver cells, host-cell adaptation for improved replication in Vero cells, or attenuation in mice, which mutations are useful in fine tuning the attenuation and growth characteristics of dengue virus vaccines.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows growth of wt DEN4 2A and vaccine candidate, 2AΔ30, in Vero and HuH-7 cells. Vero (A) or HuH-7 (B) cells were infected with DEN4 2A or 2AΔ30 at a multiplicity of infection (MOI) of 10 or 0.01. Confluent cell monolayers in 25-mm tissue culture flasks were washed and overlaid with a 1.5 ml inoculum containing the indicated virus. After a two hour incubation at 37° C., cells were washed three times in PBS and 7 ml of culture media supplemented with 2% FBS was added. A 1 ml aliquot of tissue culture medium was removed, replaced with fresh medium, and designated the 0 hour time-point. At the indicated time points post-infection, samples of tissue culture media were removed and frozen at -70° C. The level of viral replication was assayed by plaque titration in Vero cells. Briefly, serial ten-fold dilutions of cell culture media samples were inoculated onto confluent Vero cell monolayers in 24-well plates in duplicate and overlaid with Opti-MEM containing 0.8% methylcellulose. After five days, plaques were visualized by immunoperoxidase staining as described in Example 1.

FIG. 2 shows generation of temperature-sensitive (ts) DEN4 viruses by 5-fluorouracil (5-FU) chemical mutagenesis. The wild-type DEN4 2A virus was derived from a cDNA clone of DEN4 strain 814669 (Dominica, 1981). Vero cells were infected with DEN4 2A and overlaid with culture media containing 1 mM 5-fluorouracil (5-FU) which resulted in a reduction of approximately 100-fold in viral replication when compared to untreated controls. Viral progeny from the 1 mM 5-FU-treated cultures were subjected to a single round of terminal dilutions generating 1,248 biologically cloned viruses which were screened for ts phenotypes by assessing virus replication at 35° C. and 39° C. in Vero and HuH-7 cells. Virus clones which demonstrated a 100-fold or greater reduction in titer at 39° C. were terminally diluted an additional two times and amplified in Vero cells. Temperature-sensitive phenotypes of the 3× biologically cloned viruses were confirmed by evaluating efficiency of plaque formation (EOP) in the indicated cells as described in Example 1.

FIG. 3 shows plaque size phenotypes of representative 5-FU mutant DEN4 viruses. Serial ten-fold dilutions of wild-type DEN4 2A-13 (A), 5-FU mutant viruses #569 and #1189 (B), and 5-FU mutant viruses #1083 and #311 (C) were inoculated onto confluent Vero and HuH-7 cell monolayers in 24-well plates. After incubation at 35° C. for two hours, monolayers were overlaid with 0.8% methylcellulose culture media. Following incubation at 35° C. for five days, plaques were visualized by immunoperoxidase staining. Viruses which had a plaque size that was ≤1 mm (approximately ≤50% the size of wt DEN4 2A-13) at the permissive temperature of 35° C. were designated as having the small-plaque (sp) phenotype. Mutant viruses #569 and #1189 (B) were sp in both Vero and HuH-7 cells, and #311 and #1083 (C) were sp in only HuH-7 cells.

FIG. 4 shows generation of recombinant DEN4 viruses. (A), The p4 cDNA clone is represented which was constructed from the 2A cDNA clone (derived from DEN4 814669) by site-directed mutagenesis. Restriction enzyme sites were introduced or removed to facilitate subsequent cloning of DEN4 recombinants bearing introduced attenuating mutations. Restriction enzyme sites are shown and define fragments of the genome that were sub-cloned into modified pUC-119 vectors for site-directed mutagenesis to introduce mutations identified in the 5-FU mutant viruses. (B), An outline of the methods used to generate rDEN4 viruses is also represented and described in Example 1.

FIG. 5 shows amino acid sequence of the rDEN4 NS5 gene (SEQ ID NO: 1). Eighty underlined amino acid pairs were mutagenized to alanine pairs; 32 pairs in boldface represent mutant viruses that could be recovered in either Vero or C6/36 cells; pairs in normal type represent mutant viruses that could not be recovered in either Vero or C6/36 cells. Boxed regions indicate putative functional domains, including an S-adenosylmethionine utilizing methyltransferase domain (SAM), an importin-β binding domain adjacent to a nuclear localization sequence (importin-β-binding+NLS) and an RNA-dependent RNA polymerase domain (Polymerase).

FIG. 6 shows plaque size of mutant 5-1A1 in C6/36 cells. Note that 5-1A1 has a small plaque phenotype in C6/36 cells relative to that of the wild type virus.

FIG. 7 shows growth of wild type rDEN4 and 5-1A1 in C6/36 cells. Cells were inoculated in triplicate with each virus at an MOI of 0.01, and the amount of virus present in the supernatants that were harvested on the indicated days was determined by plaque enumeration in Vero cells. The titers are expressed as \log_{10} PFU/ml ± standard error.

FIG. 8 shows nucleotide alignment of the 3' UTR of mosquito-borne and tick-borne flaviviruses. cDNA sequences are shown 5' to 3' and represent a portion of the UTR corresponding to DEN4 nucleotides 10417 to 10649 (3' genome end). Nucleotide numbering represents the position in the alignment. Regions deleted or swapped are indicated using the nucleotide numbering of DEN4. GenBank accession numbers for mosquito-borne viruses: DEN4 (SEQ ID NO: 2): AF326825, DEN1 (SEQ ID NO: 3): U88535, DEN2 (SEQ ID NO: 4): AF038403, DEN3 (SEQ ID NO: 5): M93130, West Nile virus (WN) (SEQ ID NO: 6): M12294, Japanese encephalitis virus (JE) (SEQ ID NO: 7): AF315119, Yellow fever virus (YF) (SEQ ID NO: 8): U17067; GenBank accession numbers for tick-borne viruses: Powassan virus (POW) (SEQ ID NO: 9): L06436, Louping Ill virus (LI) (SEQ ID NO: 10): Y07863, Tick-borne encephalitis virus (TBE) (SEQ ID NO: 11): U27495, and Langat virus (LGT) (SEQ ID NO: 12): AF253419.

FIG. 9 shows genetic map of plasmid p4. Dengue cDNA is shown as bold line, with the C-prM-E region exchanged during construction of chimeric dengue virus cDNAs indicated.

FIG. 10 shows plaque size phenotypes of rDEN4 viruses encoding Vero adaptation mutations. Serial three-fold dilutions of the indicated viruses were inoculated onto confluent Vero and C6/36 cell monolayers in 6-well plates. After incubation at 37° C. (Vero) or 32° C. (C6/36) for two hours, monolayers were overlaid with 0.8% methylcellulose culture media. Following incubation for five days, plaques were visualized by immunoperoxidase staining. Values below each well are the average plaque size in mm ± standard error. For each of the virus-infected wells, 36 plaques were measured on the digital image of the 6-well plate on Adobe Photoshop at 300% view.

FIG. 11 shows growth curve in Vero cells of rDEN4 viruses encoding single Vero adaptation mutations. Vero cells were infected with the indicated viruses at an MOI of 0.01. Confluent cell monolayers in 25-cm² tissue culture flasks were washed and overlaid with a 1.5 ml inoculum containing the indicated virus. After a two hour incubation at 37° C., cells were washed three times in PBS and 5 ml of culture medium supplemented with 2% FBS was added. A 1 ml aliquot of tissue culture medium was removed, replaced with fresh medium, and designated the 0 hour time-point. At the indicated time points post-infection, samples of tissue culture medium were removed, clarified, and frozen at -70° C. The level of virus replication was assayed by plaque titration in Vero cells. Briefly, serial ten-fold dilutions of cell culture media samples were inoculated onto confluent Vero cell monolayers in 24-well plates in duplicate and overlaid with Opti-MEM containing 0.8% methylcellulose. After five days, plaques were visualized by immunoperoxidase staining as described in Example 1. Limit of detection (L.O.D.) is $\geq 0.7 \log_{10}$ PFU/ml.

FIG. 12 shows growth curve in Vero cells of rDEN4 viruses encoding combined Vero cell adaptation mutations. Vero cells were infected with the indicated viruses at an MOI of 0.01. Confluent cell monolayers in 25-cm² tissue culture flasks were washed and overlaid with a 1.5 ml inoculum containing the indicated virus. After a two hour incubation at 37° C., cells were washed three times in PBS and 5 ml of culture medium supplemented with 2% FBS was added. A 1 ml aliquot of tissue culture medium was removed, replaced with fresh medium, and designated the 0 hour time-point. At the indicated time points post-infection, samples of tissue culture medium were removed, clarified, and frozen at -70° C. The level of virus replication was assayed by plaque titration in Vero cells. Limit of detection (L.O.D.) is $\geq 0.7 \log_{10}$ PFU/ml.

BRIEF DESCRIPTION OF THE TABLES

Table 1. Susceptibility of mice to intracerebral DEN4 infection is age-dependent.

Table 2. Temperature-sensitive (ts) and mouse brain attenuation (att) phenotypes of 5-FU mutant DEN4 viruses.

Table 3. Nucleotide and amino acid differences of the 5-FU mutant viruses which are ts in both Vero and HuH-7 cells.

Table 4. Nucleotide and amino acid differences of the 5-FU mutant viruses which are ts in only HuH-7 cells.

Table 5. Mutations which are represented in multiple 5-FU mutant DEN4 viruses.

Table 6. Addition of ts mutation 4995 to rDEN4 Δ 30 confers a ts phenotype and further attenuates its replication in suckling mouse brain.

Table 7. Temperature-sensitive (ts) and mouse brain attenuation (att) phenotypes of 5-FU DEN4 mutant viruses which exhibit a small plaque (sp) phenotype.

Table 8. Viruses with both ts and sp phenotypes are more restricted in replication in mouse brain than those with only a ts phenotype.

Table 9. Nucleotide and amino acid differences of the 5-FU mutant DEN4 viruses which produce small plaques in both Vero and HuH-7 cells.

Table 10. Nucleotide and amino acid differences of the 5-FU mutant DEN4 viruses which produce small plaques in only HuH-7 cells.

Table 11. Putative Vero cell adaptation mutations derived from the full set of 5-FU mutant viruses.

Table 12. Mutagenic oligonucleotides used to generate recombinant DEN4 viruses containing single 5-FU mutations.

Table 13. sp, ts and mouse attenuation phenotypes of rDEN4 mutant viruses encoding single mutations identified in six sp 5-FU mutant viruses.

Table 14. Phenotypes of rDEN4 mutant viruses encoding single mutations identified in 10 5-FU mutant viruses that are ts in both Vero and HuH-7 cells.

Table 15. sp, ts and mouse attenuation phenotypes of rDEN4 mutant viruses encoding single mutations identified in 3 HuH-7 cell-specific ts 5-FU mutant viruses.

Table 16. Temperature-sensitive (ts) and mouse brain attenuation (att) phenotypes of additional rDEN4 viruses encoding single 5-FU mutations.

Table 17. Growth of wt DEN-4 2A-13 in SCID mice transplanted with HuH-7 cells.

Table 18. Combination of ts mutations, NS3 4995 and NS5 7849, in rDEN4 results in an additive ts phenotype.

Table 19. The 5-FU mutations are compatible with the Δ 30 mutation for replication in the brain of suckling mice.

Table 20. Temperature-sensitive and mouse brain attenuation phenotypes of viruses bearing charge-cluster-to-alanine mutations in the NS5 gene of DEN4.

Table 21. SCID-HuH-7 attenuation phenotypes of viruses bearing charge-cluster-to-alanine mutations in the NS5 gene of DEN4.

Table 22. Combination of paired charge-cluster-to-alanine mutations into double-pair mutant viruses.

Table 23. Temperature-sensitive and mouse brain attenuation phenotypes of double charge-cluster-to-alanine mutants of the NS5 gene of rDEN4.

Table 24. SCID-HuH-7 attenuation phenotypes of double charge-cluster-to-alanine mutants of the NS5 gene of rDEN4.

Table 25. Phenotypes (temperature sensitivity, plaque size and replication in mouse brain and SCID-HuH-7 mice) of wt DEN4 and viruses containing the Δ 30 and 7129 mutations.

Table 26. The 5-fluorouracil 5-1A1 small plaque mutant demonstrates a restriction of midgut infection following oral infection of *Aedes aegypti* mosquitoes.

Table 27. The 5-fluorouracil 5-1A1 small plaque mutant demonstrates a restriction of infection following intrathoracic inoculation of *Toxorhynchites splendens* mosquitoes.

Table 28. Mutagenesis primers for the deletion or swap of sequences in DEN4 showing conserved differences from tick-borne flaviviruses.

Table 29. Virus titer and plaque size of 3' UTR mutant viruses in Vero and C6/36 cells.

Table 30. Infectivity of wt DEN4 and 3' UTR mutants for *Toxorhynchites splendens* via intrathoracic inoculation.

Table 31. Infectivity of 3' UTR swap mutant viruses for *Aedes aegypti* fed on an infectious bloodmeal.

Table 32. Putative Vero cell adaptation mutations derived from the set of 5-FU mutant viruses and other DEN4 viruses passaged in Vero cells.

Table 33. Sequence analysis of rDEN2/4 Δ 30 clone 27(p4)-2-2A2.

Table 34. Sequence analysis of rDEN2/4 Δ 30 clone 27(p3)-2-1A1.

Table 35. Recombinant virus rDEN2/4 Δ 30 bearing Vero adaptation mutations can be recovered and titered on Vero cells.

Table 36. Putative Vero cell adaptation mutations of dengue type 4 virus and the corresponding wildtype amino acid residue in other dengue viruses.

Table 37. Mutations known to attenuate dengue type 4 virus and the corresponding wildtype amino acid residue in other dengue virus.

BRIEF DESCRIPTION OF THE APPENDICES

Appendix 1. Sequence of recombinant dengue type 4 virus strain 2A (amino acid sequence SEQ ID NO: 13 and nucleotide sequence SEQ ID NO: 14).

Appendix 2. Sequence of recombinant dengue type 4 virus strain rDEN4 (amino acid sequence SEQ ID NO: 15 and nucleotide sequence SEQ ID NO: 16).

Appendix 3. Sequence of recombinant dengue type 2 chimeric virus strain rDEN2/4Δ30 (amino acid sequence SEQ ID NO: 17 and nucleotide sequence SEQ ID NO: 18).

Appendix 4. Alignment of dengue virus polyproteins. DEN4 (SEQ ID NO: 19); DEN1-WP (SEQ ID NO: 20); DEN2-NGC (SEQ ID NO: 21); DEN3-H87 (SEQ ID NO: 22).

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

To assemble a collection of useful mutations for incorporation in recombinant live dengue virus vaccines, site-directed and random mutagenesis techniques were used to introduce mutations into the dengue virus genome. The resulting mutant viruses were screened for several valuable phenotypes, including temperature sensitivity in Vero cells or human liver cells, host cell restriction in mosquito cells or human liver cells, host-cell adaptation for improved replication in Vero cells, and attenuation in mice. The genetic basis for each observed phenotype was determined by direct sequence analysis of the virus genome. Mutations identified through these sequencing efforts have been further evaluated by their re-introduction, singly, or in combination, into recombinant dengue virus and characterization of the resulting phenotypes. In this manner, a menu of mutations was developed that is useful in fine-tuning the attenuation and growth characteristics of dengue virus vaccines.

Example 1

Chemical Mutagenesis of Dengue Virus Type 4 Yields Temperature-Sensitive and Attenuated Mutant Viruses

A recombinant live attenuated dengue virus type 4 (DEN4) vaccine candidate, 2AΔ30, was found previously to be generally well-tolerated in humans, but a rash and an elevation of liver enzymes in the serum occurred in some vaccines. 2AΔ30, a non-temperature-sensitive (ts) virus, contains a 30 nucleotide deletion in the 3' untranslated region (UTR) of the viral genome. In the present study, chemical mutagenesis of DEN4 has been utilized to generate attenuating mutations which may be useful to further attenuate the incompletely attenuated 2AΔ30 candidate vaccine. Wild-type DEN4 2A virus was grown in Vero cells in the presence of 5-fluorouracil, and, from a panel of 1,248 clones that were isolated in Vero cells, twenty ts mutant viruses were identified which were ts in both Vero and HuH-7 cells (n=13) or in HuH-7 cells only (n=7). Each of the twenty ts mutations possessed an attenuation (att) phenotype as indicated by restricted replication in the brains of seven day old mice. The complete nucleotide sequence of the 20 ts mutant viruses identified nucleotide substitutions in structural and non-structural genes as well as in the 5' and 3' UTR with more than one change occurring, in general, per mutant virus. A ts mutation in the NS3 protein (nucleotide position 4,995) was introduced into a recombinant DEN4 virus possessing the Δ30 deletion creating the rDEN4Δ30-4995 recombinant virus which was

found to be ts and to be more attenuated than rDEN4Δ30 in the brains of mice. A menu of attenuating mutations is being assembled that should be useful in generating satisfactorily attenuated recombinant dengue vaccine viruses and in increasing our understanding of the pathogenesis of dengue virus.

The mosquito-borne dengue (DEN) viruses (serotypes 1 to 4) are members of the Flavivirus genus and contain a single-stranded positive-sense RNA genome of approximately 10,600 nucleotides (nt) (Monath, T. P. & Heinz, F. X. 1996 in: *Fields Virology* B. N. Fields, et al. Eds. pp. 961-1034 Lippincott-Raven Publishers, Philadelphia). The genome organization of DEN viruses is 5'-UTR-C-prM-E-NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5-UTR-3' (UTR—untranslated region, C—capsid, PrM—pre-membrane, E—envelope, NS—non-structural) (Chang, G.-J. 1997 in: *Dengue and dengue hemorrhagic fever* D. J. Gubler & G. Kuno, eds. pp. 175-198 CAB International, New York; Rice, C. M. 1996 in: *Fields Virology* B. N. Fields et al. Eds. pp. 931-959 Lippincott-Raven Publishers, Philadelphia). A single viral polypeptide is co-translationally processed by viral and cellular proteases generating three structural proteins (C, M, and E) and seven NS proteins. The disease burden associated with DEN virus infection has increased over the past several decades in tropical and semitropical countries. Annually, there are an estimated 50-100 million cases of dengue fever (DF) and 500,000 cases of the more severe and potentially lethal dengue hemorrhagic fever/dengue shock syndrome (DHF/DSS) (Gubler, D. J. & Meltzer, M. 1999 *Adv Virus Res* 53:35-70).

The site of viral replication in DEN virus-infected humans and the pathogenesis of DF and DHF/DSS are still incompletely understood (Innis, B. L. 1995 in: *Exotic viral infections* J. S. Porterfield, ed. pp. 103-146 Chapman and Hall, London). In humans, DEN virus infects lymphocytes (Kurane, I. et al. 1990 *Arch Virol* 110:91-101; Theofilopoulos, A. N. et al. 1976 *J Immunol* 117:953-61), macrophages (Halstead, S. B. et al. 1977 *J Exp Med* 146:218-29; Scott, R. M. et al. 1980 *J Infect Dis* 141:1-6), dendritic cells (Libraty, D. H. et al. 2001 *J Virol* 75:3501-8; Wu, S. J. et al. 2000 *Nat Med* 6:816-20), and hepatocytes (Lin, Y. L. et al. 2000 *J Med Virol* 60:425-31; Marianneau, P. et al. 1996 *J Gen Virol* 77:2547-54). The liver is clearly involved in DEN virus infection of humans, as indicated by the occurrence of transient elevations in serum alanine aminotransferase (ALT) and aspartate aminotransferase (AST) levels in the majority of dengue virus-infected patients and by the presence of hepatomegaly in some patients (Kalayanaraj, S. et al. 1997 *J Infect Dis* 176: 313-21; Kuo, C. H. et al. 1992 *Am J Trop Med Hyg* 47:265-70; Mohan, B. et al. 2000 *Trop Pediatr* 46:40-3; Wahid, S. F. et al. 2000 *Southeast Asian J Trop Med Public Health* 31:259-63). DEN virus antigen-positive hepatocytes are seen surrounding areas of necrosis in the liver of fatal cases (Couvelard, A. et al. 1999 *Hum Pathol* 30:1106-10; Huerre, M. R. et al. 2001 *Virchows Arch* 438:107-15), and dengue virus sequences were identified in such cases using RT-PCR (Rosen, L. et al. 1999 *Am J Trop Med Hyg* 61:720-4). Of potential importance to the etiology of severe dengue virus infection, three studies have demonstrated that the mean levels of serum ALT/AST were significantly increased in patients with DHF/DSS versus those with DF (Kalayanaraj, S. et al. 1997 *J Infect Dis* 176:313-21; Mohan, B. et al. 2000 *J Trop Pediatr* 46:40-3; Wahid, S. F. et al. 2000 *Southeast Asian J Trop Med Public Health* 31:259-63).

A vaccine for DEN viruses is not presently licensed. Since previous infection with one dengue virus serotype can increase the risk for DHF/DSS following infection with a different serotype (Burke, D. S. et al. 1988 *Am J Trop Med*

Hyg 38:172-80; Halstead, S. B. et al. 1969 *Am J Trop Med Hyg* 18:997-1021; Thein, S. et al. 1997 *Am J Trop Med Hyg* 56:566-72), it is clear that a dengue virus vaccine will need to protect against each of the four dengue virus serotypes, namely DEN1, DEN2, DEN3, and DEN4. Several strategies are currently being actively pursued in the development of a live attenuated tetravalent DEN virus vaccine (Bancroft, W. H. et al. 1984 *J Infect Dis* 149:1005-10; Bhamarapravati, N. & Sutee, Y. 2000 *Vaccine* 18:44-7; Guirakhoo, F. et al. 2000 *J Virol* 74:5477-85; Huang, C. Y. et al. 2000 *J Virol* 74:3020-8). Recently, we demonstrated that a live attenuated DEN4 vaccine candidate, 2AΔ30, was attenuated and immunogenic in a group of 20 human volunteers (see Example 8). This recombinant DEN4 virus contains a 30 nt deletion in the 3' UTR which removes nucleotides 10,478-10,507 and was restricted in replication in rhesus monkeys. Levels of viremia in humans were low or undetectable, and virus recovered from the vaccinees retained the Δ30 mutation. An asymptomatic rash was reported in 50% of patients. The only laboratory abnormality observed was an asymptomatic, transient rise in the serum ALT level in 5 of 20 vaccinees. All vaccinees developed serum-neutralizing antibody against DEN4 virus (mean titer: 1:580). Importantly, 2AΔ30 was not transmitted to mosquitoes fed on vaccinees and has restricted growth properties in mosquitoes (Troyer, J. M. et al. 2001 *Am J Trop Med Hyg* 65:414-9). The presence of a rash and of the elevated ALT levels suggests that the 2AΔ30 vaccine candidate is slightly under-attenuated in humans. Because of the overall set of desirable properties conferred by the Δ30 mutation, chimeric vaccine candidates are being constructed which contain the structural genes of dengue virus type 1, 2, and 3 and the DEN4 attenuated backbone bearing the genetically stable Δ30 mutation.

Although the initial findings indicate the utility of the 2AΔ30 vaccine candidate, many previous attempts to develop live attenuated dengue virus vaccines have yielded vaccine candidates that were either over- or under-attenuated in humans (Eckels, K. H. et al. 1984 *Am J Trop Med Hyg* 33:684-9; Bhamarapravati, N. & Yoksan, S. 1997 in: *Dengue and dengue hemorrhagic fever* D. J. Gubler & G. Kuno eds. pp. 367-377 CAB International, New York; Innis, B. L. et al. 1988 *J Infect Dis* 158:876-80; McKee, K. T., Jr. et al. 1987 *Am J Trop Med Hyg* 36:435-42). Therefore, we developed a menu of point mutations which confer temperature-sensitive (ts) and attenuation (att) phenotypes upon DEN4. These mutations are envisioned as being useful to attenuate DEN4 viruses to different degrees and therefore as having purpose in fine-tuning the level of attenuation of vaccine candidates such as 2AΔ30. Addition of such mutations to 2AΔ30 or to other dengue virus vaccine candidates is envisioned as resulting in the generation of a vaccine candidate that exhibits a satisfactory balance between attenuation and immunogenicity for humans.

In the present example, chemical mutagenesis of DEN4 has been utilized to identify point mutations which confer the ts phenotype, since such viruses often are attenuated in humans. Additionally, because of the reported involvement of the liver in natural dengue infection and the elevated ALT levels in a subset of 2AΔ30 vaccinees, mutagenized DEN4 viruses were also evaluated for ts phenotype in HuH-7 liver cells derived from a human hepatoma. Here, we describe the identification of 20 DEN4 ts mutant viruses each of which replicates efficiently in Vero cells, the proposed substrate for vaccine manufacture, and each of which is attenuated in mice. Finally, the feasibility of modifying the attenuation phenotype of the 2AΔ30 vaccine candidate by introduction of a point mutation in NS3 is demonstrated.

Cells and viruses. WHO Vero cells (African green monkey kidney cells) were maintained in MEM (Life Technologies, Grand Island, N.Y.) supplemented with 10% fetal bovine serum (FBS) (Summit Biotechnologies, Fort Collins, Colo.), 2 mM L-glutamine (Life Technologies), and 0.05 mg/ml gentamicin (Life Technologies). HuH-7 cells (human hepatoma cells) (Nakabayashi, H. et al. 1982 *Cancer Res* 42:3858-63) were maintained in D-MEM/F-12 (Life Technologies) supplemented with 10% FBS, 1 mM L-glutamine and 0.05 mg/ml gentamicin. C6/36 cells (*Aedes albopictus* mosquito cells) were maintained in complete MEM as described above supplemented with 2 mM non-essential amino acids (Life Technologies).

The wild type (wt) DEN4 2A virus was derived from a cDNA clone of DEN4 strain 814669 (Dominica, 1981) (Men, R. et al. 1996 *J Virol* 70:3930-7). Sequence of the cDNA of DEN 4 2A virus is presented in Appendix 1. The full-length 2A cDNA clone has undergone several subsequent modifications to improve its ability to be genetically manipulated. As previously described, a translationally-silent XhoI restriction enzyme site was engineered near the end of the E region at nucleotide 2348 to create clone 2A-XhoI (Bray, M. & Lai, C. J. 1991 *PNAS USA* 88:10342-6). The viral coding sequence of the 2A-XhoI cDNA clone was further modified using site-directed mutagenesis to create clone p4: a unique BbvCI restriction site was introduced near the C-prM junction (nucleotides 447-452); an extra XbaI restriction site was ablated by mutation of nucleotide 7730; and a unique SacII restriction site was created in the NS5 region (nucleotides 9318-9320). Each of these engineered mutations is translationally silent and does not change the amino acid sequence of the viral polypeptide. Also, several mutations were made in the vector region of clone p4 to introduce or ablate additional restriction sites. The cDNA clone p4Δ30 was generated by introducing the Δ30 mutation into clone p4. This was accomplished by replacing the MluI-KpnI fragment of p4 (nucleotides 10403-10654) with that derived from plasmid 2AΔ30 containing the 30 nucleotide deletion. The cDNA clones p4 and p4Δ30 were subsequently used to generate recombinant viruses rDEN4 (Appendix 2) and rDEN4Δ30, respectively. (The GenBank accession number for rDEN4 is AF326825 and the accession for rDEN4Δ30 is AF326827).

Chemical mutagenesis of DEN4. Confluent monolayers of Vero cells were infected with wt DEN4 2A at a multiplicity of infection (MOI) of 0.01 and incubated for 2 hours at 32° C. Infected cells were then overlaid with MEM supplemented with 2% FBS and 5-fluorouracil (5-FU) (Sigma, St. Louis, Mo.) at concentrations ranging from 10 mM to 10 nM. After incubation at 32° C. for five days, cell culture medium was harvested, clarified by centrifugation, and frozen at -70° C. Clarified supernatants were then assayed for virus titer by plaque titration in Vero cells. Serial ten-fold dilutions of the clarified supernatant were prepared in Opti-MEM I (Life Technologies) and inoculated onto confluent Vero cell monolayers in 24-well plates. After incubation at 35° C. for two hours, monolayers were overlaid with 0.8% methylcellulose (EM Science, Gibbstown, N.J.) in Opti-MEM I supplemented with 2% FBS, gentamicin, and L-glutamine. Following incubation at 35° C. for five days, plaques were visualized by immunoperoxidase staining. Vero cell monolayers were fixed in 80% methanol for 30 minutes and washed for 10 minutes with antibody buffer which consists of 3.5% (w/v) nonfat dry milk (Nestle, Solon, Ohio) in phosphate buffered saline (PBS). Cells were then incubated for one hour at 37° C. with an anti-DEN4 rabbit polyclonal antibody preparation (PRNT₅₀ of >1:2000) diluted 1:1,000 in antibody buffer. After one wash with antibody buffer, cells were incubated for

one hour with peroxidase-labeled goat-anti-rabbit IgG (KPL, Gaithersburg, Md.) diluted 1:500 in antibody buffer. Monolayers were washed with PBS, allowed to dry briefly, overlaid with peroxidase substrate (KPL), and plaques were counted.

Virus yields in cultures treated with 1 mM 5-FU were reduced 100-fold compared to untreated cultures, and the virus present in the supernatant from the 1 mM 5-FU-treated culture was terminally diluted to derive clones for phenotypic characterization. Briefly, 96 well plates of Vero cells were inoculated with the 5-FU-treated virus at an MOI that yielded 10 or fewer virus-positive wells per plate. After a five-day incubation at 35° C., cell culture media from the 96 well plates were temporarily transferred to 96 well plates lacking cells, and the positive cultures were identified by immunoperoxidase staining of the infected-cell monolayers. Virus from each positive well was transferred to confluent Vero cell monolayers in 12 well plates for amplification. Cell culture medium was harvested from individual wells five or six days later, clarified by centrifugation, aliquoted to 96 deep-well polypropylene plates (Beckman, Fullerton, Calif.) and frozen at -70° C. A total of 1,248 virus clones were prepared from the 1 mM 5-FU-treated cultures. Two wt virus clones, 2A-1 and 2A-13, were generated in the same manner from the 5-FU untreated control cultures.

Screening of clones for ts and att phenotypes. The 1,248 virus clones were screened for ts phenotype by assessing virus replication at 35° C. and 39° C. in Vero and HuH-7 cells. Cell monolayers in 96 well plates were inoculated with serial ten-fold dilutions of virus in L-15 media (Quality Biologicals, Gaithersburg, Md.) supplemented with 2% FBS, L-glutamine and gentamicin. Cells were incubated at the indicated temperatures for five days in temperature-controlled water baths, and presence of virus was determined by immunoperoxidase staining as described above. Virus clones which demonstrated a 100-fold or greater reduction in titer at 39° C. were terminally diluted an additional two times and amplified in Vero cells. The efficiency of plaque formation (EOP) at permissive and restrictive temperatures of each triply biologically cloned virus suspension was determined as follows. Plaque titration in Vero and HuH-7 cells was performed as described above except virus-infected monolayers were overlaid with 0.8% methylcellulose in L-15 medium supplemented with 5% FBS, gentamicin, and L-glutamine. After incubation of replicate plates for five days at 35, 37, 38, or 39° C. in temperature-controlled water baths, plaques were visualized by immunoperoxidase staining and counted.

The replication of DEN4 5-FU ts mutant viruses was evaluated in Swiss Webster suckling mice (Taconic Farms, Germantown, N.Y.). Groups of six one-week-old mice were inoculated intracranially with 10⁴ PFU of virus diluted in 30 µl Opti-MEM I. Five days later, mice were sacrificed and brains were removed and individually homogenized in a 10% suspension of phosphate-buffered Hank's balanced salt solution containing 7.5% sucrose, 5 mM sodium glutamate, 0.05 mg/ml ciprofloxacin, 0.06 mg/ml clindamycin, and 0.0025 mg/ml amphotericin B. Clarified supernatants were frozen at -70° C. and subsequently virus titer was determined by titration in Vero cells, and plaques were stained by the immunoperoxidase method described above.

Sequence analysis of viral genomes. The nucleotide sequence of the 5-FU-mutagenized DEN4 viruses was determined. Briefly, genomic viral RNA was isolated from virus clones with the QIAamp viral RNA mini kit (Qiagen, Valencia, Calif.) and reverse transcription was performed using the SuperScript First Strand Synthesis System for RT-PCR (Life Technologies) and random hexamer primers. Advantage cDNA polymerase (Clontech, Palo Alto, Calif.) was used to

generate overlapping PCR fragments of approximately 2,000 nt which were purified by HighPure PCR Product Purification System (Roche Diagnostics, Indianapolis, Ind.). DEN-specific primers were used in BigDye terminator cycle sequencing reactions (Applied Biosystems, Foster City, Calif.) and reactions were analyzed on a 3100 genetic analyzer (Applied Biosystems). Primers were designed to sequence both strands of the PCR product from which consensus sequences were assembled.

The nucleotide sequence of the 5' and 3' regions of the viral genome were determined as above after circularization of the RNA genome. The 5' cap nucleoside of the viral RNA was excised using tobacco acid pyrophosphatase (Epicentre Technologies, Madison, Wis.) and the genome was circularized by RNA ligase (Epicentre Technologies). A RT-PCR fragment was generated which overlapped the ligation junction (5' and 3' ends) and was sequenced as described above.

Generation of recombinant DEN4 viruses. The mutation at nt position 4,995 in NS3 was introduced into the p4 cDNA construct by site-directed mutagenesis (Kunkel, T. A. 1985 PNAS USA 82:488-92). The StuI-BstBI (nt 3,619-5,072) fragment of p4 was sub-cloned into a modified pUC119 vector. The U>C mutation at nt position 4,995 was engineered by site-directed mutagenesis into the p4 fragment, cloned back into the p4 cDNA construct, and the presence of the mutation was confirmed by sequence analysis. The Δ30 mutation was introduced into the 3' UTR of the p4-4995 cDNA clone by replacing the MluI-KpnI fragment with that derived from the p4Δ30 cDNA clone, and the presence of the deletion was confirmed by sequence analysis. Full length RNA transcripts were prepared from the above cDNA clones by in vitro transcription. Briefly, transcription consisted of a 50 µl reaction mixture containing 1 µg linearized plasmid, 60 U SP6 polymerase (New England Biolabs (NEB), Beverly, Mass.), 1×RNA polymerase buffer (40 mM Tris-HCl, pH 7.9, 6 mM MgCl₂, 2 mM spermidine, 10 mM dithiothreitol), 0.5 mM m⁷G(5')ppp(5')G cap analog (NEB), 1 mM each nucleotide triphosphate, 1 U pyrophosphatase (NEB), and 80 U RNase inhibitor (Roche, Indianapolis, Ind.). This reaction mixture was incubated at 40° C. for 90 min and the resulting transcripts were purified using RNeasy mini kit (Qiagen, Valencia, Calif.).

For transfection of C6/36 cells, RNA transcripts were combined with DOTAP liposomal transfection reagent (Roche) in HEPES-buffered saline (pH 7.6) and added to cell monolayers in 6 well plates. After incubation at 32° C. for 12-18 hours, the cell culture media were removed and replaced with MEM supplemented with 5% FBS, L-glutamine, gentamicin and non-essential amino acids. Cell monolayers were incubated for an additional 5 to 7 days and cell culture media were harvested, clarified by centrifugation, and assayed for the presence of virus by plaque titration in Vero cells. Recovered viruses were terminally diluted twice as described above, and virus suspensions for further analysis were prepared in Vero cells.

In vitro (tissue culture) and in vivo replication of wt DEN4 and DEN4Δ30. The level of replication of both wt DEN4 2A and the vaccine candidate, 2AΔ30, was evaluated in Vero (monkey kidney) and HuH-7 (human hepatoma) cells (FIG. 1), the latter of which has recently been found to efficiently support the replication of DEN2 virus (Lin, Y. L. et al. 2000 J Med Virol 60:425-31). The pattern of replication of wt DEN4 2A and 2AΔ30 was similar in both cell lines. Viral titers from cultures infected with 2AΔ30 at an MOI of 0.01 were slightly reduced compared to wt DEN4 2A at 72 hours, but at later time points their level of replication was equivalent. The efficient replication of both DEN4 viruses in each cell line

indicated that these continuous lines of cells would be useful for characterization of the ts phenotype of the 1248 potential mutant viruses.

The level of replication of DEN4 virus administered intracerebrally to Swiss Webster mice was first determined to assess whether mice could be used to efficiently evaluate and quantify the attenuation phenotype of a large set of mutant viruses. Since the susceptibility of mice to DEN infection is age dependent (Cole, G. A. & Wisseman, C. L. Jr. 1969 *Am J Epidemiol* 89:669-80; Cole, G. A. et al. 1973 *J Comp Pathol* 83:243-52), mice aged 7 to 21 days were infected with 2A-13 (a clone of DEN4 wild type virus—see below), rDEN4 or rDEN4Δ30, and after five days the brain of each mouse was removed, and the level of viral replication was quantitated by plaque assay (Table 1). The results indicated that the two wt DEN4 viruses and the rDEN4Δ30 vaccine candidate replicated to high titer ($>6.0 \log_{10}$ PFU/g brain) in 7-day old mice and that the mean viral titers were similar among the three viruses. These results demonstrated the feasibility of using 7-day old mice to screen a large set of mutant viruses, and the high level of replication of wild type and vaccine candidate permits one to quantitate the magnitude of the restriction of replication specified by an attenuating mutation over a 10,000-fold range.

Generation and in vitro characterization of DEN4 5-FU mutant viruses. A panel of 1,248 DEN4 virus clones was generated from a 5-FU-mutagenized suspension of wt DEN4 2A as described above (FIG. 2). Each clone was tested in Vero and HuH-7 cells for the ts phenotype at 39° C., and putative ts mutant viruses were subjected to two additional rounds of biological cloning by terminal dilution, and the ts phenotype of each further cloned virus population was examined in more detail by determining their efficiency of plating (EOP) at permissive temperature (35° C.) and at various restrictive temperatures (Table 2). One virus (clone 2A-13) without a ts mutant viruses, served as the virus to which each of the ts mutant viruses was directly compared for both the ts and att phenotypes.

Thirteen 5-FU mutant viruses were identified which have a ts phenotype in both Vero and HuH-7 cells, and seven mutant viruses were ts only in HuH-7 cells (Table 2). Mutant viruses which were ts in Vero cells but not in HuH-7 cells were not identified. Temperature-sensitivity was defined as a ≥ 2.5 or $\geq 3.5 \log_{10}$ PFU/ml reduction in virus titer in Vero or HuH-7 cells, respectively, at an indicated temperature when compared to the permissive temperature of 35° C. Wild type DEN4 2A was found to have approximately a 0.5 and 1.5 \log_{10} PFU/ml reduction in virus titer in Vero or HuH-7 cells at 39° C., respectively. The Δ30 deletion did not confer a ts phenotype in Vero or HuH-7 cells and exhibited only a slight reduction in virus titer ($2.2 \log_{10}$ PFU/ml) at 39° C. in HuH-7 cells, which was less than 10-fold greater than the reduction of wt DEN4 2A at that temperature. Several 5-FU mutant viruses had a greater than 10,000-fold reduction in virus titer at 39° C. in both Vero and HuH-7 cells. A complete shut-off in viral replication at 39° C. in HuH-7 cells was observed in five virus clones (#571, 605, 631, 967, and 992) which were not ts in Vero cells. Mutations that selectively restrict replication in HuH-7 liver cells may be particularly useful in controlling the replication of dengue virus vaccine candidates in the liver of vaccinees.

Replication of DEN4 5-FU mutant viruses in suckling mice. The level of replication of each of the 20 ts DEN4 mutant viruses in mouse brain was determined (Table 2). The titers obtained were compared to that of the two wt viruses, 2A-13 and rDEN4, which each replicated to a level of greater

than 10^6 PFU/g of brain tissue, and to that of the 2AΔ30 mutant, which conferred only a limited $0.5 \log_{10}$ PFU/g reduction in mean virus titer compared to the wt controls. The observed reduction in the level of rDEN4Δ30 replication was consistent among 11 separate experiments. Interestingly, the rDEN4Δ30 virus, which was attenuated in both rhesus monkeys and humans (Example 8), was only slightly restricted in replication in mouse brain. Varying levels of restriction of replication were observed among the mutant viruses ranging from a 10-fold (#473) to over 6,000-fold (#686) reduction. Mutant viruses with ts phenotypes in both Vero and HuH-7 cells, as well as in HuH-7 cells alone, were found to have significant att phenotypes. Five of 13 5-FU mutant viruses with ts phenotypes in both Vero and HuH-7 cells and five of seven mutant viruses with ts phenotypes in HuH-7 cells alone had greater than a 100-fold reduction in virus replication. There appeared to be no direct correlation between the magnitude of the reduction in replication at restrictive temperature in tissue culture and the level of attenuation in vivo. The similar level of temperature sensitivity and replication of the rDEN4 wt and clone 2A-13 in mouse brain indicated that observed differences in replication between the ts mutant viruses and clone 2A-13 was not simply a function of passage in Vero cells, but reflects the sequence differences between these viruses.

Sequence analysis of DEN4 5-FU mutant viruses. To determine the genetic basis of the observed ts and att phenotypes, the complete nucleotide sequence of each ts mutant and of clone 2A-13 was determined and summarized in Table 3 (ts in Vero and HuH-7 cells) and Table 4 (ts in only HuH-7 cells).

The only type of mutation identified in the 20 mutant viruses sequenced was a nucleotide substitution (no deletions or insertions occurred), and these were present in each of the coding regions except C and NS4A. Three mutant viruses (#239, 489, and 773) contained only a single missense point mutation in NS3 at nt position 4,995 resulting in a Ser to Pro amino acid (a.a.) change at a.a. position 1,632. For #773, this was the sole mutation present (Table 3). The non-coding mutations in coding regions are not considered to be significant. The 17 additional mutant viruses had multiple mutations (two to five) in a coding region or in an UTR which could potentially confer the observed ts or att phenotypes. Five of the 17 mutant viruses with multiple mutations (#473, 718, 759, 816, and 938) also encoded the point mutation at nt position 4,995. The presence of the 4,995 mutation was found in only DEN4 mutant viruses with ts phenotypes in both Vero and HuH-7 cells.

The sequence analysis indicated that 10 mutant viruses which were ts in Vero and HuH-7 cells and three mutant viruses which were ts in only HuH-7 cells contained mutations in only the 5' and 3' UTR and/or in a nonstructural protein. These mutations are especially suitable for inclusion in chimeric dengue virus vaccine candidates in which the structural genes derive from a DEN1, DEN2, or DEN3 serotype and the remaining coding and non-coding regions come from an attenuated DEN4 vector. Mutations identified in 5-FU DEN4 mutant viruses which were ts in only HuH-7 cells (Table 4) may potentially be utilized in vaccine candidates, such as rDEN4Δ30, to selectively control the replication and pathogenesis of DEN4 in the liver. These combined results from the sequence analysis of 5-FU mutant viruses demonstrate the utility of chemical mutagenesis as a means of introducing attenuating mutations into the dengue virus genome.

The presence of a point mutation at nt position 4,995 in eight separate mutant viruses was described above. Five additional point mutations were also represented in multiple viruses including nt changes at position 1,455 in E, 7,162,

7,163 and 7,564 in NS4B, and 10,275 in the 3' UTR (Table 5). The significance of the occurrence of these "sister" mutations in multiple viruses is discussed in Example 6. Interestingly, the wild-type, parallel-passaged virus, 2A-13, also contained a single mutation at the 7,163 nt position in NS4B.

Introduction of a ts mutation into rDEN4 and rDEN4Δ30. The presence of a single nucleotide substitution (U>C mutation at nt position 4,995 in NS3) in three separate mutant viruses (clones 239, 489, and 773) indicated that this mutation specified the ts and att phenotypes in each of the three mutant viruses. This mutation was cloned into cDNA construct of p4 and p4Δ30 and recombinant viruses were recovered and designated rDEN4-4995 and rDEN4Δ30-4995, respectively. These recombinant viruses were tested for ts and att phenotypes as described above (Table 6). As expected, introduction of mutation 4995 into rDEN4 wt resulted in a significant ts phenotype at 39° C. in both Vero and HuH-7 cells. rDEN4-4995 grew to nearly wild-type levels at the permissive temperature, 35° C., in both cell types, but demonstrated a greater than 10,000-fold reduction at 39° C. (shut-off temperature) in both Vero and HuH-7 cells. The addition of the 4995 mutation to rDEN4Δ30 yields a recombinant virus, rDEN4Δ30-4995, that exhibits the same level of temperature sensitivity as rDEN4-4995 (Table 6).

The rDEN4 viruses encoding the 4995 mutation were next tested for replication in the brains of suckling mice (Table 6). The 4995 mutation conferred an att phenotype upon both rDEN4 and rDEN4Δ30. There was an approximately 1,000-fold reduction in virus replication compared to that of wt virus. The combination of point mutation 4995 and the Δ30 deletion did not appear to result in an additive reduction of virus replication. These results confirmed that the 4995 point mutation indeed specifies the ts and att phenotypes. Importantly, the utility of modifying tissue culture and in vivo phenotypes of the rDEN4Δ30 vaccine candidate by introduction of additional mutations was also demonstrated.

Discussion. Herein we teach how to prepare a tetravalent, live-attenuated dengue virus vaccine using rDEN4Δ30 as the DEN4 component and three antigenic chimeric viruses expressing the structural proteins (C, prM, and E) of DEN1, DEN2, and DEN3 from the attenuated rDEN4Δ30 vector (Example 8). DEN4 virus rDEN4Δ30 containing the Δ30 deletion mutation in the 3' UTR manifests restricted replication in humans while retaining immunogenicity. Since rDEN4Δ30 retains a low level of residual virulence for humans despite this restricted replication, the present study was initiated to generate additional attenuating mutations that are envisioned as being useful to further attenuate rDEN4Δ30 or other dengue viruses and that are envisioned as being incorporated into any of the three antigenic chimeric viruses or other dengue viruses as needed. Temperature-sensitive mutants of dengue viruses (Bhamarapravati, N. & Yoksan, S. 1997 in: *Dengue and Dengue Hemorrhagic Fever* D. J. Gubler & G. Kuno eds. pp. 367-377 CAB International, New York; Eckels, K. H. et al. 1980 *Infect Immun* 27:175-80) as well as other viruses (Skiadopoulos, M. H. et al. 1998 *J Virol* 72:1762-8; Whitehead, S. S. et al. 1999 *J Virol* 73:871-7) manifest restricted replication in vivo. We have generated a panel of 20 ts DEN4 mutant viruses, determined their genomic sequence, and assessed their in vivo attenuation phenotypes. The 20 ts DEN4 mutant viruses were generated by growth in the presence of 5-FU and were first selected for viability in Vero cells, the substrate planned for use in the manufacture of these vaccines, to ensure that the mutant viruses can be grown efficiently in a suitable substrate.

Two classes of mutant viruses were obtained; those ts in both Vero and HuH-7 cells (n=13) or those ts in only HuH-7

cells (n=7). The viruses exhibited a range in their level of temperature sensitivity from a 100- to 1,000,000-fold reduction in replication at the restrictive temperature of 39° C. Since our DEN4 vaccine candidate retains a low level of virulence for the liver and other findings support the ability of dengue viruses to infect hepatocytes (Lin, Y. L. et al. 2000 *J Med Virol* 60:425-31; Marianneau, P. et al. 1997 *J Virol* 71:3244-9) and cause liver pathology (Couvelard, A. et al. 1999 *Hum Pathol* 30:1106-10; Huerre, M. R. et al. 2001 *Virchows Arch* 438:107-15), we sought to develop mutations that would selectively restrict replication of dengue 4 virus in liver cells. Toward this end, we identified seven mutant viruses which have a HuH-7 cell-specific ts phenotype. The mutations present in these viruses are the first reported in DEN viruses that confer restricted replication in liver cells and are envisioned as being useful in limiting virus replication and pathogenesis in the liver of vaccine recipients. The contribution of individual mutations identified in the HuH-7 cell-specific ts viruses to the observed phenotypes is envisioned as being assessed by introduction of the individual mutations into recombinant DEN4 viruses.

Recent evidence has indicated that the magnitude of the viremia in DEN-infected patients positively correlates with disease severity, i.e., the higher the titer of viremia the more severe the disease (Murgue, B. et al. 2000 *J Med Virol* 60:432-8; Vaughn, D. W. et al. 2000 *J Infect Dis* 181:2-9). This indicates that mutations that significantly restrict replication of vaccine candidates in vivo are the foundation of a safe and attenuated vaccine. Evaluation of DEN virus vaccine candidates for in vivo attenuation is complicated by the lack of a suitable animal model which accurately mimics the disease caused by dengue viruses in humans. In the absence of such a model, the replication of the panel of 5-FU mutant viruses in the brains of Swiss Webster suckling mice was assessed as a means to identify an in vivo attenuation phenotype since this animal model is well-suited for the evaluation of a large set of mutant viruses. Each of the 20 ts mutant viruses exhibited an att phenotype manifesting a 10- to 6,000-fold reduction in replication in the brain of mice as compared to wt DEN4 virus (Table 2). This indicates that there is a correlation between the presence of the ts phenotype in tissue culture and attenuation of the mutant in vivo confirming the utility of selecting viruses with this marker as vaccine candidates. However, there was no correlation between the level of temperature sensitivity and the level of restriction in vivo. Furthermore, Sabin observed a dissociation between mouse neurovirulence and attenuation in humans by generating an effective live attenuated virus vaccine against DEN by passage of virus in mouse brain. This research actually resulted in a highly mouse-neurotropic DEN virus which, paradoxically, was significantly attenuated in humans (Sabin, A. B. 1952 *Am J Trop Med Hyg* 1:30-50). Despite this, attenuation for the suckling mouse brain has been reported for other live-attenuated DEN virus vaccine candidates including the DEN2 PDK-53 vaccine strain which is non-lethal in mice and DEN-2 PR-159/S-1 vaccine strain which was significantly attenuated compared to its parental wild-type virus (Bhamarapravati, N. & Yoksan, S. 1997 in: *Dengue and Dengue Hemorrhagic Fever* D. J. Gubler & G. Kuno eds. pp. 367-377 CAB International, New York; Butrapet, S. et al. 2000 *J Virol* 74:3011-9; Eckels, K. H. et al. 1980 *Infect Immun* 27:175-80; Innis, B. L. et al. 1988 *J Infect Dis* 158:876-80). Replication in rhesus monkeys has been reported to be predictive of attenuation for humans (Innis, B. L. et al. 1988 *J Infect Dis* 158:876-80). Recently, murine models of DEN virus infection have been developed using SCID mice transplanted with human macrophage (Lin, Y. L. et al. 1998 *J Virol* 72:9729-37) or liver cell

lines (An, J. et al. 1999 *Virology* 263:70-7), but these mice have not as yet been used to assess att phenotypes of candidate vaccine viruses. Mutant viruses or recombinant viruses bearing one or more of these mutations described herein are envisioned as being tested for replication in rhesus monkeys (or other suitable animal model) as predictive for attenuation in humans.

The chemical mutagenesis of DEN4 virus and sequence analysis of resulting viruses described here has resulted in the identification of a large number of point mutations resulting in amino acid substitutions in all genes except C and NS4A as well as point mutations in the 5' and 3' UTR (Tables 3 and 4). This approach of whole-genome mutagenesis has the benefit of identifying mutations dispersed throughout the entire genome which are pre-selected for viability in the Vero cell substrate. Ten 5-FU mutant viruses which were ts in Vero and HuH-7 cells and three viruses which were selectively ts in HuH-7 cells contained only mutations outside of the genes encoding the structural proteins, i.e., in the 5' and 3' UTR or NS genes. These mutations along with the Δ 30 deletion in the 3' UTR are particularly suited for inclusion in antigenic, chimeric vaccines which consist of an attenuated DEN4 vector bearing the wild-type structural genes (C, prM, E) of the other DEN virus serotypes. Use of this strategy has several advantages. Each antigenic chimeric virus that possesses structural proteins from a wild-type virus along with attenuating mutations in their UTRs or NS genes should maintain its infectivity for humans, which is mediated largely by the E protein, and, therefore, each vaccine component should be immunogenic (Huang, C. Y. et al. 2000 *J Virol* 74:3020-8). The replicative machinery of the tetravalent vaccine strains would share the same attenuating mutations in the NS genes or in the UTR which should attenuate each vaccine component to a similar degree and thereby minimize interference or complementation among the four vaccine viruses. In addition, wild-type E protein would be expected to most efficiently induce neutralizing antibodies against each individual DEN virus.

Sequence analysis of dengue viruses (Blok, J. et al. 1992 *Virology* 187:573-90; Lee, E. et al. 1997 *Virology* 232:281-90; Puri, B. et al. 1997 *J Gen Virol* 78:2287-91) and yellow fever viruses (Dunster, L. M. et al. 1999 *Virology* 261:309-18; Holbrook, M. R. et al. 2000 *Virus Res* 69:31-9) previously generated by serial passage in tissue culture have mutations throughout much of the genome, a pattern we have observed in the present study. Recent analysis of the DEN2 PDK-53 vaccine strain has identified the important mutations involved in attenuation which were located in non-structural regions including the 5' UTR, NS1 and NS3 (Butrapet, S. et al. 2000 *J Virol* 74:3011-9). This DEN2 vaccine strain has been used to generate a chimeric virus with DEN1 C-prM-E genes (Huang, C. Y. et al. 2000 *J Virol* 74:3020-8). In separate studies, the sequence of the DEN1 vaccine strain 45AZ5 PDK-27 was determined and compared to parental viruses, but the mutations responsible for attenuation have not yet been identified (Puri, B. et al. 1997 *J Gen Virol* 78:2287-91).

Several amino acid substitutions were identified in more than one ts 5-FU mutant virus (Table 5). Lee et al. have previously reported finding repeated mutations in separate DEN3 virus clones after serial passage in Vero cells (Lee, E. et al. 1997 *Virology* 232:281-90). A mutation (K>N) identified in E at a.a. position 202 in a single DEN3 passage series was also found in our 5-FU mutant virus #1012 (K>E). Mutations observed in the 5-FU sister mutant viruses are envisioned as representing adaptive changes that confer an increased efficiency of DEN4 replication in Vero cells. Such

mutations are envisioned as being beneficial for inclusion in a live-attenuated DEN virus vaccine by increasing the yield of vaccine virus during manufacture. Interestingly, three distinct amino acid substitutions were found in NS4B of the 5-FU sister mutant viruses. The exact function of this gene is unknown, but previous studies of live-attenuated yellow fever vaccines (Jennings, A. D. et al. 1994 *J Infect Dis* 169:512-8; Wang, E. et al. 1995 *J Gen Virol* 76:2749-55) and Japanese encephalitis vaccines (Ni, H. et al. 1995 *J Gen Virol* 76:409-13) have identified mutations in NS4B associated with attenuation phenotypes.

The mutation at nt position 4995 of NS3 (S1632P) was present as the only significant mutation identified in three 5-FU mutant viruses (#239, #489, and #773). This mutation was introduced into a recombinant DEN4 virus and found to confer a ts and att phenotype (Table 6). These observations clearly identify the 4995 mutation as an attenuating mutation. Analysis of a sequence alignment (Chang, G.-J. 1997 in: *Dengue and Dengue Hemorrhagic Fever* D. J. Gubler & G. Kuno, eds. pp. 175-198 CAB International, New York) of the four dengue viruses indicated that the Ser at a.a. position 1632 is conserved in DEN1 and DEN2, while DEN3 contains an Asn at this position indicating that the mutation is predicted to be useful in modifying the phenotypes of the other DEN virus serotypes. The NS3 protein is 618 a.a. in length and contains both serine protease and helicase activities (Bazan, J. F. & Fletterick, R. J. 1989 *Virology* 171:637-9; Brinkworth, R. I. et al. 1999 *J Gen Virol* 80:1167-77; Valle, R. P. & Falgout, B. 1998 *J Virol* 72:624-32). The 4995 mutation results in a change at a.a. position 158 in NS3 which is located in the N-terminal region containing the protease domain. Amino acid position 158 is located two a.a. residues away from an NS3 conserved region designated homology box four. This domain has been identified in members of the flavivirus family and is believed to be a critical determinant of the NS3 protease substrate specificity (Bazan, J. F. & Fletterick, R. J. 1989 *Virology* 171:637-9; Brinkworth, R. I. et al. 1999 *J Gen Virol* 80:1167-77). However, the exact mechanism which results in the phenotype associated with the 4995 mutation has not yet been identified. The identification of the 4995 mutation as an attenuating mutation permits a prediction of its usefulness for the further attenuation of rDEN4 Δ 30.

We have determined the contribution of individual 5-FU mutations to the observed phenotypes by introduction of the mutations into recombinant DEN4 viruses as was demonstrated herein for the 4995 mutation (see Example 3). In addition, combination of individual mutations with each other or with the Δ 30 mutation is useful to further modify the attenuation phenotype of DEN4 virus candidate vaccines. The introduction of the 4995 mutation into rDEN4 Δ 30 described herein rendered the rDEN4 Δ 30-4995 double mutant ts and 1000-fold more attenuated for the mouse brain than rDEN4 Δ 30. This observation has demonstrated the feasibility of modifying both tissue culture and in vivo phenotypes of this and other dengue virus vaccine candidates. Once the mutations responsible for the HuH-7 cell-specific ts phenotype are identified as described above and introduced into the rDEN4 Δ 30 vaccine candidate, we envision confirming that these mutations attenuate rDEN4 Δ 30 vaccine virus for the liver of humans. A menu of attenuating mutations is envisioned as being assembled that is predicted to be useful in generating satisfactorily attenuated recombinant dengue vaccine viruses and in increasing our understanding of the pathogenesis of dengue virus (see Example 7).

Chemical Mutagenesis of DEN4 Virus Results in
Small-Plaque Mutant Viruses with
Temperature-Sensitive and Attenuation Phenotypes

Mutations that restrict replication of dengue virus have been sought for the generation of recombinant live-attenuated dengue virus vaccines. Dengue virus type 4 (DEN4) was previously grown in Vero cells in the presence of 5-fluorouracil, and the characterization of 1,248 mutagenized, Vero cell-passaged clones identified 20 temperature-sensitive (ts) mutant viruses that were attenuated (att) in suckling mouse brain (Example 1). The present investigation has extended these studies by identifying an additional 22 DEN4 mutant viruses which have a small-plaque size (sp) phenotype in Vero cells and/or the liver cell line, HuH-7. Five mutant viruses have a sp phenotype in both Vero and HuH-7 cells, three of which are also ts. Seventeen mutant viruses have a sp phenotype in only HuH-7 cells, thirteen of which are also ts. Each of the sp viruses was growth restricted in the suckling mouse brain, exhibiting a wide range of reduction in replication (9- to 100,000-fold). Complete nucleotide sequence was determined for the 22 DEN4 sp mutant viruses, and nucleotide substitutions were found in the 3' untranslated region (UTR) as well as in all coding regions except NS4A. Identical mutations have been identified in multiple virus clones indicating that they are involved in the adaptation of DEN4 virus to efficient growth in Vero cells.

The DEN viruses cause more disease and death of humans than any other arbovirus, and more than 2.5 billion people live in regions with endemic dengue infection (Gubler, D. J. 1998 *Clin Microbiol Rev* 11:480-96). Annually, there are an estimated 50-100 million cases of dengue fever (DF) and 500,000 cases of the more severe and potentially lethal dengue hemorrhagic fever/dengue shock syndrome (DHF/DSS) (Gubler, D. J. & Meltzer, M. 1999 *Adv Virus Res* 53:35-70). Dengue fever is an acute infection characterized by fever, retro-orbital headache, myalgia, and rash. At the time of defervescence during DF, a more severe complication of DEN virus infection, DHF/DSS, may occur which is characterized by a second febrile period, hemorrhagic manifestations, hepatomegaly, thrombocytopenia, and hemoconcentration, which may lead to potentially life-threatening shock (Gubler, D. J. 1998 *Clin Microbiol Rev* 11:480-96).

The sites of DEN virus replication in humans and their importance and relationship to the pathogenesis of DF and DHF/DSS are still incompletely understood (Innis, B. L. 1995 in: *Exotic Viral Infections* J. S. Porterfield, ed. pp. 103-146 Chapman and Hall, London). In addition to replication in lymphoid cells, it has become evident that the liver is involved in DEN infection of humans. Transient elevations in serum alanine aminotransferase (ALT) and aspartate aminotransferase (AST) levels are observed in the majority of DEN virus-infected patients and hepatomegaly is observed in some patients (Kalayanarooj, S. et al. 1997 *J Infect Dis* 176:313-21; Kuo, C. H. et al. 1992 *Am J Trop Med Hyg* 47:265-70; Mohan, B. et al. 2000 *J Trop Pediatr* 46:40-3; Wahid, S. F. et al. 2000 *Southeast Asian J Trop Med Public Health* 31:259-63). DEN virus antigen-positive hepatocytes are seen surrounding areas of necrosis in the liver of fatal cases (Couvillard, A. et al. 1999 *Hum Pathol* 30:1106-10; Huerre, M. R. et al. 2001 *Virchows Arch* 438:107-15), from which dengue virus sequences were identified using RT-PCR (Rosen, L. et al. 1999 *Am J Trop Med Hyg* 61:720-4). Of potential importance to the etiology of severe dengue virus infection, three studies have demonstrated that the mean levels of serum ALT

and AST were significantly increased in patients with DHF/DSS compared to those with DF (Kalayanarooj, S. et al. 1997 *J Infect Dis* 176:313-21; Mohan, B. et al. 2000 *J Trop Pediatr* 46:40-3; Wahid, S. F. et al. 2000 *Southeast Asian J Trop Med Public Health* 31:259-63). As expected, elevation of serum liver enzymes has previously been observed in clinical trials of DEN virus vaccine candidates (Example 8; Eckels, K. H. et al. 1984 *Am J Trop Med Hyg* 33:684-9; Edelman, R. et al. 1994 *J Infect Dis* 170:1448-55; Kanesa-thasan, N. et al. 2001 *Vaccine* 19:3179-3188; Vaughn, D. W. et al. 1996 *Vaccine* 14:329-36).

Based on the increasing disease burden associated with DEN virus infection over the past several decades, a vaccine which confers protection against the four dengue virus serotypes is needed, but none is presently licensed. Because of the increased risk for severe DHF/DSS associated with secondary infection with a heterologous DEN virus serotype (Burke, D. S. et al. 1988 *Am J Trop Med Hyg* 38:172-80; Halstead, S. B. et al. 1977 *J Exp Med* 146:218-29; Thein, S. et al. 1997 *Am J Trop Med Hyg* 56:566-72), an effective vaccine must confer simultaneous protection against each of the four DEN virus serotypes. Several approaches are presently being pursued to develop a tetravalent vaccine against the dengue viruses (Bancroft, W. H. et al. 1984 *J Infect Dis* 149:1005-10; Bhamarapavati, N. & Sutee, Y. 2000 *Vaccine* 18:44-7; Butrapet, S. et al. 2000 *J Virol* 74:3011-9; Guirakhoo, F. et al. 2000 *J Virol* 74:5477-85; Huang, C. Y. et al. 2000 *J Virol* 74:3020-8; Kanesa-thasan, N. et al. 2001 *Vaccine* 19:3179-3188). One such approach, a live-attenuated DEN4 vaccine candidate, termed 2AΔ30, was both attenuated and immunogenic in a cohort of 20 volunteers (Example 8). The recombinant 2AΔ30 virus contains a 30 nt deletion in the 3' UTR which removes nucleotides 10,478-10,507 and was found to produce a low or undetectable level of viremia in vaccinees at a dose of 10⁵ PFU/vaccinee. An asymptomatic rash was reported in 50% of volunteers, and the only laboratory abnormality observed was an asymptomatic, transient rise in the serum ALT level in 5 of the 20 vaccinees. All 2AΔ30 vaccinees developed serum neutralizing antibodies against DEN4 virus (mean titer: 1:580), and 2AΔ30 was not transmitted to mosquitoes that fed experimentally on vaccinees (Troyer, J. M. et al. 2001 *Am J Trop Med Hyg* 65:414-9). Because of the desirable properties conferred by the Δ30 mutation, chimeric vaccine candidates are being constructed which contain the structural genes of DEN virus type 1, 2, and 3, in the attenuated DEN4 background bearing the genetically stable Δ30 mutation. Attenuating mutations outside of the structural genes are particularly attractive for inclusion in antigenic chimeric vaccine candidates because they will not affect the infectivity or immunogenicity conferred by the major mediator of humoral immunity to DEN viruses, the envelope (E) protein.

The presence of rash and elevated ALT levels suggests that the 2AΔ30 vaccine candidate may be slightly under-attenuated in humans. Similarly, many previous attempts to develop live attenuated dengue virus vaccines have yielded vaccine candidates that were either over- or under-attenuated in humans, some of which also induced elevation of serum ALT and AST levels (Bhamarapavati, N. & Yoksan, S. 1997 in: *Dengue and Dengue Hemorrhagic Fever* D. J. Gubler & G. Kuno eds. pp. 367-377 CAB International, New York; Eckels, K. H. et al. 1984 *Am J Trop Med Hyg* 33:684-9; Innis, B. L. et al. 1988 *J Infect Dis* 158:876-80; Kanesa-thasan, N. et al. 2001 *Vaccine* 19:3179-3188; McKee, K. T., Jr. et al. 1987 *Am J Trop Med Hyg* 36:435-42). Therefore, we have developed a menu of point mutations conferring temperature-sensitive (ts), small-plaque (sp), and attenuation (att) phenotypes

capable of attenuating DEN4 viruses to a varying degree (Example 1). We have previously described 20 mutant viruses that exhibit a ts, but not sp, phenotype in Vero cells or HuH-7 liver cells and that show attenuated replication in mouse brain (Example 1). Addition of such mutations to 2AΔ30 or to other dengue virus vaccine candidates is envisioned as yielding vaccine candidates that exhibit a more satisfactory balance between attenuation and immunogenicity.

In the present Example, we have extended our analysis of the panel of 1,248 DEN4 virus clones previously generated by mutagenesis with 5-fluorouracil (5-FU) (Example 1), by identifying a set of 22 sp mutant viruses, some of which also have a ts phenotype. Small plaque mutant viruses were sought since such viruses are often attenuated in humans (Bhamarapavati, N. & Yoksan, S. 1997 in: *Dengue and Dengue Hemorrhagic Fever* D. J. Gubler & G. Kuno eds. pp. 367-377 CAB International, New York; Butrapet, S. et al. 2000 *J Virol* 74:3011-9; Crowe, J. E. Jr. et al. 1994 *Vaccine* 12:783-790; Crowe, J. E. Jr. et al. 1994 *Vaccine* 12:691-699; Eckels, K. H. et al. 1980 *Infect Immun* 27:175-80; Innis, B. L. et al. 1988 *J Infect Dis* 158:876-80; Murphy, B. R. & Chanock, R. M. 2001 in: *Fields Virology* D. M. Knipe, et al. Eds. Vol. 1, pp. 435-468 Lippincott Williams & Wilkins, Philadelphia; Takemoto, K. K. 1966 *Prog Med Virol* 8:314-48). Because natural infection with dengue viruses and vaccination with 2AΔ30 may be associated with liver toxicity in humans, we identified mutant viruses with restricted replication in human liver cells. Accordingly, viruses were screened for plaque size and temperature-sensitivity in the human hepatoma cell line, HuH-7, as well as in Vero cells. Here we describe the ts phenotype, nucleotide sequence, and growth properties in suckling mice of 22 sp DEN4 mutant virus clones.

Cells and viruses. WHO Vero cells (African green monkey kidney cells) and HuH-7 cells (human hepatoma cells) (Nakabayashi, H. et al. 1982 *Cancer Res* 42:3858-63) were maintained as described in Example 1. DEN4 2A virus is a wild type virus derived from a cDNA clone of DEN4 strain 814669 (Dominica, 1981) (Lai, C. J. et al. 1991 *PNAS USA* 88:5139-43; Mackow, E. et al. 1987 *Virology* 159:217-28). The nucleotide sequence of DEN4 2A, the parent of the 5-FU mutant viruses, was previously assigned GenBank accession number AF375822 (Example 1). The DEN4 vaccine candidate, 2AΔ30, (Example 8) contains a 30 nt deletion in the 3' untranslated region (UTR) which removes nucleotides 10,478-10,507 (Men, R. et al. 1996 *J Virol* 70:3930-7). The cDNA clones p4, a modified derivative of the DEN4 2A cDNA clone, and p4Δ30 were used to generate recombinant wild type and attenuated viruses, rDEN4 and rDEN4Δ30, respectively (Example 8). GenBank accession numbers were previously assigned as follows (virus: accession number): DEN4 strain 814669: AF326573; 2AΔ30: AF326826; rDEN4: AF326825; rDEN4Δ30: AF326827.

Generation and biological cloning of mutant viruses with a sp phenotype. The generation of 1,248 virus clones from a pool of 5-fluorouracil-mutagenized DEN4 2A has been previously described (Example 1). Briefly, monolayers of Vero cells were infected with DEN4 2A at a multiplicity of infection (MOI) of 0.01 and overlaid with MEM supplemented with 2% FBS and 1 mM 5-fluorouracil (5-FU) (Sigma, St. Louis, Mo.), which reduced replication of DEN4 2A 100-fold. Vero cells in 96-well plates were inoculated with the 5-FU treated virus suspension, and virus clones were harvested from plates receiving terminally-diluted virus. A total of 1,248 virus clones were generated from the cultures treated with 1 mM 5-FU. Two virus clones, 2A-1 and 2A-13, were generated in the same manner from control cultures not

treated with 5-FU and served as parallel-passaged control viruses with a wild type phenotype.

Evaluation of in vitro plaque size and temperature sensitivity. The 1,248 5-FU-mutagenized virus clones were screened for temperature sensitivity by assessing virus replication at 35° C. (permissive temperature) and 39° C. (restrictive temperature) in Vero and HuH-7 cells. Cell monolayers in 96-well plates were inoculated with serial ten-fold dilutions of virus and replicate plates were incubated at 35° C. and 39° C. for five days in temperature-controlled water baths. Virus replication was determined by immunoperoxidase staining as previously described (Example 1). A collection of 193 5-FU virus clones demonstrated a 100-fold or greater reduction in titer at 39° C. in either cell line, and these presumptive ts viruses were further characterized. The efficiency of plaque formation (EOP) at permissive and restrictive temperatures and the plaque size of each of the 193 virus clones were determined as follows. Serial ten-fold dilutions of virus suspension were inoculated onto confluent Vero cell and HuH-7 cell monolayers in replicate 24-well plates. After incubation at 35° C. for two hours, monolayers were overlaid with 0.8% methylcellulose (EM Science, Gibbstown, N.J.) in L-15 medium (Quality Biologicals, Gaithersburg, Md.) supplemented with 2% FBS, gentamicin, and L-glutamine. After incubation of replicate plates for five days at 35, 37, 38, or 39° C. in temperature-controlled water baths, plaques were visualized by immunoperoxidase staining and counted as previously described. Plaque size of each of the 193 viruses was evaluated at the permissive temperature (35° C.) and compared to that of DEN4 2A-13 parallel-passaged control virus with a wild type plaque size. Mutant viruses incubated at the permissive temperature of 35° C. which had a plaque size ≤ 1 mm or ≤ 0.4 mm (approximately $\leq 50\%$ the size of wild type DEN4 2A-13) in Vero or HuH-7 cells, respectively, were designated as having a sp phenotype. The level of temperature sensitivity and plaque size of each virus was confirmed in at least two separate experiments. Seventy-five viruses which were confirmed to have a putative ts and/or sp phenotype were biologically cloned an additional two times and phenotypes were re-assessed. Twenty-two of the 75 terminally diluted viruses were found to have a sp phenotype. Sixteen of the 22 sp mutant viruses were also found to have a ts phenotype as defined by a 2.5 or 3.5 \log_{10} PFU/ml reduction in virus titer in Vero or HuH-7 cells, respectively, at restrictive temperature compared to the permissive temperature of 35° C. as previously described (Example 1). Twenty of the 75 terminally-diluted viruses were found to have a ts phenotype without a sp phenotype and were previously described (Example 1). The remainder of the 75 viruses did not meet either criteria for a ts or sp mutant virus.

Evaluation of sp mutant viruses for restricted replication in suckling mice Animal experiments were carried out in accordance with the regulations and guidelines of the National Institutes of Health, Bethesda, Md. Growth of DEN4 5-FU mutant viruses was determined in Swiss Webster suckling mice (Taconic Farms, Germantown, N.Y.). Groups of six seven-day-old mice were inoculated intracerebrally with 10^4 PFU of virus in 30 μ l Opti-MEM I (Invitrogen) and the brain of each mouse was removed five days later and individually analyzed as previously described (Example 1). Clarified supernatants of 10% suspensions of mouse brain were frozen at -70° C., and the virus titer was determined by plaque assay in Vero cells.

Determination of the complete genomic sequence of the sp mutant viruses. The nucleotide sequence of the 5-FU-mutagenized DEN4 viruses was determined as described in Example 8. Briefly, genomic RNA was isolated from virus

clones and cDNA was prepared by reverse transcription and served as template for the generation of overlapping PCR fragments. A panel of primers was designed to sequence both strands of the PCR product from which consensus sequences were assembled and analyzed. The nucleotide sequence of the 5' and 3' regions of the virus genome was determined after circularization of the RNA genome as described in Example 8.

Identification of DEN45-fluorouracil mutant viruses with a sp phenotype. The generation of a panel of 1,248 virus clones from a wild type DEN4 2A virus suspension mutagenized by 5-FU has been described previously (Example 1). In the present study twenty-two mutant viruses with a sp phenotype were identified. The plaque size of representative mutant viruses is illustrated in FIG. 3. The plaque size of DEN4 2A-13 virus (a parallel-passaged virus with a wild type phenotype derived from control cultures not treated with 5-FU) was consistently smaller in HuH-7 cells than that observed in Vero cells (FIG. 3A). Mutant viruses #569 and #1189 (FIG. 3B) were sp in both Vero and HuH-7 cells. In contrast, 5-FU mutant virus clones #311 and #1083 (FIG. 3C) were sp in only HuH-7 cells, suggesting a liver cell-specific defect in replication within this phenotypic group. As indicated in Table 7, five mutant viruses were found to have a sp phenotype in both Vero and HuH-7 cells while 17 viruses had a sp phenotype in only HuH-7 cells. Each 5-FU mutant virus clone was compared for a sp or ts phenotype with three control viruses, 2A-13, wild type rDEN4, and rDEN4Δ30. The recombinant viruses, rDEN4 and rDEN4Δ30, each had a plaque size in Vero and HuH-7 cells similar to that of DEN4 2A-13 indicating that the Δ30 mutation does not confer a sp phenotype (Table 7).

Most of the sp 5-FU mutant viruses also had a ts phenotype in Vero and/or HuH-7 cells (Table 7) since mutant viruses were initially screened for temperature sensitivity. Temperature-sensitivity was defined as a 2.5 or 3.5 log₁₀PFU/ml reduction in virus titer in Vero or HuH-7 cells, respectively, at restrictive temperature compared to the permissive temperature of 35° C. as previously defined (Example 1). Three mutant viruses (#574, #1269 and #1189) were sp and ts in both Vero and HuH-7 cells, while nine mutant viruses (#506-326 in Table 7) were found to be ts in both cell types but sp only in HuH-7 cells. Four viruses (#1104, 952, 738, and 1083) were found to have a wild type phenotype in Vero cells but were both sp and ts in HuH-7 cells. These four mutant viruses each had a 6,000- to 600,000-fold reduction in virus titer at 39° C. in HuH-7 cells with only a 6- to 40-fold reduction at 39° C. in Vero cells. Finally, sp mutant viruses were identified which did not have a ts phenotype in either cell line; two of these viruses (#569 and #761) were sp in both Vero and HuH-7 cells and four viruses (#1096-1012) were sp in only HuH-7 cells (Table 7). As described previously, the Δ30 mutation did not confer temperature-sensitivity in either cell line (Example 1).

The sp 5-FU mutant viruses have restricted replication in suckling mouse brain. The 22 sp DEN4 5-FU mutant viruses were evaluated for their ability to replicate in the brain of one-week-old suckling mice. As a marker for in vivo attenuation, their level of replication was compared with that of the parallel-passaged control virus with a wild type phenotype, 2A-13 (Table 7). Nineteen of 22 sp mutant viruses had a greater than 100-fold reduction in virus replication in the brain of suckling mice compared to 2A-13 and nine viruses had a reduction of greater than 10,000-fold.

The five mutant viruses which were sp in both Vero and HuH-7 cells were 5,000-fold to 100,000-fold restricted in replication compared to 2A-13. Two of these mutant viruses,

#569 and #761, were not ts in either cell line but had a reduction in virus titer of greater than 10,000-fold in mouse brain, indicating that the sp phenotype in both Vero and HuH-7 cells is an important surrogate marker for attenuated replication in suckling mouse brain. 5-FU mutant viruses which were sp in only HuH-7 cells had a more variable range of replication in mouse brain. Three viruses had a mean reduction in virus titer of less than 10-fold when compared to 2A-13 virus. However, 8 of 13 viruses which were ts in Vero and/or HuH-7 cells but sp in only HuH-7 cells had a greater than 5,000-fold reduction in virus replication. The results of the in vivo replication analysis of the previously described 20 ts 5-FU mutant viruses (Example 1) and the 22 sp mutant viruses are summarized in Table 8. Mutant viruses with both a sp and ts phenotype were found to have a significantly greater level of attenuation in the brain of suckling mice when compared to viruses with only a ts phenotype.

Sequence analysis of the sp 5-FU mutant viruses. To initiate an analysis of the genetic basis of the ts, sp, or att phenotype of the 22 sp mutant viruses, the complete nucleotide sequence of each virus genome was determined and is summarized in Table 9 (sp in Vero and HuH-7 cells) and Table 10 (sp in only HuH-7 cells). All identified mutations were nucleotide substitutions, as deletions or insertions were not observed. Point mutations were distributed throughout the genome, including the 3' UTR as well as in all coding regions. Because all 5-FU mutant viruses were found to have at least two mutations (two to six), the observed phenotypes cannot be directly attributed to a specific mutation. The majority of sp viruses also contained translationally silent point mutations (none to four) in the structural or non-structural coding regions. However, these silent mutations are not expected to contribute to the observed phenotypes. Six of the 22 sp mutant viruses (Tables 9 and 10) were found to have mutations in only the NS genes and/or the 3' UTR, indicating that the sp phenotype can be conferred by mutations outside of the structural genes.

Presence of identical mutations in multiple 5-FU mutant viruses. Analysis of the complete nucleotide sequence data for the 5-FU mutant viruses identified several repeated mutations which were present in two or more viruses. Such mutations were also identified previously during our analysis of twenty 5-FU mutant viruses with a ts but not sp phenotype (Example 1). Because these mutations occurred in viruses together with additional mutations, the contribution of the repeated mutations to the observed sp, ts, and att phenotypes remains empirical. Table 11 lists the repeated mutations found among the 20 ts (not sp) mutant viruses described previously (Example 1) and the 22 sp mutant viruses described here. Repeated mutations were identified in the following genes: two in E, two in NS3, five in NS4B, one in NS5, and two in the 3' UTR. Interestingly, within a thirty nucleotide region of NS4B (nt 7153-7182), there were five different nucleotide substitutions which were found in sixteen viruses. Also at nt 7,546 in NS4B, an amino acid substitution (Ala→Val) was found in 10 different 5-FU mutant viruses. The significance of these repeated mutations in NS4B as well as in other DEN4 genomic regions remains empirical, but a reasonable explanation for this phenomenon is that these mutations are involved in adaptation of DEN4 virus for efficient growth in Vero cells, as further discussed in Example 6.

Discussion. As part of a molecular genetic vaccine strategy, we have developed attenuating mutations that are envisioned as being useful in the development of a live attenuated tetravalent dengue virus vaccine. Specifically, mutations which restrict replication of the vaccine virus in human liver cells

were generated since there was some residual virulence of the rDEN4 Δ 30 vaccine candidate for the liver of humans. Mutant viruses with a sp phenotype were sought in both Vero cells and HuH-7 human liver cells, in order to identify host-range mutant viruses that were specifically restricted in replication in HuH-7 cells (sp in HuH-7 but not in Vero). Such mutations are envisioned as being useful in limiting replication of a candidate vaccine in the liver of vaccinees while preserving both efficient replication in Vero cells and immunogenicity in vivo.

Several observations from the present study indicate that sp mutations confer an att phenotype in vivo. This is not surprising since attenuation in suckling mouse brain has been reported for live DEN virus vaccine candidates possessing sp phenotypes, including the DEN2 PDK-53 and DEN2 PR-159/S-1 vaccine strains (Bhamarapavati, N. & Yoksan, S. 1997 in: *Dengue and Dengue Hemorrhagic Fever* D. J. Gubler & G. Kuno eds. pp. 367-377 CAB International, New York; Butrapet, S. et al. 2000 *J Virol* 74:3011-9; Eckels, K. H. et al. 1980 *Infect Immun* 27:175-80; Innis, B. L. et al. 1988 *J Infect Dis* 158:876-80). Each of 22 DEN4 5-FU mutant viruses with a sp phenotype (some of which were also ts) in either Vero or HuH-7 cells manifested restricted replication in the brains of mice. Six 5-FU mutant viruses with a sp phenotype in the absence of a ts phenotype were more attenuated in the brains of suckling mice than mutant viruses with solely a ts phenotype (Example 1), indicating that the sp phenotype specifies a greater level of attenuation for mouse brain than does the ts phenotype. Mutant viruses with both a ts and sp phenotype had an even greater reduction in replication, further indicating that the attenuation conferred by the ts and sp phenotypes can be additive. Importantly, seventeen of the 22 sp mutant viruses were host-range sp mutant viruses, being sp only in HuH-7 cells. Since such mutations are envisioned as being useful in restricting the replication of a DEN4 virus in human liver cells, we used nucleotide sequence analysis to determine the genetic basis of the sp phenotype.

Analysis of the complete genomic sequence of the 22 sp DEN4 viruses revealed substitutions in the 3' UTR as well as coding mutations in all genes except NS4A. It was first noted that several specific mutations were present in two or more of the 22 sp DEN4 mutant viruses and that many of these same mutations were also previously identified among the set of 20 ts DEN4 mutant viruses (Example 1). Since flaviviruses can rapidly accumulate mutations during passage in tissue culture (Dunster, L. M. et al. 1999 *Virology* 261:309-18; Mandl, C. W. et al. 2001 *J Virol* 75:5627-37), many of these over-represented mutations, previously referred to as putative Vero cell adaptation mutations (Example 1), likely promote efficient replication in Vero cells and were selected unintentionally during the biological cloning of the mutant viruses. The effect of these mutations on DEN virus replication in Vero cells, the proposed substrate for vaccine manufacture, is discussed in Example 6.

The sp mutations identified among the 5-FU mutant viruses are envisioned as being useful in several different approaches for the development of DEN virus vaccine strains. As described above for the generation of antigenic chimeric viruses, one or more sp attenuating mutations are envisioned as being added to the attenuated DEN4 Δ 30 genetic background to supplement the att phenotype of the Δ 30 mutation. A second approach is to introduce a sp attenuating mutation, with or without Δ 30, into infectious cDNA clones of the other three DEN serotypes. The ability to transfer mutations among genetically-related viruses and maintain similar att phenotypes has been previously demonstrated (Skiadopoulos, M. H. et al. 1999 *Virology* 260:125-35). These distinct strategies

are envisioned as being useful as separate or complementary approaches to the construction of a tetravalent DEN virus vaccine, underlining the importance of the identification of a large panel of att mutations within the DEN viruses.

Example 3

Recombinant DEN4 Viruses Containing Mutations Identified in 5-FU Mutant Viruses Show Restricted Replication in Suckling Mouse Brain and in SCID Mice Transplanted with Human Liver Cells

Data was presented, in Examples 1 and 2 that summarizes the generation, characterization and sequence analysis of 42 attenuated mutant DEN4 viruses. For three of the mutant viruses (#239, 489, and 773) with a single missense mutation at nt position 4995 in NS3, it was clear that the identified mutation specified the ts and att phenotypes. This conclusion was confirmed in Example 1 by tissue culture and in vivo characterization of rDEN4-4995, a recombinant virus into which the 4995 mutation had been introduced by site-directed mutagenesis. In this analysis, rDEN4-4995 exhibited the same level of temperature sensitivity and attenuation as 5-FU mutant viruses #239, 489, and 773. The individual mutation(s) in the remaining 5-FU mutant viruses that specify the observed phenotypes remains to be identified, since most of these viruses possess more than one nucleotide substitution. We have conducted an analysis to identify the mutations in a subset of the other 39 mutant viruses that specify the ts, sp, and att phenotypes by introduction of each mutation into the wt DEN4 cDNA (p4) and evaluation of the phenotypes of the resulting recombinant DEN4 viruses bearing the individual mutations. Previous studies of a DEN2 virus vaccine candidate (Butrapet, S. et al. 2000 *J Virol* 74:3011-9) as well as other virus vaccines (Whitehead, S. S. et al. 1999 *J Virol* 73:871-7) have demonstrated the utility of this approach for the identification of the genetic basis of attenuation.

As described in Examples 1 and 2, 19 5-FU mutant viruses were identified which were found to contain coding mutations in only the NS genes and/or nucleotide substitutions in the 5' or 3' UTR which would facilitate the generation of antigenic chimeric viruses. In the present example, the genetic basis of the observed sp, ts, and mouse brain att phenotypes was identified for these 19 viruses using reverse genetics to generate recombinant DEN4 (rDEN4) viruses containing individual mutations identified in the panel of DEN4 mutant viruses. In addition, the 19 5-FU mutant viruses were evaluated for replication in a novel small animal model for DEN4 virus replication, SCID mice transplanted with HuH-7 cells (SCID-HuH-7), and the genetic basis of the att viruses was identified using mutant rDEN4 viruses. Also presented are findings describing the generation and characterization of a recombinant virus containing two of the identified attenuating mutations as well as combination of select 5-FU mutations with the Δ 30 mutation.

Generation of rDEN4 viruses containing 5-FU mutations. The methods used for the generation of rDEN4 viruses are outlined in FIG. 4 and are similar to those described in Example 1. Briefly, the p4 cDNA was digested with the appropriate restriction enzymes and the resulting fragments were subcloned into a modified pUC119 vector. For Kunkel mutagenesis, single-stranded DNA preparations of the pUC-NS vectors were made, and primers were designed to individually introduce mutations that were present in the 5-FU mutant viruses. The sequences of the 41 mutagenic oligonucleotides used to generate the single-mutation recombinant viruses are presented in Table 12. Primers were designed to

co-introduce or co-ablate a translationally-silent restriction enzyme site in the cDNA, which greatly facilitates the screening and identification of cDNA clones possessing the mutant sequence. Fragments containing the introduced mutations were cloned back into p4, and nucleotide sequence analysis confirmed the presence of the nucleotide changes. A total of 33 rDEN4 viruses was generated which contained each of the individual mutations present in the 19 5-FU mutant viruses containing only coding mutations in the NS genes and/or nucleotide substitutions in the 5' or 3' UTR. An additional 8 rDEN4 viruses were generated from mutations identified in the remaining panel of 42 5-FU mutant viruses.

A cDNA clone was also generated which combined the mutations identified at nt position 4995 in NS3 and 7849 in NS5. The 7849 mutation was introduced into the p4-4995 cDNA clone by replacing the XmaI-PstI fragment with that derived from the p4-7849 cDNA clone. The presence of both mutations was confirmed by sequence analysis. The Δ 30 mutation was introduced into the 3' UTR of the individual mutant cDNA clones by replacing the MluI-KpnI fragment with that derived from the p4 Δ 30 cDNA clone, and the presence of the deletion was confirmed by sequence analysis.

Recombinant viruses were recovered by transfection of Vero or C6/36 cells with RNA transcripts derived from the mutant cDNA clones as described in Example 1. Recovered viruses were terminally diluted twice and working stocks of viruses were prepared in Vero cells. Each of the mutant cDNA clones was recovered after transfection as expected since the 5-FU mutant viruses containing these mutations were viable.

Characterization of ts and att phenotypes of the rDEN4 viruses containing introduced mutations. Of the 19 5-FU mutant viruses with mutations in only NS genes and/or the 5' or 3' UTR, six had an sp phenotype (Table 13), ten had a ts phenotype in Vero and HuH-7 cells (Table 14), and three had a ts phenotype in only HuH-7 cells (Table 15). For the six sp 5-FU mutant viruses, #738, 922, 1081, 1083, 1136, and 1189, seventeen mutations identified by sequence analysis resulted in a coding change or a nucleotide change in the UTR and each was engineered into an individual DEN4 cDNA clone. Virus containing each defined mutation was successfully recovered and propagated and was tested for efficiency of plaque formation in Vero and HuH-7 cells at various temperatures, plaque size phenotype, and growth properties in suckling mice using methods previously described in Examples 1 and 2.

Table 13 lists the phenotypes of the six sp 5-FU mutant parent viruses and those of the 17 rDEN4 viruses encoding single mutations present in the parent virus. For example, 5-FU mutant #1189 (parent), which was ts and sp in both cell lines and had an almost 10,000-fold reduction in replication in suckling mouse brain, contained 4 coding mutations at nt position 3303 in NS1, 4812 and 5097 in NS3, and 7182 in NS4B. Analysis of the four rDEN4 viruses containing each of these mutations indicated that rDEN4-5097 had a ts, sp, and att phenotype while rDEN4-3303, rDEN4-4812, and rDEN4-7182 had no discernible phenotypes, indicating that the mutation at nt 5097 was responsible for the phenotype observed in the 5-FU parent, #1189. Thus, analysis of the relative contributions of the four mutations present in the 5-FU mutant #1189 to its attenuation phenotype provides the framework for a similar analysis of the remaining 5-FU mutant viruses. This analysis specifically demonstrates the methods used to identify mutations contributing to the observed phenotype. The ts, sp, and att phenotypes of 5-FU parent viruses #738, 922, 1081, and 1083, were similarly attributed to single mutations 3540, 4306, 2650, and 10634, respectively. However,

two separate mutations (3771 and 4891) contributed to the phenotypes of 5-FU mutant virus #1136.

Table 14 lists the genetic basis of the ts and mouse brain attenuation for the ten 5-FU mutant viruses with ts phenotypes in both Vero and HuH-7 cells. As described in Example 1, the 4995 mutation which is the only mutation present in three 5-FU mutant viruses, #239, #489, and #773, was found to confer a ts and att phenotype, confirming the genetic basis for the phenotypes exhibited by these viruses. In three separate experiments, the rDEN4-4995 virus was found to have an approximately 1,000-fold decrease in replication in the brains of suckling mice when compared to that of wild-type virus (Table 6 and 14). The 4995 mutation is also present in 5-FU mutant viruses #473, #759, and #816, each of which has additional mutations. The ts and att phenotypes observed in these viruses can be attributed to the 4995 mutation since the additional mutations did not show discernible phenotypes. Interestingly, 5-FU mutant virus #938 has the 4995 mutation and an additional mutation at nt 3442 in NS1 with both mutations independently conferring restricted replication in mouse brain. The remaining three 5-FU parent viruses in Table 14, #173, #509, and #1033, were found to each contain a single mutation responsible for the att phenotype: 7849, 8092, and 4907, respectively.

Three 5-FU mutant viruses, #686, #992, and #1175 with HuH-7 cell-specific ts phenotypes are listed in Table 15. Mutations in NS3 (5695) and NS5 (10186) were found to confer the phenotypes observed for parent virus #992 and #1175. Interestingly, two mutations in NS2A, 3575 and 4062, were found to result in a synergistic increase in the level of attenuation. Both individual mutations had an approximately 100-fold decrease in virus replication in the brain while the parent virus with both mutations had an almost 10,000-fold reduction. Table 16 lists two additional mutations with an att phenotype, 4896 and 6259 in NS3.

Replication of DEN4 viruses in SCID mice transplanted with HuH-7 cells. Since DEN viruses replicate poorly in the liver of mice and corresponding studies are impractical to conduct in non-human primates, an animal model that evaluates the in vivo level of replication of DEN virus in liver cells was developed based on a recent report examining the replication of DEN virus in SCID mice transplanted with a continuous cell line of human liver tumor cells (An, J. et al. 1999 Virology 263:70-7). SCID mice transplanted with human continuous cell lines, primary cells, or organized tissues have similarly been used to study the replication of other viruses which lack a suitable small animal model (Mosier, D. E. 2000 Virology 271:215-9). In our study, SCID mice were transplanted with HuH-7 cells since DEN4 virus replicated efficiently in these cells in tissue culture and since these were the cells used to define the host-range phenotype. These studies are envisioned as addressing the utility of examining DEN virus infection in SCID mouse-xenograft models for vaccine development (An, J. et al. 1999 Virology 263:70-7; Lin, Y. L. et al. 1998 J Virol 72:9729-37).

To further examine the in vivo growth properties of the 19 5-FU mutant DEN4 viruses with mutations in only the NS genes and/or the 3' UTR and selected corresponding rDEN4 mutant viruses, replication was assessed in SCID mice transplanted with HuH-7 cells (SCID-HuH-7). For analysis of DEN4 virus replication in SCID-HuH-7 mice, four to six week-old SCID mice (Tac:Icr:Ha(ICR)-Prkdc^{scid}) (Taconic Farms) were injected intraperitoneally with 10⁷ HuH-7 cells suspended in 200 μ l phosphate-buffered saline (PBS). In preparation for transplantation, HuH-7 cells were propagated in cell culture as described above and harvested by trypsinization at approximately 80% confluence. Cells were washed

twice in PBS, counted, resuspended in an appropriate volume of PBS, and injected into the peritoneum of mice. Tumors were detected in the peritoneum five to six weeks after transplantation, and only mice with apparent tumors were used for inoculation. Mice were infected by direct inoculation into the tumor with 10^4 PFU of virus in 50 μ l Opti-MEM1. Mice were monitored daily for seven days and serum for virus titration was obtained by tail-nicking on day 6 and 7. Approximately 400 μ l blood was collected in a serum separator tube (Sarstedt, Germany), centrifuged, and serum was aliquoted and stored at -70° C. The virus titer was determined by plaque assay in Vero cells. Seven days after infection, most mice developed morbidity and all mice were sacrificed. Tumors were excised and weighed to confirm uniformity of the experimental groups.

Preliminary experiments indicated that SCID-HuH-7 mice inoculated with DEN4 2A-13 directly into the tumor developed viremia with maximum levels (up to $8.0 \log_{10}$ PFU/ml serum) achieved on day 5 (Table 17). Virus could also be detected in brain, liver, and tumor homogenates.

The level of viremia in SCID-HuH-7 mice infected with parental 5-FU or rDEN4 mutant viruses was compared with that of the parallel-passaged control virus, 2A-13, or rDEN4, respectively. Results of 4 separate experiments indicated that the vaccine candidate, rDEN4 Δ 30, had an almost 10-fold reduction in virus replication compared to wild type rDEN4 (Table 13) which reflects the apparent attenuation of the rDEN4 Δ 30 vaccine candidate in humans (Example 8). Results in Tables 13 to 15 indicate that three 5-FU mutant viruses had a greater than 100-fold reduction in viremia in the SCID-HuH-7 mice compared to wild type 2A-13 virus: #1081, #1083, and #1189. The common phenotype among these viruses was a sp phenotype in HuH-7 cells. Analysis of the genetic basis of the att phenotype in these parent 5-FU mutant viruses identified three individual mutations in NS1, NS3, and the 3' UTR which conferred at least a 100-fold reduction in viremia. Specifically, rDEN4-2650 (NS1), rDEN4-5097 (NS3), and rDEN4-10634 (3' UTR) manifested a 2.2, 3.6, and 4.3 \log_{10} PFU/ml reduction in peak titer of viremia compared to rDEN4, respectively. These mutations also conferred the att phenotype in suckling mouse brain. 5-FU mutant virus #738 and #509 had a reduction in viremia in the SCID-HuH-7 mice compared to wild type 2A-13 of 1.9 and 1.5 \log_{10} PFU/ml, respectively, and the genetic basis for these phenotypes is envisioned as being assessed on an empirical basis.

This analysis of the genetic basis of the phenotypes specified by the mutations in the 5-FU mutant viruses that manifested restricted replication in SCID-HuH-7 mice indicated that (1) three separate mutations conferred the att phenotype; (2) these mutations were located in two proteins, NS1 and NS3, and in the 3' UTR; (3) these three mutations were fully responsible for each of the cell culture (ts or sp) and in vivo (attenuation in mouse brain and SCID-HuH-7 mice) phenotypes of the parent viruses; and (4) two of the three mutations specify the host-range sp phenotype (sp on HuH-7 only) and therefore are envisioned as being useful in a vaccine virus. Although the relevance of such SCID-transplant models to virus replication and disease in humans is unknown, the identification of three novel mutations which restrict DEN4 virus replication in SCID-HuH-7 mice is envisioned as facilitating an examination of the correlation between the att phenotype in SCID-HuH-7 mice with that in rhesus monkeys or humans. Such mutations, specifically the host-range sp mutations, are envisioned as being useful in conjunction with the Δ 30 or other mutation to decrease the residual virulence of rDEN4 Δ 30 or other dengue virus for the human liver, and

studies are envisioned as being conducted to construct such rDEN4 viruses and evaluate them in monkeys and humans (Example 8).

Combination of two 5-FU mutations results in an additive ts phenotype. The ability to combine individual mutations in rDEN4 virus as a means to modulate the phenotype of the resulting double mutant virus is a major advantage of using recombinant cDNA technology to generate or modify dengue virus vaccine candidates. Addition of multiple ts and att mutations to recombinant vaccine viruses is envisioned as improving the phenotypic stability of the double recombinant due to the decreased possibility of co-reversion of the two mutations to wild-type virulence (Crowe, J. E. Jr. et al. 1994a Vaccine 12:783-790; Skiadopoulou, M. H. et al. 1998 J Virol 72:1762-8; Subbarao, E. K. et al. 1995 J Virol 69:5969-5977; Whitehead, S. S. et al. 1999 J Virol 73:871-7). The mutations identified at nt position 4995 in NS3 and 7849 in NS5 were combined in a single p4 cDNA clone and a recombinant virus, designated rDEN4-4995-7849, was recovered and evaluated for its ts and att phenotypes (Table 18). rDEN4-4995-7849 was more ts than either recombinant virus containing the individual mutations (Table 18), indicating the additive effect of the two ts mutations. The rDEN4-4995-7849 virus had a greater than 10,000-fold reduction in replication in the brains of suckling mice. The reduction in replication of the double mutant virus was only slightly increased over that of rDEN4-7849, however, a difference in the level of replication between rDEN4-4995-7849 and rDEN4-7849 would be difficult to detect since the level of replication of both viruses was close to the lower limit of detection ($2.0 \log_{10}$ PFU/g brain).

Combination of selected 5-FU mutations with the Δ 30 mutation confers increased attenuation of rDEN4 Δ 30 for the brains of suckling mice. To define the effect of adding individual mutations to the attenuated rDEN4 Δ 30 background, five combinations have been constructed: rDEN4 Δ 30-2650, rDEN4 Δ 30-4995, rDEN4 Δ 30-5097, rDEN4 Δ 30-8092, and rDEN4 Δ 30-10634. Addition of such missense mutations with various ts, sp, and att phenotypes is envisioned as serving to decrease the reactogenicity of rDEN4 Δ 30 while maintaining sufficient immunogenicity.

The Δ 30 mutation was introduced into the 3' UTR of the individual mutant cDNA clones by replacing the MluI-KpnI fragment with that derived from the p Δ 30 cDNA clone, and the presence of the deletion was confirmed by sequence analysis. Recombinant viruses were recovered by transfection in C6/36 cells for each rDEN4 virus. However, upon terminal dilution and passage, the rDEN4 Δ 30-5097 virus was found to not grow to a sufficient titer in Vero cells and was not pursued further. This is an example of a cDNA in which the 5-FU mutation and the Δ 30 mutation are not compatible for efficient replication in cell culture. To begin the process of evaluating the in vivo phenotypes of the other four viruses which replicated efficiently in cell culture, rDEN4 viruses containing the individual mutations and the corresponding rDEN4 Δ 30 combinations were tested together for levels of replication in suckling mouse brain. The results in Table 19 indicate that addition of each of the mutations confers an increased level of attenuation in growth upon the rDEN4 Δ 30 virus, similar to the level conferred by the individual 5-FU mutation. No synergistic effect in attenuation was observed between the missense mutations and Δ 30. These results indicate that the missense mutations at nucleotides 2650, 4995, 8092, and 10634 are compatible with Δ 30 for growth in cell culture and in vivo and can further attenuate the rDEN4 Δ 30 virus in mouse brain. Further studies in SCID-HuH-7 mice, rhesus monkeys, and humans are envisioned as establishing

the effect of the combination of individual mutations and $\Delta 30$ upon attenuation and immunogenicity (Example 8).

By identifying the specific mutations in the 5-FU mutant viruses which confer the observed phenotypes, a menu of defined ts, sp, and att mutations is envisioned as being assembled (see Example 7). Numerous combinations of two or more of these mutations are envisioned as being selected with or without the $\Delta 30$ mutation. Such mutations and their combinations are envisioned as being useful for the construction of recombinant viruses with various levels of in vivo attenuation, thus facilitating the generation of candidate vaccines with acceptable levels of attenuation, immunogenicity, and genetic stability.

Example 4

Generation of DEN4 Mutant Viruses with Temperature-Sensitive and Mouse Attenuation Phenotypes Through Charge-Cluster-to-Alanine Mutagenesis

The previous Examples described the creation of a panel of DEN4 mutant viruses with ts, sp, and att phenotypes obtained through 5-FU mutagenesis. As indicated in these Examples, the attenuating mutations identified in the 5-FU mutant viruses are envisioned as having several uses including (1) fine tuning the level of attenuation of existing dengue virus vaccine candidates and (2) generation of new vaccine candidates by combination of two or more of these attenuating mutations. In the current example, we created a second panel of mutant viruses through charge-cluster-to-alanine mutagenesis of the NS5 gene of DEN4 and examined the resulting mutant viruses for the ts, sp, and att phenotypes as described in Examples 1 and 2. The charge-cluster-to-alanine mutant viruses recovered demonstrated a range of phenotypes including ts in Vero cells alone, ts in HuH-7 cells alone, ts in both cell types, att in suckling mouse brains, and att in SCID-HuH-7 mice.

The usefulness of mutant viruses expressing these phenotypes has already been described, however charge-cluster-to-alanine mutant viruses possess some additional desirable characteristics. First, the relevant mutations are envisioned as being designed for use in the genes encoding the non-structural proteins of DEN4, and therefore are envisioned as being useful to attenuate DEN1, DEN2, and DEN3 antigenic chimeric recombinants possessing a DEN4 vector background. Second, the phenotype is usually specified by three or more nucleotide changes, rendering the likelihood of reversion of the mutant sequence to that of the wild type sequence less than for a single point mutation, such as mutations identified in the panel of 5-FU mutant viruses. Finally, charge-cluster-to-alanine attenuating mutations are envisioned as being easily combinable among themselves or with other attenuating mutations to modify the attenuation phenotype of DEN4 vaccine candidates or of DEN1, DEN2, and DEN3 antigenic chimeric recombinant viruses possessing a DEN4 vector background.

Charge-Cluster-to-Alanine-Mutagenesis. The cDNA p4, from which recombinant wild type and mutant viruses were generated, has been described in Examples 1, 2, and 3 and in FIG. 4. Charge-cluster-to-alanine mutagenesis (Muylaert, I. R. et al. 1997 J Virol 71:291-8), in which pairs of charged amino acids are replaced with alanine residues, was used to individually mutagenize the coding sequence for 80 pairs of contiguous charged amino acids in the DEN4 NS5 gene. Subclones suitable for mutagenesis were derived from the full length DEN4 plasmid (p4) by digestion with XmaI/PstI

(pNS5A), PstI/SacII (pNS5B) or SacII/MluI (pNS5C) at the nucleotide positions indicated in FIG. 4. These fragments were then subcloned and Kunkel mutagenesis was conducted as described in Examples 1 and 3. To create each mutation, oligonucleotides were designed to change the sequence of individual pairs of codons to GCAGCX (SEQ ID NO: 69), thereby replacing them with two alanine codons (GCX) and also creating a BbvI restriction site (GCAGC) (SEQ ID NO: 70). The BbvI site was added to facilitate screening of cDNAs and recombinant viruses for the presence of the mutant sequence. Restriction enzyme fragments bearing the alanine mutations were cloned back into the full-length p4 plasmid as described in Examples 1 and 3.

Initial evaluation of the phenotype of the 32 charge-cluster-to-alanine mutant viruses revealed a range in restriction of replication in suckling mouse brain and SCID-HuH-7 mice. To determine whether attenuation could be enhanced by combining mutations, double mutant viruses carrying two pairs of charge-cluster-to-alanine mutations were created by swapping appropriate fragments carrying one pair of mutations into a previously-mutagenized p4 cDNA carrying a second pair of mutations in a different fragment using conventional cloning techniques.

Transcription and Transfection. 5'-capped transcripts were synthesized in vitro from mutagenized cDNA templates using AmpliCap SP6 RNA polymerase (Epicentre, Madison, Wis.). Transfection mixtures, consisting of 1 μ g of transcript in 60 μ l of HEPES/saline plus 12 μ l of dioleoyl trimethylammonium propane (DOTAP) (Roche Diagnostics Corp., Indianapolis, Ind.), were added, along with 1 ml Virus production-serum free medium (VP-SFM) to subconfluent monolayers of Vero cells in 6-well plates. Transfected monolayers were incubated at 35° C. for approximately 18 hr, cell culture medium was removed and replaced with 2 ml VP-SFM, and cell monolayers were incubated at 35° C. After 5 to 6 days, cell culture medium was collected, and the presence of virus was determined by titration in Vero cells followed by immunoperoxidase staining as previously described. Recovered virus was amplified by an additional passage in Vero cells, and virus suspensions were combined with SPG (sucrose-phosphate-glutamate) stabilizer (final concentration: 218 mM sucrose, 6 mM L-glutamic acid, 3.8 mM potassium phosphate, monobasic, and 7.2 mM potassium phosphate, dibasic, pH 7.2), aliquoted, frozen on dry ice, and stored at -70° C.

cDNA constructs not yielding virus after transfection of Vero cells were used to transfect C6/36 cells as follows. Transfection mixtures, as described above, were added, along with 1 ml of MEM containing 10% fetal bovine serum (FBS), 2 mM L-glutamine, 2 mM non-essential amino acids, and 0.05 mg/ml gentamicin, to monolayers of C6/36 cells. Transfected cell monolayers were incubated at 32° C. for 18 hr, cell culture medium was removed and replaced with 2 ml fresh medium, and cell monolayers were incubated at 32° C. After 5 to 6 days, cell culture media were then used to infect Vero cells and incubated for 5-6 days, at which time cell culture media were collected, frozen and titered as described above.

Recovered viruses were biologically cloned by two rounds of terminal dilution in Vero cells followed by an additional amplification in Vero cells. Briefly, virus was initially diluted to a concentration of approximately 20 PFU/ml in VP-SFM and then subjected to a series of two-fold dilutions across a 96-well plate. Virus dilutions were used to infect Vero cell monolayers in a 96-well plate and incubated for 5 to 6 days at 35° C. Following incubation, cell culture media were removed and temporarily stored at 4° C., and the virus-positive cell monolayers were identified by immunoperoxidase

staining. Terminal dilution was achieved when $\leq 25\%$ of cell monolayers were positive for virus. Cell culture medium from a positive monolayer at the terminal dilution was subjected to an additional round of terminal dilution. Following the second terminal dilution, virus was amplified in Vero cells (75 cm² flask), collected and frozen as previously described.

Assays for temperature-sensitivity and mouse attenuation. Assay of the level of temperature sensitivity of the charge-cluster-to-alanine mutant viruses in Vero and HuH-7 cells and their level of replication in the brain of suckling mice were conducted as described in Example 1 and assay of the level of replication in SCID-HuH-7 mice was conducted as described in Example 3.

Charge-cluster-to-alanine mutant viruses are viable and show temperature-sensitive and mouse attenuation phenotypes. Of 80 full-length DEN4 cDNA constructs containing a single pair of charge-to-alanine mutations, virus was recovered from 32 in either Vero or C6/36 cells (FIG. 5). The level of temperature sensitivity of wt rDEN4, rDEN4 Δ 30, and the 32 mutant viruses is summarized in Table 20. One mutant virus (645-646) was ts in Vero but not HuH-7 cells and 7 mutant viruses were ts in HuH-7 but not Vero cells. Such mutants whose temperature sensitivity is host-cell dependent are referred to as temperature-sensitive, host-range (tshr) mutants. Thirteen mutant viruses were ts in both cell types, and 11 mutant viruses were not ts on either cell type. Thus a total of 21 mutant viruses were ts with 8 mutant viruses exhibiting an tshr specificity. None of the mutant viruses showed a small plaque phenotype at permissive temperature. Mutant viruses showed a wide range (0 to 10,000-fold) of restricted replication in suckling mouse brain (Table 20). Fourteen mutant viruses were attenuated in suckling mouse brain, arbitrarily defined as a ≥ 1.5 log₁₀-unit reduction in virus titer. There was no correlation between attenuation in mouse brain and temperature sensitivity in either Vero cells (Kendall Rank correlation: P=0.77) or HuH-7 cells (Kendall Rank correlation: P=0.06).

Thirteen mutant viruses that either showed an att phenotype in suckling mouse brain or whose unmutated charged amino acid pair was highly conserved among the four DEN serotypes (see Example 7) were assayed for att in SCID-HuH-7 mice (Table 21). Three of these mutant viruses showed >100-fold decrease in replication relative to wild type DEN4. Overall, mean log reduction from wild type in suckling mice did not show significant correlation with mean log reduction in SCID-HuH-7 mice (Spearman rank correlation, N=13, P=0.06). However, mutant virus 200-201 was unusual in that it showed a high level of restriction in SCID-HuH-7 mice but little restriction in suckling mouse brain. When virus 200-201 was removed from the analysis, restriction of replication in suckling and SCID-HuH-7 mice showed a significant correlation (Spearman rank correlation, N=12, P=0.02).

Combining charge-cluster-to-alanine mutations present in two viruses into one virus can enhance its ts and att phenotypes. Six paired mutations were combined into fourteen double-pair mutant viruses, of which six could be recovered in Vero or C6/36 cells (Table 22). All of the individual paired mutations used in double-pair mutant viruses were ts on HuH-7 cells, none was ts in Vero cells, and for all combinations at least one mutation pair conferred an att phenotype in suckling mouse brain. Evaluation of four of the double-pair mutant viruses (Table 23) revealed that combining charge-cluster-to-alanine mutation pairs invariably resulted in the acquisition of a ts phenotype in Vero cells (4 out of 4 viruses) and often resulted in a lowered shutoff temperature in HuH-7 cells (3 out of 4 viruses). In half of the viruses assayed, combination of charge-cluster-to-alanine mutation pairs

resulted in enhanced restriction of replication (10-fold greater than either component mutation) in suckling mouse brain (Table 23) and in SCID-HuH-7 mice (Table 24).

Summary. The major usefulness of the charge-cluster-to-alanine mutations stems from their design: they are located in the DEN4 non-structural gene region and therefore are envisioned as being useful to attenuate DEN4 itself as well as antigenic chimeric viruses possessing the DEN4 NS gene region. Furthermore, they are predicted to be phenotypically more stable than the single-nucleotide substitution mutant viruses such as the 5-FU mutant viruses. Finally, combinations of mutations are envisioned as being created in order to fine-tune attenuation and to further stabilize attenuation phenotypes.

Example 5

Identification and Characterization of DEN4 Mutant Viruses Restricted in Replication in Mosquitoes

Section 1. Identification of Viruses Showing Restriction of Replication in Mosquitoes.

In Examples 1 and 4, DEN4 mutant viruses were generated through 5-FU mutagenesis and charge-cluster-to-alanine mutagenesis, respectively, in order to identify mutations that confer ts, sp and att phenotypes. Another highly desirable phenotype of a dengue virus vaccine is restricted growth in the mosquito host. A dengue virus vaccine candidate should not be transmissible from humans to mosquitoes in order to prevent both the introduction of a dengue virus into an environment in which it is currently not endemic and to prevent the possible loss of the attenuation phenotype during prolonged replication in an individual mosquito host. Loss of the attenuation phenotype could also occur following sustained transmission between humans and mosquitoes. Recently, loss of attenuation of a live attenuated poliovirus vaccine was seen following sustained transmission among humans (CDC 2000 MMWR 49:1094).

In the present example, a panel of 1248 DEN4 mutant viruses generated through 5-FU mutagenesis and 32 DEN4 mutant viruses generated through charge-cluster-to-alanine mutagenesis were assayed for restricted growth in mosquito cells. This is a useful preliminary assay for restriction in vivo, since restriction in cultured mosquito cells is often, though not always, associated with poor infectivity for mosquitoes (Huang, C. Y et al. 2000 J Virol 74:3020-8). Mutant viruses that showed restriction in mosquito cells and robust growth in Vero cells (the substrate for vaccine development, as discussed in Example 6) were targeted for further characterization.

Generation and characterization of the 5-1A1 mutant. The generation and isolation of the panel of 1248 5-FU mutant viruses and the panel of 32 charge-cluster-to-alanine mutant viruses have been described in Examples 1, 2, and 4. Vero and C6/36 cells were maintained as described in Example 1.

Each of the 1248 5-FU mutant viruses and 32 charge-cluster-to-alanine mutant viruses was titered in C6/36 cell monolayers in 24-well plates at 32° C. and 5% CO₂. After 5 days, plaques were immunostained with anti-DEN4 rabbit polyclonal antibody and counted as described in the preceding Examples. Mutant viruses were assayed for one of two phenotypes indicating restricted growth in mosquito cells: either sp in C6/36 cells relative to Vero cells or a ≥ 3.5 log₁₀PFU/ml decrease in titer between Vero and C6/36 cells at the permissive temperature for each cell type. Two mutant viruses, one generated by 5-FU mutagenesis (#5) and one generated by charge-cluster-to-alanine mutagenesis (rDEN4-

356,357), showed reduced plaque size in C6/36 cells. After three terminal dilutions, the 5-FU mutant #5, designated 5-1A1, maintained the reduced plaque size phenotype. Additionally, recombinant virus rDEN4-7546, tested for Vero cell adaptation (discussed in detail in Example 6) also showed reduced plaque size in C6/36 (FIG. 10).

The multicycle growth kinetics of both 5-1A1 and the recombinant wild type rDEN4 in C6/36 cells were determined as described in Example 1. Briefly, cells were infected in triplicate at a multiplicity of infection of 0.01 and samples were harvested at 24-hr intervals. Samples were flash frozen and titered in a single assay in Vero cell monolayers.

Oral infection of mosquitoes. *Aedes aegypti* is one of the primary vectors of dengue virus (Gubler, D. J. 1998 Clin Microbiol Rev 11:480-96). This species was reared at 26° C. and 80% relative humidity (RH) with a 16 hr daylight cycle. Adults were allowed continuous access to a cotton pad soaked in a 10% sucrose solution. Five to ten day old female *Ae. aegypti* which had been deprived of a sugar source for 48 hr were fed a bloodmeal consisting of equal volumes of washed human red blood cells, 10% sucrose solution, and dengue virus suspension. The infected blood meal was prepared immediately prior to feeding and offered to mosquitoes in a water-jacketed feeder covered in stretched parafilm and pre-heated to 38° C. (Rutledge, L. C. et al. 1964 Mosquito News 24:407-419). Mosquitoes that took a full bloodmeal within 45 min were transferred to a new container by aspirator and maintained as described above. After 21 days, mosquitoes were stored at -20° C. until dissection.

Intrathoracic inoculation of mosquitoes. The large, non-haematophagous mosquito *Toxorhynchites splendens* is a sensitive host for determining the infectivity of dengue virus. This species was reared at 24° C. and 75% RH with a 12 hr daylight cycle. Larvae and pupae were fed on appropriately sized *Aedes* larvae; adults were allowed continuous access to a cotton pad soaked in a 10% sucrose solution. Groups of one to ten day old adult *T. splendens* of both sexes were immobilized by immersion of their container in an icewater bath and inoculated intrathoracically with undiluted virus and serial tenfold dilutions of virus in 1×PBS. Virus was inoculated in a 0.22 µl dose using a Harvard Apparatus microinjector (Medical Systems Corp, Greenvale N.Y.) and a calibrated glass needle (technique is a modification of the method described in Rosen and Gubler, 1974).

Detection of viral antigen in body and head tissues by immunofluorescence assay (IFA). Head and midgut preparations of *Aedes aegypti* and head preparations of *Toxorhynchites splendens* were made on glass slides as described in Sumanochitrapon et al. (Sumanochitrapon, W. et al. 1998 Am J Trop Med Hyg 58:283-6). Slides were fixed in acetone for 20 min, and placed at 4° C. until processed by IFA. The primary antibody, hyperimmune mouse ascites fluid specific for DEN-4 (HMAF), was diluted 1/100 in PBS-Tween 20 (0.05%). Slides were incubated at 37° C. in a humid chamber for 30 min, and subsequently rinsed in PBS-Tween 20. The secondary antibody, FITC conjugated goat anti-mouse IgG (KPL, Gaithersburg, Md.), was diluted 1/200 in PBS-Tween 20 with 0.002% Evan's Blue. Slides were viewed on an Olympus BX60 microscope. The infectious dose required to infect 50% of mosquitoes (ID₅₀) was determined by the method of Reed and Muench (Reed, L. J. & Muench, H. 1938 Am J Hyg 27:493-497). For *Aedes aegypti* infections, two OID₅₀ (oral infectious dose 50) values were calculated for each virus: the OID₅₀ required to produce an infection in the midgut, with or without dissemination to the head, and the OID₅₀ required to produce disseminated infection. For *Tx. splendens* one MID₅₀ (mosquito infectious dose 50) value was calculated.

Statistical Analysis. The percentage of mosquitoes infected by different viruses were compared using logistic regression analysis (Statview, Abacus Inc.).

Mutations restricting growth of DEN4 in mosquito cells but not Vero cells are rare. Out of 1280 mutant viruses initially assayed, only two, #5 and rDEN4-356,357, showed reduced plaque size in C6/36 cells and normal plaque size in Vero cells. One additional virus, rDEN4-7546 (described in Example 6), with reduced plaque size in C6/36 was detected in subsequent assays. Mutant virus #5 was cloned by three successive terminal dilutions and designated 5-1A1; rDEN4-7546 and rDEN4-356,357 had already been twice-terminally diluted when they were tested in C6/36 cells. Virus 5-1A1 has been extensively characterized and its phenotypes are described in detail in the following section. rDEN4-356,357 and rDEN4-7546 are envisioned as being characterized in a similar fashion.

Plaque size and growth kinetics of 5-1A1. 5-1A1 replicated to 6.7 log₁₀PFU/ml in Vero cells with normal plaque size and replicated to 7.6 log₁₀PFU/ml in C6/36 cells with small plaque size (FIG. 6, Table 25). In comparison, wild type DEN4 used as a concurrent control replicated to 7.3 log₁₀PFU/ml in Vero cells, 8.3 log₁₀PFU/ml in C6/36 cells, and showed normal plaque size in both cell types (FIG. 6, Table 25). The growth kinetics of 5-1A1 was compared to that of wild type DEN4 by infecting C6/36 cells at an MOI of 0.01 and monitoring the production of infectious virus. The kinetics and magnitude of replication of 5-1A1 in C6/36 cells was comparable to that of wild type DEN4 (FIG. 7).

5-1A1 is restricted in its ability to infect mosquitoes. 5-1A1 was evaluated for its ability to infect *Aedes aegypti* mosquitoes through an artificial bloodmeal (Table 26). In this assay the ability to infect the midgut of the mosquito and the ability for a midgut infection to disseminate to the head are measured separately. The oral infectious dose 50 (OID₅₀) of wild type DEN4 for the midgut was 3.3 log₁₀PFU; the OID₅₀ of wild type DEN4 for a disseminated infection was 3.9 log₁₀PFU. In contrast, 5-1A1 never infected 50% of mosquitoes at the doses used. In order to calculate the OID₅₀ for midgut infections by 5-1A1, it was assumed that at a 10-fold higher dose, 100% of 25 mosquitoes would have become infected. Using this assumption, the conservative estimate of the OID₅₀ for midgut infections by 5-1A1 was ≥3.9 log₁₀PFU. Because 5-1A1 produced only 3 disseminated infections, we did not attempt to calculate an OID₅₀ for this category. 5-1A1 was significantly restricted in its ability to infect the midgut relative to wild type DEN4 (logistic regression, N=150, P<0.001). Additionally, 5-1A1 produced very few disseminated infections, but because of low numbers this result was not amenable to statistical analysis.

5-1A1 was also significantly restricted in its ability to infect *Tx. splendens* mosquitoes following intrathoracic inoculation (Table 27). The MID₅₀ of wild type DEN4 was 2.3 log₁₀PFU whereas the MID₅₀ of 5-1A1 was estimated to be >3.0 log₁₀ PFU (logistic regression, N=36, P<0.01).

5-1A1 does not show a ts or an att phenotype. 5-1A1 was tested for temperature sensitivity in Vero and HuH-7 cells and for attenuation in suckling mouse brains as described in Example 1. The mutant virus was not temperature sensitive, as defined in Example 1, and was not attenuated in suckling mouse brain (Table 25).

Identification and confirmation of the mutation responsible for the phenotype of 5-1A1. The nucleotide sequence of the entire genome of 5-1A1 was determined as described in Example 1. Sequencing of 5-1A1 revealed three changes from the wild type sequence: two translationally-silent point mutations at positions 7359 and 9047, and one coding point

mutation (C to U) at position 7129 in the NS4B gene which resulted in a proline to leucine substitution.

To formally confirm the effect of the C7129U mutation, the mutation was inserted into the cDNA p4, which has been described in Examples 1, 2, and 3 and in FIG. 4, using Kunkel mutagenesis as described in Examples 1 and 3. The mutagenized cDNA was transcribed and transfected as described in Example 3, and the resulting virus, after two terminal dilutions, was designated rDEN4-7129-1A. Like 5-1A1, rDEN4-7129-1A showed normal plaque size and titer in Vero cells and reduced plaque size and normal titer in C6/36 cells (Table 25). rDEN4-7129-1A was not ts on either Vero or HuH-7 cells and was not att in suckling mouse brain. Additionally, rDEN4-7129-1A did not show the SCID-HuH-7 att phenotype described in Example 3 (Table 25). The ability of rDEN4-7129-1A to infect mosquitoes is envisioned as being tested in both *Ae. aegypti* and *Tx. splendens*.

To test the compatibility of the C7129U mutation and the Δ30 deletion, the C7129U mutation was inserted into rDEN4Δ30 using previously described techniques. The resulting virus, designated rDEN4Δ30-7129, is envisioned as being tested for the phenotypes listed in Table 25.

In summary, three mutant viruses, 5-1A1, rDEN4-356,357 and rDEN4-7546, showed a particular combination of phenotypes characterized by normal plaque size and replication to high titers in Vero cells and small plaque size but unrestricted growth in mosquito cells. 5-1A1 was further characterized and lacked temperature sensitivity in either Vero or HuH-7 cells and showed normal levels of replication in mouse brain and in SCID-HuH-7 mice and restricted infectivity for both *Ae. aegypti* and *Tx. splendens* mosquitoes. In comparison to wild type rDEN4, the 5-1A1 mutant had one coding mutation: a point mutation (C to U) at nucleotide 7129 in NS4B resulting in a replacement of Pro with Leu. Because 5-1A1 contains only a single missense mutation, the phenotype of this mutant virus can be attributed to the effect of the mutation at position 7129. These results indicate that the 7129 mutation is responsible for the phenotype of decreased infectivity for mosquitoes and is predicted to be useful to restrict replication of vaccine candidates in mosquitoes. To formally confirm this, we have inserted the 7129 mutation into a recombinant DEN4 virus. The resulting virus, designated rDEN4-7129-1A, shows an absence of ts and att phenotypes similar to 5-1A1. It is envisioned as being tested for mosquito infectivity.

The 7129 mutation is a valuable point mutation to include in a DEN4 vaccine candidate and into each of the dengue virus antigenic chimeric vaccine candidates since its biological activity is host specific, i.e., it is restricted in replication in mosquitoes but not in mammals. Moreover, as discussed in Example 6, the 7129 mutation has also been shown to enhance replication in Vero cells. Thus, its insertion into a vaccine candidate is envisioned as enhancing vaccine production in tissue culture without affecting the biological properties specified by other attenuating mutations. It is also envisioned as providing a useful safeguard against mosquito transmission of a dengue virus vaccine.

Section II. Design of Mutations to Restrict Replication in Mosquitoes

In Section 1 of Example 5, we screened a large panel of mutant viruses carrying both random mutations (generated with 5-fluorouracil) and specific mutations (generated through charge-cluster-to-alanine mutagenesis) for restricted growth in C6/36 cells, a proxy measure for restriction in mosquitoes. However, in neither case were mutations designed for the specific purpose of restricting replication in mosquitoes. In this section, we identified nucleotide

sequences in the 3' UTR that show conserved differences between the mosquito-transmitted and tick-transmitted flaviviruses. We then altered those sequences in the DEN4 cDNA p4 by either deleting them altogether or exchanging them with the homologous sequence of the tick-transmitted Langat virus. The resulting viruses were assayed for reduced plaque size and titer in both Vero and C6/36 cells and for infectivity for *Ae. aegypti* and *Tx. splendens*.

Identification and modification of particular 3' UTR sequences showing conserved differences between vectors. Several studies (Olsthoom, R. C. & Bol, J. F. 2001 RNA 7:1370-7; Proutski, V. et al. 1997 Nucleic Acids Res 25:1194-202) have identified conserved differences in the nucleotide sequences of the 3' UTR of mosquito-transmitted and tick-transmitted flaviviruses. Such differences are concentrated in the 3' terminal core region, the approximately 400 3' terminal nucleotides. It has been suggested that these sequences may have a vector-specific function (Proutski, V. et al. 1997 Nucleic Acids Res 25:1194-202). While such a function has not been identified, it may nonetheless be possible to disrupt vector infectivity by deleting or otherwise altering these nucleotides.

To identify target sequences for this type of alteration, we constructed an alignment of the 3' UTR nucleotide sequences of seven mosquito-transmitted flaviviruses and four tick-transmitted flaviviruses (FIG. 8). From this alignment, we identified several sequences that showed conserved differences between the mosquito-transmitted flaviviruses and tick-transmitted flaviviruses. We then designed primers to alter these sequences in the wt DEN4 cDNA p4 (FIG. 4) in one of two ways: 1) deletion of the nucleotides (Δ) or 2) replacement of the nucleotides with the homologous sequence from the tick-transmitted flavivirus Langat (swap). Langat was chosen as the template for swapped nucleotides because it is naturally attenuated (Pletnev, A. G. 2001 Virology 282:288-300), and therefore unlikely to enhance the virulence of rDEN4 virus derived from the modified cDNA. The DEN4 sequences altered and the mutagenesis primers used to do so are listed in Table 28. Nucleotides 10508-10530 correspond to the CS2 region identified in previous studies (Proutski, V. et al. 1997 Nucleic Acids Res 25:1194-202).

Mutagenesis of p4, transcription and transfection were conducted as previously described in Section I of this Example. All five of the engineered viruses were recovered, and all were subjected to two rounds of terminal dilution as previously described.

Evaluation of phenotypes: cell culture. Viruses were titered in Vero and C6/36 cells as previously described, and the results are listed in Table 29. All of the viruses replicated to >5.0 log₁₀PFU/ml; one of them (rDEN4Δ10508-10530) replicated to >8.0 log₁₀PFU/ml. Only one of the viruses (rDEN4Δ10535-10544) was small plaque in C6/36 cells; this virus showed wild-type plaque size in Vero cells. Interestingly, another virus (rDEN4swap10508-10539) showed wild type plaque size in C6/36 cells but was sp in Vero cells.

Evaluation of phenotypes: mosquito infectivity. To date one of the five viruses has been tested for infectivity via intrathoracic inoculation in *Tx. splendens*, using previously described methods. Virus rDEN4Δ10508-10530 was dramatically restricted in infectivity relative to the wild type (Table 30). So few mosquitoes were infected that it was not possible to calculate an MID₅₀ for this virus.

One of the five viruses has been tested for infectivity of *Ae. aegypti* fed on an infectious bloodmeal using previously described methods. rDEN4swap10535-10544 (Table 31) caused significantly fewer midgut infections than wild type rDEN4, but the percentage of disseminated infections did not

differ between rDEN4swap10535-10544 and wild type rDEN4. All of the viruses are envisioned as being tested for mosquito infectivity using both methods.

Summary. In this example we have outlined two different strategies for preventing mosquito transmission of a dengue vaccine. First, several small substitution mutations, including two point mutations and one paired charge-to-alanine substitution, have been shown to restrict the replication of DEN4 in mosquito C6/36 cells in cell culture, and one of these mutations (C7129U) has been shown to restrict the ability of DEN4 virus to infect mosquitoes. Second, we have created a variety of deletion and substitution mutations in regions of the DEN4 3' UTR that show conserved differences between mosquito-transmitted and tick-transmitted flaviviruses. One of these viruses is sp in C6/36 cells and at least two of these viruses show some degree of restriction of mosquito infectivity. By design, the nucleotide sequences in which these mutations were made are highly conserved among the four dengue serotypes and among mosquito-transmitted flaviviruses in general, indicating that they are portable to other vaccine candidates for mosquito-borne flaviviruses. All of the mutations discussed in this Example lie outside the structural genes and so are envisioned as being useful in constructing antigenic-chimeric vaccine candidates.

Example 6

Adaptation Mutations which Enhance the Replication of DEN4 and DEN4 Chimeric Viruses in Vero Cells

Vero cells are a highly characterized substrate that should be suitable for the manufacture of live attenuated flavivirus vaccines, such as dengue virus and tick-borne encephalitis virus. In addition, Vero cells can also be used to grow flaviviruses to high titer for the preparation of an inactivated virus vaccine. Optimal sequences for the efficient growth of dengue viruses in Vero cells have not been identified, but it is well known that flaviviruses accumulate mutations during passage in various cell cultures (Dunster, L. M. et al. 1999 *Virology* 261:309-18; Theiler, M. & Smith, H. H. 1937 *J Exp Med* 65:787-800). Inclusion of specific sequences in live attenuated viruses that enhance their replication in Vero cells and increase the number of doses of vaccine produced per unit substrate would greatly facilitate their manufacture. Similarly, inclusion of Vero cell growth-promoting sequences in wild type viruses used for the preparation of an inactivated virus vaccine would also greatly facilitate the manufacture of the vaccine. The present example identifies mutations that occur following passage of DEN4 virus and DEN2/4 chimeric viruses in Vero cells. Data derived from five sources provided information for this analysis making it possible to generate a list of Vero cell growth-promoting sequences.

Presence of identical mutations in multiple 5-FU mutant viruses. First, as described in Examples 1 and 2, the genomes of 42 dengue virus clones isolated from a 5-FU mutagenized stock of virus were completely sequenced. If mutations that enhance replication occurred during the passage of these 42 mutant viruses in Vero cells, then such mutations should reveal themselves by representation in more than one clone. Analysis of the 42 sequences revealed the occurrence of specific missense mutations in coding regions or nucleotide substitutions in UTRs in multiple clones that are not present in the 2A parental virus genome (Tables 11 and 32). These mutations, many of which occur within a 400 nucleotide section of the NS4B coding region, represent Vero cell-adaptation mutations. One mutation, such as the 4995 mutation,

present in eight viruses was found to specify both ts and att phenotypes (Examples 1 and 3). In contrast, the 7163 mutation, present in six viruses, does not specify a ts or att phenotype (Table 13) and thus is an example of a specific Vero cell growth-promoting mutation.

Presence of Vero cell adaptation mutations in other DEN4 viruses and DEN2/4 antigenic chimeric viruses. Second, the 2A-13 dengue virus that was used as a parallel passaged wild type control during the 5-FU experiments described in Example 1 was grown and cloned in Vero cells in the absence of 5-FU in a manner identical to that of the 5-FU treated viruses. Sequence analysis of this 5-FU untreated virus, designated 2A-13-1A1, revealed that the virus genome contained a mutation at nucleotide 7163 (Example 1 and Table 32), identical to the missense mutation previously identified in 6 of the 5-FU mutant viruses (Tables 11 and 32). This indicates that growth and passage of DEN4 virus in Vero cells is sufficient to acquire this specific mutation, i.e. mutagenesis with 5-FU is not required. Thus, information from two separate sources indicates that the 7163 mutation appeared in separate Vero cell passaged viruses, thereby strengthening the interpretation that this mutation is growth promoting.

Third, following passage of the 2AΔ30 and rDEN4Δ30 in Vero cells, sequence analysis revealed the presence of a mutation at nucleotides 7153 and 7163, respectively. These two mutations were also previously identified among the 5-FU treated viruses (Table 32). Again, identical mutations appeared following independent passage of virus in Vero cells, corroborating the hypothesis that these mutations confer a growth advantage in Vero cells.

Fourth, an antigenic chimeric dengue virus vaccine candidate was generated that expressed the structural proteins C, prM, and E from DEN2 on a DEN4 wild type genetic background or an attenuated Δ30 genetic background. To construct this virus, the C, prM and E region of wild type cDNA plasmid p4 was replaced with a similar region from DEN2 virus strain NGC (FIG. 10). Specifically, nucleotides between restriction sites Bg/II (nt 88) and XhoI (nt 2345) of p4 were replaced with those derived from dengue type 2 virus. RNA transcripts synthesized from the resulting p4-D2 plasmid were transfected into Vero cells and rDEN2/4 virus was recovered. A further attenuated version of this chimeric virus containing the Δ30 mutation, rDEN2/4Δ30, was recovered in C6/36 mosquito cells following transfection of cells with RNA transcripts derived p4Δ30-D2. However, rDEN2/4Δ30 could not be recovered directly in Vero cells. The rDEN2/4Δ30 mutant virus recovered in C6/36 cells replicated to very low levels in Vero cells (<1.0 log₁₀PFU/ml) but grew to high titer in C6/36 cells (>6.0 log₁₀PFU/ml). Genomic sequence of the C6/36-derived virus matched the predicted cDNA sequence and is shown in Appendix 3. Nevertheless, when C6/36-derived rDEN2/4Δ30 was serially passaged 3 to 4 times in Vero cells, a virus population adapted for growth in Vero cells emerged. Virus from this Vero cell-adapted preparation was cloned and amplified in Vero cells to a titer >6.0 log₁₀PFU/ml. The genomic sequence was determined for 2 independent virus clones and compared to the predicted cDNA sequence (Table 33 and 34). Each cloned virus contains a mutation in a non-structural gene which coincides closely in location or sequence with a mutation previously identified among the panel of 5-FU mutagenized viruses. The other mutations in these two clones also might confer a growth advantage in Vero cells. Importantly, the mutations identified in Tables 33 and 34 are absolutely required for replication in Vero cells, and it would not be possible to

produce the rDEN2/4Δ30 vaccine candidate in Vero cells without the growth-promoting mutations identified in Tables 33 and 34.

Fifth, sequence analysis of the dengue 4 wild-type virus strain 814669 (GenBank accession no. AF326573) following passage in Vero cells identified a mutation in the NS5 region at nucleotide 7630 which had previously been identified among the panel of 5-FU mutagenized viruses (Table 32). This mutation at nucleotide 7630 was introduced into recombinant virus rDEN4 by site-directed mutagenesis as described in Table 16. The resulting virus, rDEN4-7630, was not temperature sensitive when tested at 39° C., indicating that mutation 7630 does not contribute to temperature sensitivity.

Characterization of rDEN2/4Δ30 chimeric viruses containing single and multiple Vero cell adaptation mutations. The generation of chimeric virus rDEN2/4Δ30 provided a unique opportunity for evaluating the capacity of individual mutations to promote increased growth in Vero cells. Because rDEN2/4Δ30 replicates to very low titer in Vero cells, yet can be efficiently generated in C6/36 mosquito cells, recombinant virus bearing putative Vero-cell adapting mutations were first generated in C6/36 cells and then virus titers were determined in both C6/36 and Vero cells. As shown in Table 35, addition of a single mutation to rDEN2/4Δ30 resulted in a greater than 1000-fold increase in titer in Vero cells, confirming the Vero cell adaptation phenotype conferred by these mutations. However, the combination of two separate mutations into a single virus did not increase the titer in Vero cells beyond the level observed for viruses bearing a single adaptation mutation. Inclusion of either the 7182 or 7630 mutation in the cDNA of rDEN2/4Δ30 allowed the virus to be recovered directly in Vero cells, circumventing the need to recover the virus in C6/36 cells.

Characterization of the growth properties of rDEN4 viruses containing single and multiple defined Vero cell adaptation mutations. To confirm the ability of Vero cell adaptation mutations to enhance growth of DEN4 viruses, site-directed mutagenesis was used to generate rDEN4 viruses encoding selected individual mutations as described in Examples 1 and 3. Five mutations in NS4B (7153, 7162, 7163, 7182, and 7546) from the list of repeated mutations in the 5-FU mutant viruses (Table 32) were introduced singly into the p4 cDNA clone. In addition, the mosquito-restricted, rDEN4-7129 virus was evaluated for enhanced growth in Vero cells since the location of this mutation is in the same region of NS4B. Each virus, including wild-type rDEN4, was recovered, terminally diluted, and propagated in C6/36 cells to prevent introduction of additional Vero cell adaptation mutations, however, because of its restricted growth in C6/36 cells, rDEN4-7129 was propagated only in Vero cells.

Plaque size was evaluated for each mutant rDEN4 virus in Vero cells and C6/36 cells and compared to wild-type rDEN4. Six-well plates of each cell were inoculated with dilutions of virus and plaques were visualized five days later. Representative plaques are illustrated in FIG. 10 and demonstrate that the presence of a Vero cell adaptation mutation does indeed confer increased virus cell to cell spread and growth specifically in Vero cells. In C6/36 cells, average plaque size was approximately 0.50 mm for both wild-type rDEN4 and each mutant virus (except for rDEN4-7546 and rDEN4-7129 which were smaller than wild-type; see Example 5). However, rDEN4 viruses expressing mutation 7162, 7163, 7182, and 7129 had a greater than two-fold increase in plaque size in Vero cells compared to wild-type rDEN4 virus. A smaller but consistent increase in plaque size was observed for rDEN4-7153 and rDEN4-7546.

Growth kinetics and virus yield in Vero cells was assessed for the same panel of rDEN4 viruses. Vero cells were infected at an MOI of 0.01 and samples were removed daily for 10 days, titered on Vero cells, and plaques were visualized. The results in FIG. 11 indicate that the presence of a Vero cell adaptation mutation increased the kinetics of virus growth, but had only a marginal effect on the peak virus yield. At day four post-infection, wild-type rDEN4 grew to 5.2 log₁₀PFU/ml while the level of replication in rDEN4-7129-infected cells was 100-fold higher. The rest of the mutant rDEN4 viruses had an increased yield at day four ranging from 0.9 (rDEN4-7153) to 1.6 (rDEN4-7162 and -7163) log₁₀PFU/ml. Interestingly, enhanced kinetics of virus growth correlated with increased plaque size in Vero cells. The peak virus yield was reached by day 6 post-infection for rDEN4-7129, -7162, -7163, and -7182 while wild-type rDEN4 did not reach peak titer until day 10. However, the peak virus yield was only slightly higher in rDEN4 viruses expressing Vero cell adaptation mutations.

In an effort to further enhance rDEN4 replication, especially the peak virus yield, combinations of selected Vero cell adaptation mutations were introduced into the rDEN4 background. Three viruses with dual mutations were generated: rDEN4-7153-7163, rDEN4-7153-7182, and rDEN4-7546-7630 and tested in a Vero cell time course infection as described above along with rDEN4 and rDEN4-7162 as a positive control (FIG. 12). The viruses expressing combined mutations grew in a nearly identical manner to rDEN4-7162 indicating that these selected combinations did not enhance the kinetics or peak virus yield. Additional combinations of these and other Vero cell adaptation mutations are envisioned as increasing peak virus yield.

Discussion. Some of the growth promoting mutations listed in Table 32 are also found in homologous regions of DEN1, DEN2, and DEN3 and are envisioned as serving to promote the replication of these viruses in Vero cells. Specifically, the growth promoting mutations indicated in Table 32 that are present in a DEN4 virus are envisioned as being useful for importation into homologous regions of other flaviviruses, such as DEN1, DEN2 and DEN3. Examples of such conserved regions are shown in Appendix 4 and are listed in Table 36. The nucleotides for both mutation 7129 and 7182 are conserved in all four dengue virus serotypes. It is also interesting to note that mutation 7129 not only increases growth in Vero cells (FIG. 10), but it also forms small plaques in mosquito cells (FIG. 6, Table 25). Lee et al. previously passaged DEN3 virus in Vero cells and performed limited sequence analysis of only the structural gene regions of the resulting viruses (Lee, E. et al. 1997 Virology 232:281-90). From this analysis a menu of Vero adaptation mutations was assembled. Although none of these mutations correspond to the Vero adaptation mutations identified in this Example, a single mutation at amino acid position 202 in DEN3 corresponds to mutation 1542 identified in 5-FU mutant virus #1012. The current Example emphasizes the importance in this type of study of determining the sequence of the entire viral genome.

Vero cell growth optimized viruses are envisioned as having usefulness in the following areas. First, the yield of a live attenuated vaccine virus in Vero cells is predicted to be augmented. The live attenuated vaccine candidate is conveniently a DEN4 or other dengue virus or a DEN 1/4, DEN2/4, or DEN3/4 antigenic chimeric virus, or a chimeric virus of another flavivirus based on the DEN4 background. The increased yield of vaccine virus is envisioned as decreasing the cost of vaccine manufacture. Second, Vero cell adaptation mutations that are attenuating mutations, such as the 4995

mutation, are envisioned as being stable during the multiple passage and amplification of virus in Vero cell cultures that is required for production of a large number of vaccine doses. Third, Vero cell adaptation mutations are actually required for the growth of the rDEN2/4 Δ 30 vaccine candidate in Vero cells. Fourth, the increase in yield of a DEN wild type or an attenuated virus is envisioned as making it economically feasible to manufacture an inactivated virus vaccine. Fifth, the presence of the Vero cell growth promoting mutations in the DEN4 vector of the rDEN1/4, rDEN2/4, and rDEN3/4 antigenic chimeric viruses or other flavivirus chimeric viruses based on DEN4 is envisioned as permitting the viruses to grow to a high titer and as thereby being useful in the manufacture of an inactivated virus vaccine. Sixth, the insertion of Vero cell growth promoting mutations into cDNAs such as rDEN2/4 Δ 30 is envisioned as permitting recovery of virus directly in Vero cells, for which there are qualified master cell banks for manufacture, rather than in C6/36 cells for which qualified cell banks are not available. And seventh, insertion of the 7129 and 7182 mutations into DEN1, DEN2, or DEN3 wt viruses is envisioned as increasing their ability to replicate efficiently and be recovered from cDNA in Vero cells.

Example 7

Assembly of a List of Attenuating Mutations

The data presented in these examples permits the assembly of a list of attenuating mutations that is summarized in Table 37. This list contains individual mutations identified in Tables 13-16, 20, and 21 that are known to independently specify an attenuation phenotype. Mutation 7129 is also included since it is derived from virus 5-1A1 shown to be attenuated in mosquitoes. We envision using various combinations of mutations from this list to generate viruses with sets of desirable properties such as restricted growth in the liver or in the brain as taught in Example 3 (Table 18) and Example 4 (Tables 23 and 24). These mutations are also combinable with other previously described attenuating mutations such as the Δ 30 mutation, as taught in Example 1 (Table 6) and Example 3 (Table 19) to produce recombinant viruses that are satisfactorily attenuated and immunogenic. Mutations listed in Table 37 are also envisioned as being combined with other previously described attenuating mutations such as other deletion mutations or other point mutations (Blok, J. et al. 1992 *Virology* 187:573-90; Butrapet, S. et al. 2000 *J Virol* 74:3011-9; Men, R. et al. 1996 *Virology* 70:3930-7; Puri, B. et al. 1997 *J Gen Virol* 78:2287-91).

The possibility of importing an attenuating mutation present in one paramyxovirus into a homologous region of a second paramyxovirus has recently been described (Durbin, A. P. et al. 1999 *Virology* 261:319-30; Skiadopoulos, M. H. et al. 1999 *Virology* 260:125-35). Such an importation confers an att phenotype to the second virus or, alternatively, further attenuates the virus for growth in vivo. Similarly we envision importing an attenuating mutation present in one flavivirus to a homologous region of a second flavivirus which would confer an att phenotype to the second flavivirus or, alternatively, would further attenuate the virus for growth in vivo. Specifically, the attenuating mutations indicated in Table 37 are envisioned as being useful for importation into homologous regions of other flaviviruses. Examples of such homologous regions are indicated in Appendix 4 for the mutations listed in Table 37.

Example 8

Evaluation of Dengue Virus Vaccine in Humans and Rhesus Monkeys

The present example evaluates the attenuation for humans and rhesus monkeys (as an animal model) of a DEN-4 mutant bearing a 30 nucleotide deletion (Δ 30) that was introduced into its 3' untranslated region by site-directed mutagenesis and that was found previously to be attenuated for rhesus monkeys (Men, R. et al. 1996 *J Virol* 70:3930-7), as representative of the evaluation of any dengue virus vaccine for attenuation in humans and rhesus monkeys (as an animal model).

Viruses and cells. The wild type (wt) DEN-4 virus strain 814669 (Dominica, 1981), originally isolated in *Aedes pseudoscutellaris* (AP61) cells, was previously plaque-purified in LLC-MK2 cells and amplified in C6/36 cells as described (Mackow, E. et al. 1987 *Virology* 159:217-28). For further amplification, the C6/36 suspension was passaged 2 times in Vero (WHO) cells maintained in MEM-E (Life Technologies, Grand Island, N.Y.) supplemented with 10% FBS. Viruses derived from RNA transfection or used for clinical lot development were grown in Vero (WHO) cells maintained in serum-free media, VP-SFM (Life Technologies).

Construction of DEN-4 deletion mutants. A 30 nucleotide (nt) deletion was previously introduced into the 3' untranslated region of the 2A cDNA clone of wt DEN-4 strain 814669 as described (Men, R. et al. 1996 *J Virol* 70:3930-7). This deletion removes nucleotides 10478-10507, and was originally designated 3'd 172-143, signifying the location of the deletion relative to the 3' end of the viral genome. In the current example, this deletion is referred to as Δ 30. The full-length 2A cDNA clone has undergone several subsequent modifications to improve its ability to be genetically manipulated. As previously described, a translationally-silent *XhoI* restriction enzyme site was engineered near the end of the E region at nucleotide 2348 to create clone 2A-*XhoI* (Bray, M. & Lai, C. J. 1991 *PNAS USA* 88:10342-6). In this example, the viral coding sequence of the 2A-*XhoI* cDNA clone was further modified using site-directed mutagenesis to create clone p4: a unique *BbvCI* restriction site was introduced near the C-prM junction (nucleotides 447-452); an extra *XbaI* restriction site was ablated by mutation of nucleotide 7730; and a unique *SacII* restriction site was created in the NS5 region (nucleotides 9318-9320). Each of these engineered mutations is translationally silent and does not change the amino acid sequence of the viral polypeptide. Also, several mutations were made in the vector region of clone p4 to introduce or ablate additional restriction sites. The cDNA clone p4 Δ 30 was generated by introducing the Δ 30 mutation into clone p4. This was accomplished by replacing the *MluI*-*KpnI* fragment of p4 (nucleotides 10403-10654) with that derived from plasmid 2A Δ 30 containing the 30 nucleotide deletion. The cDNA clones p4 and p4 Δ 30 were subsequently used to generate recombinant viruses rDEN4 and rDEN4 Δ 30, respectively.

Generation of viruses. Full-length RNA transcripts were synthesized from cDNA clones 2A and 2A Δ 30 using SP6 RNA polymerase as previously described (Lai, C. J. et al. 1991 *PNAS USA* 88:5139-43; Men, R. et al. 1996 *J Virol* 70:3930-7). The reaction to generate full-length RNA transcripts from cDNA clones p4 and p4 Δ 30 was modified and consisted of a 50 μ l reaction mixture containing 1 μ g linearized plasmid, 60 U SP6 polymerase (New England Biolabs (NEB), Beverly, Mass.), 1 \times RNA polymerase buffer (40 mM Tris-HCl, pH 7.9, 6 mM MgCl₂, 2 mM spermidine, 10 mM

dithiothreitol), 0.5 mM m7G(5')ppp(5')G cap analog (NEB), 1 mM each nucleotide triphosphate, 1 U pyrophosphatase (NEB), and 80 U RNase inhibitor (Roche, Indianapolis, Ind.). This reaction mixture was incubated at 40° C. for 90 min and the resulting transcripts were purified using RNeasy mini kit (Qiagen, Valencia, Calif.). For transfection of Vero cells, purified transcripts (1 µg) were mixed with 12 µl DOTAP liposome reagent (Roche) in saline containing 20 mM HEPES buffer (pH 7.6) and added to cell monolayer cultures in a 6-well plate. After 5-17 days, tissue culture medium was harvested, clarified by centrifugation, and virus was amplified in Vero cells. The presence of virus was confirmed by plaque titration. It should be noted that during the course of transfection and amplification of 2AΔ30 to create the vaccine lot, the virus underwent a total of 6 passages entirely in Vero cells. The remaining viruses, rDEN4 and rDEN4Δ30 were passaged 5 times in Vero cells to generate the virus suspension used for sequence analysis and studies in rhesus monkeys.

Vaccine Production. An aliquot of clarified tissue culture fluid containing vaccine candidate 2AΔ30 was submitted to DynCorp (Rockville, Md.) for amplification of virus in Vero cells and production of a vaccine lot. For vaccine production, 2AΔ30 infected tissue culture supernatant was harvested, SPG buffer added (final concentration: 218 mM sucrose, 6 mM L-glutamic acid, 3.8 mM potassium phosphate, monobasic, and 7.2 mM potassium phosphate, dibasic, pH 7.2), and the virus suspension was clarified by low speed centrifugation. To degrade residual Vero cell DNA, the vaccine suspension was treated with Benzonase endonuclease (American International Chemical, Natick, Mass.), 100 U/ml and incubated for 1 hr at 37° C., followed by high-speed centrifugation (17,000×g, 16 hr). The resulting virus pellet was gently rinsed with MEM-E, resuspended in MEM-E containing SPG, sonicated, distributed into heat-sealed ampoules, and stored frozen at -70° C. Final container safety testing confirmed microbial sterility, tissue culture purity, and animal safety. The 2AΔ30 vaccine lot (designated DEN4-9) has a titer of 7.48 log₁₀ PFU/ml, with a single dose of 5.0 log₁₀ PFU/ml containing <1 pg/ml Vero cell DNA and <0.001 U/ml Benzonase endonuclease.

Sequence of cDNA clones and viral genomes. The nucleotide sequence of the viral genome region of cDNA plasmids 2A and p4 was determined on a 310 genetic analyzer (Applied Biosystems, Foster City, Calif.) using vector-specific and DEN-4-specific primers in BigDye terminator cycle sequencing reactions (Applied Biosystems). The nucleotide sequence of the genomes of the parental wt DEN-4 strain 814669 and of recombinant viruses 2A wt, 2AΔ30 (vaccine lot), rDEN4, and rDEN4Δ30 was also determined. Viral RNA was extracted from virus preparations and serum samples using the QIAamp Viral RNA mini kit (Qiagen). Reverse transcription (RT) was performed using random hexamers and the SuperScript First-Strand Synthesis System for RT-PCR (Life Technologies). Overlapping PCR fragments of approximately 2000 base pairs were generated using optimized DEN-4 specific primers and Advantage cDNA polymerase (Clontech, Palo Alto, Calif.). Both strands of purified PCR fragments were sequenced directly using dye-terminator reactions as described above and results were assembled into a consensus sequence. To determine the nucleotide sequence of the viral RNA 5' and 3' regions, the 5' cap nucleoside of the viral RNA was removed with tobacco acid pyrophosphatase (Epicentre, Madison, Wis.) followed by circularization of the RNA using RNA ligase (Epicentre). RT-PCR was performed as described and a cDNA fragment spanning the ligation junction was sequenced using DEN-4 specific primers. GenBank acces-

sion numbers have been assigned as follows (virus: accession number): 814669: AF326573, 2AΔ30: AF326826, rDEN4: AF326825, and rDEN4Δ30: AF326827.

Human Vaccine Recipients. 20 normal healthy adult volunteers were recruited by the Johns Hopkins School of Hygiene and Public Health Center for Immunization Research (CIR) located in Baltimore, Md. The clinical protocol was reviewed and approved by the Joint Committee for Clinical Investigation of the Johns Hopkins University School of Medicine and informed consent was obtained from each volunteer. Volunteers were enrolled in the study if they met the following inclusion criteria: 18-45 years of age; no history of chronic illness; a normal physical examination; human immunodeficiency virus antibody negative, hepatitis B surface antigen negative, and hepatitis C antibody negative; no stool occult blood; and normal values for complete blood cell count (CBC) with differential, hematocrit, platelet count, serum creatinine, serum aspartate amino transferase (AST), alanine amino transferase (ALT), alkaline phosphatase, bilirubin, prothrombin time (PT), partial thromboplastin time (PTT), and urinalysis. Female volunteers were required to have a negative urine pregnancy test prior to vaccination and on the day of vaccination and to agree to use contraception or abstain from sexual intercourse for the duration of the study. Volunteers also lacked serological evidence of prior flavivirus infection as defined by hemagglutination-inhibition antibody titer <1:10 to DEN-1, DEN-2, DEN-3, DEN-4, St. Louis encephalitis virus, Japanese encephalitis virus, or yellow fever virus and a plaque-reduction neutralization titer <1:10 to DEN-4 and yellow fever virus.

Studies in Humans. Volunteers were immunized in three successive cohorts of four, six, and ten volunteers to assess the safety of the vaccine. In this study, an illness was defined as the following: dengue virus infection associated with a platelet count of <90,000/mm³; serum ALT >4 times normal; oral temperature >38° C. for >2 successive days; or headache and/or myalgia lasting >2 successive days. Systemic illness was defined as the occurrence of fever >38° C. for >2 consecutive days, or any 2 of the following for at least two consecutive study days: headache, malaise, anorexia, and myalgia/arthralgia. The trials were conducted between October and April, a time of low mosquito prevalence, to reduce the risk of transmission of vaccine virus from the volunteers to the community.

On the day of vaccination, vaccine candidate 2AΔ30 was diluted to 5.3 log₁₀ PFU/ml in sterile saline for injection, USP, and each volunteer was injected subcutaneously with a 0.5 ml containing 5.0 log₁₀ PFU of vaccine into the left deltoid region. Volunteers were given a home diary card on which they were to record their temperature twice daily for days 0-5 post-vaccination. The volunteers returned to the clinic each day for examination by a physician and their diary cards were reviewed. The injection site was evaluated for erythema, induration, and tenderness. Clinical signs and symptoms such as headache, rash, petechiae, lymphadenopathy, hepatomegaly, abdominal tenderness, anorexia, nausea, fatigue, myalgia, arthralgia, eye pain, and photophobia were assessed daily. Symptoms were graded as mild (no need for treatment or a change in activity), moderate (treatment needed or change in activity noted, yet still able to continue daily activity) or severe (confined to bed). Blood was drawn for CBC with differential and for virus quantitation on days 0, 2 and 4. Volunteers were admitted to the inpatient unit at the CIR on the sixth day after immunization. The study physician evaluated all volunteers each day by physical examination and interview. The volunteers had their blood pressure, pulse, and temperature recorded four times a day. Blood was drawn each

day for CBC with differential and for virus quantitation and every other day for ALT measurement. Volunteers were confined to the inpatient unit until discharge on study day 15. On study days 28 and 42, volunteers returned for physical examination and blood was drawn for virus quantitation (day 28) and for serum antibody measurement (day 28 and 42).

Virus quantitation and amplification. Serum was obtained for detection of viremia and titration of virus in positive specimens. For these purposes 8.5 ml of blood was collected in a serum separator tube and incubated at room temperature for less than 30 min. Serum was decanted into 0.5 ml aliquots, rapidly frozen in a dry ice/ethanol bath and stored at -70° C. Serum aliquots were thawed and serial 10-fold dilutions were inoculated onto Vero cell monolayer cultures in 24-well plates. After one hour incubation at room temperature, the monolayers were overlaid with 0.8% methylcellulose in OptiMEM (Life Technologies) supplemented with 5% fetal bovine serum (FBS). Following incubation at 37° C. for four days, virus plaques were visualized by immunoperoxidase staining. Briefly, cell monolayers were fixed in 80% methanol for 30 min and rinsed with antibody buffer (5% nonfat milk in phosphate buffered saline). Rabbit polyclonal DEN-4 antibodies were diluted 1:1000 in antibody buffer and added to each well followed by a one hr incubation at 37° C. Primary antibody was removed and the cell monolayers were washed twice with antibody buffer. Peroxidase-labelled goat-anti-rabbit IgG (KPL, Gaithersburg, Md.) was diluted 1:500 in antibody buffer and added to each well followed by a one hr incubation at 37° C. Secondary antibody was removed and the wells were washed twice with phosphate buffered saline. Peroxidase substrate (4 chloro-1-naphthol in H_2O_2) was added to each well and visible plaques were counted.

For amplification of virus in serum samples, a 0.3 ml aliquot of serum was inoculated directly onto a single well of a 6-well plate of Vero cell monolayers and incubated at 37° C. for 7 days. Cell culture fluid was then assayed for virus by plaque assay as described above.

Serology. Hemagglutination-inhibition (HAI) assays were performed as previously described (Clarke, D. H. & Casals, J. 1958 Am J Trop Med Hyg 7:561-73). Plaque-reduction neutralization titers (PRNT) were determined by a modification of the technique described by Russell (Russell, P. K. et al. 1967 J Immunol 99:285-90). Briefly, test sera were heat inactivated (56° C. for 30 min) and serial 2-fold dilutions beginning at 1:10 were made in OptiMEM supplemented with 0.25% human serum albumin. rDEN4 Δ 30 virus, diluted to a final concentration of 1000 PFU/ml in the same diluent, was added to equal volumes of the diluted serum and mixed well. The virus/serum mixture was incubated at 37° C. for 30 min. Cell culture medium was removed from 90% confluent monolayer cultures of Vero cells on 24-well plates and 50 μ l of virus/serum mixture was transferred onto duplicate cell monolayers. Cell monolayers were incubated for 60 min at 37° C. and overlaid with 0.8% methylcellulose in OptiMEM supplemented with 2% FBS. Samples were incubated at 37° C. for 4 days after which plaques were visualized by immunoperoxidase staining as described above, and a 60% plaque-reduction neutralization titer was calculated.

Studies in rhesus monkeys. Evaluation of the replication and immunogenicity of wt virus 814669, and recombinant viruses 2A wt, 2A Δ 30 (vaccine lot), rDEN4, and rDEN4 Δ 30 in juvenile rhesus monkeys was performed as previously described (Men R. et al. 1996 J Virol 70:3930-7). Briefly, dengue virus seronegative monkeys were injected subcutaneously with $5.0 \log_{10}$ PFU of virus diluted in L-15 medium (Quality Biological, Gaithersburg, Md.) containing SPG buffer. A dose of 1 ml was divided between two injections in

each side of the upper shoulder area. Monkeys were observed daily and blood was collected on days 0-10 and 28, and processed for serum, which was stored frozen at -70° C. Titer of virus in serum samples was determined by plaque assay on Vero cells as described above. Neutralizing antibody titers were determined for the day 28 serum samples as described above. A group of monkeys inoculated with either 2A Δ 30 (n=4) or wt virus 814669 (n=8) were challenged on day 42 with a single dose of $5.0 \log_{10}$ PFU/ml wt virus 814669 and blood was collected for 10 days. Husbandry and care of rhesus monkeys was in accordance with the National Institutes of Health guidelines for the humane use of laboratory animals.

Construction and characterization of DEN-4 wild type and deletion mutant viruses. The nucleotide and deduced amino acid sequences of the previously described wt 814669 virus, the DEN-4 2A wt virus derived from it (designated 2A wt), and the 2A Δ 30 vaccine candidate derived from 2A wt virus were first determined. Sequence analysis showed that the wt 814669 virus used in this study had apparently accumulated 2 missense mutations (nucleotides 5826 and 7630) and 3 silent mutations during its passage and amplification since these mutations were not described in previously published reports of the viral sequence (GenBank accession number M14931) and were not present in the 2A cDNA derived from the virus. Sequence comparison between viruses 2A wt and vaccine lot 2A Δ 30 revealed that 2A Δ 30 accumulated 2 missense mutations (nucleotides 7153 and 8308) and also confirmed the presence of the Δ 30 mutation (nucleotides 10478-10507) as well as an additional deletion of nucleotide 10475, which occurred during the original construction of the Δ 30 mutation (Men, R. et al. 1996 J Virol 70:3930-7). This sequence analysis revealed significant sequence divergence between the biologically-derived wt 814669 virus and its recombinant 2A wt derivative and between the 2A wt and 2A Δ 30 virus. Since the 2A wt and 2A Δ 30 viruses differed at nucleotides other than the deletion mutation, the attenuation phenotype previously reported for 2A Δ 30 (Men, R. et al. 1996 J Virol 70:3930-7) could not be formally ascribed solely to the Δ 30 mutation and may have been specified by the mutations at nucleotides 7153, 8308, 10475, or the Δ 30 deletion.

To determine whether the Δ 30 mutation was responsible for the observed attenuation of 2A Δ 30, a second pair of viruses, one with and one without the Δ 30 mutation, were produced for evaluation in monkeys. A new DEN-4 cDNA vector construct, designated p4, was derived from the 2A-XhoI cDNA clone and translationally-silent mutations were introduced to add or ablate several restriction enzyme sites. These sites were added to facilitate the future genetic manipulation of this DEN-4 wt cDNA by the introduction of other attenuating mutations if needed. The sequence of the genomic region of the p4 cDNA plasmid was identical to that of the 2A wt virus except for the engineered restriction site changes and a point mutation at nucleotide 2440 which was introduced during the original mutagenesis of the 2A cDNA plasmid to create the XhoI site (Bray, M. & Lai, C. J. 1991 PNAS USA 88:10342-6). The Δ 30 mutation and the neighboring deletion at nucleotide 10475 were co-introduced into the p4 plasmid by replacing a short restriction fragment with one derived from the cDNA clone of 2A Δ 30. RNA transcripts derived from the p4 cDNA clone and from its Δ 30 derivative each yielded virus (designated rDEN4 wt and rDEN4 Δ 30, respectively) following transfection of Vero cells. Sequence analysis of the rDEN4 virus revealed that during its passage and amplification in Vero cells it accumulated 2 missense mutations (nucleotides 4353 and 6195), a silent mutation (nucleotide 10157), and a point mutation in the 3' untranslated

region (nucleotide 10452). In addition to containing the $\Delta 30$ and the accompanying deletion at nucleotide 10475, rDEN4 $\Delta 30$ had also accumulated a missense mutation (nucleotide 7163) and a silent mutation (nucleotide 7295).

Parental wt 814669 virus and recombinant viruses 2A wt, 2A $\Delta 30$, rDEN4, and rDEN4 $\Delta 30$ each replicate in Vero cells to a titer exceeding $7.0 \log_{10}$ PFU/ml, and their replication is not temperature sensitive at 39°C .

Virus replication, immunogenicity, and efficacy in monkeys. Groups of rhesus monkeys were inoculated with wt DEN-4 814669, 2A wt, rDEN4, 2A $\Delta 30$ and rDEN4 $\Delta 30$ to assess the level of restriction of replication specified by the $\Delta 30$ mutation. Serum samples were collected daily and titer of virus present in the serum was determined by plaque enumeration on Vero cell monolayer cultures. Monkeys inoculated with wt 814669 virus or its recombinant counterparts, 2A wt or rDEN4, were viremic for 3 to 4 days with a mean peak virus titer of nearly $2 \log_{10}$ PFU/ml. Monkeys inoculated with virus 2A $\Delta 30$ or rDEN4 $\Delta 30$ had a lower frequency of viremia (83% and 50%, respectively), were viremic for only about 1 day, and the mean peak titer was 10-fold lower. Monkeys inoculated with DEN-4 814669, 2A wt, or rDEN4 viruses developed high levels of neutralizing antibody, with mean titers between 442 and 532, consistent with their presumed wild type phenotype. Monkeys inoculated with 2A $\Delta 30$ or rDEN4 $\Delta 30$ developed a lower level of neutralizing antibody, with mean titers of 198 and 223, respectively. The decrease in neutralizing antibody titer in response to 2A $\Delta 30$ and rDEN4 $\Delta 30$ is consistent with the attenuation phenotype of these viruses. Monkeys inoculated with either 2A $\Delta 30$ (n=4) or wt 814669 virus (n=8) were challenged after 42 days with wt virus 814669. Dengue virus was not detected in any serum sample collected for up to 10 days following virus challenge, indicating that these monkeys were completely protected following immunization with either wt virus or vaccine candidate 2A $\Delta 30$.

Since DEN-4 814669, 2A wt, and rDEN4 each manifest the same level of replication and immunogenicity in rhesus monkeys, it is reasonable to conclude that the identified sequence differences between these presumptive wild type viruses that arose during passage in tissue culture or during plasmid construction do not significantly affect their level of replication in vivo. Similarly, the comparable level of attenuation of 2A $\Delta 30$ and rDEN4 $\Delta 30$ indicates that the mutations shared by these viruses, namely, the $\Delta 30$ mutation and its accompanying 10475 deletion mutation, are probably responsible for the attenuation of these viruses rather than their incidental sequence differences.

Clinical Response to immunization with 2A $\Delta 30$. The 2A $\Delta 30$ vaccine candidate was administered subcutaneously at a dose of 10^5 PFU to 20 seronegative volunteers. Each of the vaccinees was infected and the virus was well tolerated by all vaccinees. Viremia was detected in 70% of the vaccinees, was present only at low titer, and did not extend beyond day 11.

None of the 20 vaccinees reported soreness or swelling at the injection site. Mild erythema (1-3 mm) around the injection site was noted on examination of 8 volunteers 30 minutes post-vaccination which resolved by the next day in 7 of those volunteers and by the third day in the remaining volunteer. Mild tenderness to pressure at the vaccination site was noted in 2 volunteers and lasted a maximum of 48 hours. During physical examination, ten volunteers (50%) were noted to have a very mild dengue-like erythematous macular rash (truncal distribution) which occurred with greatest frequency on day 10. None of the volunteers noted the rash themselves, and it was asymptomatic in each instance. Rash was seen only

in vaccinees with detectable viremia. Volunteers did not develop systemic illness. Seven volunteers noted an occasional headache that was described as mild, lasting less than 2 hours, and was not present in any volunteer on two consecutive days. One volunteer reported fever of 38.6°C and 38.2°C without accompanying headache, chills, eye pain, photophobia, anorexia, myalgia, or arthralgia as an outpatient the evening of day 3 and day 5, respectively. However, this volunteer was afebrile when evaluated by the study staff on the morning of days 3, 4, 5 and 6. All other temperature measurements recorded by the volunteer or study staff were normal. Although tourniquet tests were not performed, two volunteers were noted to have petechiae at the site of the blood pressure cuff after a blood pressure measurement was performed (one on day 6, the other on days 7 and 10). Both of these volunteers had normal platelet counts at that time and throughout the study.

Significant hematological abnormalities were not seen in any vaccinee. Three vaccinees with presumed benign ethnic neutropenia manifested an absolute neutrophil count (ANC) below $1500/\text{mm}^3$. These three volunteers had baseline ANCs which were significantly lower than the remaining 17 volunteers and which did not decrease disproportionately to the other volunteers. Two of the three volunteers who became neutropenic never had detectable viremia. A mild increase in ALT levels was noted in 4 volunteers, and a more significant increase in ALT level (up to 238 IU/L) was noted in one volunteer. These ALT elevations were transient, were not associated with hepatomegaly, and were completely asymptomatic in each of the 5 volunteers. Elevated ALT values returned to normal by day 26 post-vaccination. The volunteer with the high ALT value was also noted to have an accompanying mild elevation in AST on day 14 (10^4 IU/L) which also returned to baseline by day 26 post-vaccination. This volunteer did not have an associated increase in LDH, bilirubin, or alkaline phosphatase levels.

Serologic response of humans to immunization with 2A $\Delta 30$. Each of the twenty vaccinees developed a significant rise in serum neutralizing antibody titer against DEN-4 by day 28. The level of serum neutralizing antibody was similar in viremic (1:662) and non-viremic vaccinees (1:426). The DEN-4 neutralizing antibody titers of both groups had not changed significantly by day 42.

Genetic stability of the $\Delta 30$ mutation. RT-PCR and sequence analysis of viral RNA isolated from serum samples (n=6) collected from volunteers 6 to 10 days post-vaccination confirmed the presence of the $\Delta 30$ mutation and neighboring deletion at nucleotide 10475.

Example 9

Pharmaceutical Compositions

Live attenuated dengue virus vaccines, using replicated virus of the invention, are used for preventing or treating dengue virus infection. Additionally, inactivated dengue virus vaccines are provided by inactivating virus of the invention using known methods, such as, but not limited to, formalin or β -propiolactone treatment. Live attenuated or inactivated viruses containing the mutations described above form the basis of an improved vaccine for the prevention or treatment of dengue infection in humans.

Pharmaceutical compositions of the present invention comprise live attenuated or inactivated dengue viruses, optionally further comprising sterile aqueous or non-aqueous solutions, suspensions, and emulsions. The composition can further comprise auxiliary agents or excipients, as known in

the art. See, e.g., Berkow et al. eds. 1987 The Merck Manual, 15th edition, Merck and Co., Rahway, N.J.; Goodman et al. eds. 1990 Goodman and Gilman's The Pharmacological Basis of Therapeutics, 8th edition, Pergamon Press, Inc., Elmsford, N.Y.; Avery's Drug Treatment: Principles and Practice of Clinical Pharmacology and Therapeutics, 3rd edition, ADIS Press, LTD., Williams and Wilkins, Baltimore, Md. 1987; Osol, A. ed. 1980 Remington's Pharmaceutical Sciences Mack Publishing Co, Easton, Pa. pp. 1324-1341; Katzung, ed. 1992 Basic and Clinical Pharmacology Fifth Edition, Appleton and Lange, Norwalk, Conn.

A virus vaccine composition of the present invention can comprise from about 10^2 - 10^9 plaque forming units (PFU)/ml, or any range or value therein, where the virus is attenuated. A vaccine composition comprising an inactivated virus can comprise an amount of virus corresponding to about 0.1 to 50 μ g of E protein/ml, or any range or value therein.

The agents may be administered using techniques well known to those in the art. Preferably, agents are formulated and administered systemically. Suitable routes may include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intradermal, intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as saline, phosphate buffered saline, Tris buffered saline, Hank's buffered saline, growth media such as Eagle's Minimum Essential Medium (MEM), and the like.

When a vaccine composition of the present invention is used for administration to an individual, it can further comprise salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. Adjuvants useful with the invention include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc.; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides or bacterial cell wall components), such as for example (a) MF59 (International Publication No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE, although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, Mass.), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) RibiTTM adjuvant system (RAS), (Ribi Immunochem, Hamilton, Mont.) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL+CWS (DetoxTM); (3) saponin adjuvants, such as StimulonTM (Cambridge Bioscience, Worcester, Mass.) may be used or particle generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (IL-1, IL-2, etc.), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc.; (6) mucosal adjuvants such as those derived from cholera toxin (CT), pertussis toxin (PT), E. coli heat labile toxin (LT), and mutants thereof (see, e.g., International Publication Nos. WO 95/17211, WO 93/13202, and WO

97/02348); and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition.

The pharmacologically active compounds of this invention can be processed in accordance with conventional methods of galenic pharmacy to produce medicinal agents for administration to patients, e.g., mammals including humans.

The compounds of this invention can be employed in admixture with conventional excipients, i.e., pharmaceutically acceptable organic or inorganic carrier substances suitable for parenteral, enteral (e.g., oral) or topical application, which do not deleteriously react with the active compounds. Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions, alcohols, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid monoglycerides and diglycerides, pentaerythritol fatty acid esters, hydroxy methylcellulose, polyvinyl pyrrolidone, etc. The pharmaceutical preparations can be sterilized and if desired mixed with auxiliary agents, e.g., lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active compounds. They can also be combined where desired with other active agents, e.g., vitamins.

For parenteral application, particularly suitable are injectable, sterile solutions, preferably oily or aqueous solutions, as well as suspensions, emulsions, or implants, including suppositories. Ampoules are convenient unit dosages.

For enteral application, particularly suitable are tablets, dragees, liquids, drops, suppositories, or capsules. A syrup, elixir, or the like can be used wherein a sweetened vehicle is employed.

For topical application, there are employed as non-sprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary agents, e.g., preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze bottle or in admixture with a pressurized volatile, normally gaseous propellant, e.g., a freon.

The vaccine can also contain variable but small quantities of endotoxin, free formaldehyde, and preservative, which have been found safe and not contributing to the reactogenicity of the vaccines for humans.

Example 10

Pharmaceutical Purposes

The administration of the vaccine composition may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the compositions are provided before any symptom of dengue viral infection becomes manifest. The prophylactic administration of the composition serves to

prevent or attenuate any subsequent infection. When provided therapeutically, the live attenuated or inactivated viral vaccine is provided upon the detection of a symptom of actual infection. The therapeutic administration of the compound(s) serves to attenuate any actual infection. See, e.g., Berkow et al. eds. 1987 The Merck Manual, 15th edition, Merck and Co., Rahway, N.J.; Goodman et al. eds. 1990 Goodman and Gilman's The Pharmacological Basis of Therapeutics, 8th edition, Pergamon Press, Inc., Elmsford, N.Y.; Avery's Drug Treatment: Principles and Practice of Clinical Pharmacology and Therapeutics, 3rd edition, ADIS Press, LTD., Williams and Wilkins, Baltimore, Md. 1987; Katzung, ed. 1992 Basic and Clinical Pharmacology, Fifth Edition, Appleton and Lange, Norwalk, Conn.

A live attenuated or inactivated vaccine composition of the present invention may thus be provided either before the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection.

The vaccines of the invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby live attenuated or inactivated viruses are combined in a mixture with a pharmaceutically acceptable vehicle. A composition is said to be a "pharmacologically acceptable vehicle" if its administration can be tolerated by a recipient patient. Suitable vehicles are well known to those in the art, e.g., in Osol, A. ed. 1980 Remington's Pharmaceutical Sciences Mack Publishing Co, Easton, Pa. pp. 1324-1341.

For purposes of administration, a vaccine composition of the present invention is administered to a human recipient in a therapeutically effective amount. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. A vaccine composition of the present invention is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient that generates a host immune response against at least one dengue serotype, stimulates the production of neutralizing antibodies, or leads to protection against challenge.

The "protection" provided need not be absolute, i.e., the dengue infection need not be totally prevented or eradicated, if there is a statistically significant improvement compared with a control population or set of patients. Protection may be limited to mitigating the severity or rapidity of onset of symptoms of the dengue virus infection.

Example 11

Pharmaceutical Administration

A vaccine of the present invention may confer resistance to one or more dengue serotypes by immunization. In immunization, an live attenuated or inactivated vaccine composition is administered prophylactically, according to a method of the present invention. In another embodiment a live attenuated or inactivated vaccine composition is administered therapeutically, according to a different method of the present invention.

The present invention thus includes methods for preventing or attenuating infection by at least one dengue serotype. As used herein, a vaccine is said to prevent or attenuate a disease if its administration results either in the total or partial attenuation (i.e., suppression) of a symptom or condition of the disease, or in the total or partial immunity of the individual to the disease.

At least one live attenuated or inactivated dengue virus, or composition thereof, of the present invention may be admin-

istered by any means that achieve the intended purpose, using a pharmaceutical composition as previously described.

For example, administration of such a composition may be by various parenteral routes such as subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, oral or transdermal routes. Parenteral administration can be by bolus injection or by gradual perfusion over time. A preferred mode of using a pharmaceutical composition of the present invention is by intramuscular, intradermal or subcutaneous application. See, e.g., Berkow et al. eds. 1987 The Merck Manual 15th edition, Merck and Co., Rahway, N.J.; Goodman et al. eds. 1990 Goodman and Gilman's The Pharmacological Basis of Therapeutics, 8th edition, Pergamon Press, Inc., Elmsford, N.Y.; Avery's Drug Treatment: Principles and Practice of Clinical Pharmacology and Therapeutics, 3rd edition, ADIS Press, LTD., Williams and Wilkins, Baltimore, Md. 1987; Osol, A. ed. 1980 Remington's Pharmaceutical Sciences, Mack Publishing Co, Easton, Pa. pp. 1324-1341; Katzung, ed. 1992 Basic and Clinical Pharmacology, Fifth Edition, Appleton and Lange, Norwalk, Conn.

A typical regimen for preventing, suppressing, or treating a dengue virus related pathology, comprises administration of an effective amount of a vaccine composition as described herein, administered as a single treatment, or repeated as enhancing or booster dosages, over a period up to and including between one week and about 24 months, or any range or value therein.

It will be appreciated that the actual preferred amounts of active compound in a specific case will vary according to the specific compound being utilized, the compositions formulated, the mode of application, and the particular situs and organism being treated. Dosages for a given host can be determined using conventional considerations, e.g., by customary comparison of the differential activities of the subject compounds and of a known agent, e.g., by means of an appropriate, conventional pharmacological protocol.

The dosage of a live attenuated virus vaccine for a mammalian (e.g., human) subject can be from about 10^3 - 10^7 plaque forming units (PFU)/kg, or any range or value therein. The dose of inactivated vaccine can range from about 0.1 to 50 μ g of E protein. However, the dosage should be a safe and effective amount as determined by conventional methods, using existing vaccines as a starting point.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

TABLE 1

Susceptibility of mice to intracerebral DEN4 infection is age-dependent ^a			
Virus	Mean virus titer (log ₁₀ PFU/g brain) \pm SE following inoculation at indicated age (days)		
	7	14	21
2A-13	>6.0	4.0 \pm 0.2	3.1 \pm 0.2
rDEN4	>6.0	3.3 \pm 0.4	3.3 \pm 0.2
rDEN4A30	>6.0	3.6 \pm 0.2	2.8 \pm 0.3

^aGroups of 4 or 5 Swiss Webster mice were inoculated intracerebrally with 10^5 PFU virus in a 30 μ l inoculum. After 5 days, brains were removed, homogenized and titered in Vero cells. SE = Standard error.

TABLE 2

Temperature-sensitive (ts) and mouse brain attenuation (att) phenotypes of 5-FU mutant DEN4 viruses.														
Phenotype	Virus	Mean virus titer (\log_{10} PFU/ml) at indicated temp. ($^{\circ}$ C.)											Virus replication in suckling mice ^b	
		Vero cells					HuH-7 cells						Mean titer \pm SE	Mean \log_{10}
		35	37	38	39	Δ^a	35	37	38	39	Δ	n	(\log_{10} PFU/g brain)	reduction from wt ^d
wt (not ts)	2A-13	7.8	7.7	7.6	7.3	0.5	7.8	7.7	7.4	6.4	1.4	66	6.6 \pm 0.1 ^c	—
	rDEN4	6.5	6.4	6.4	6.0	0.5	7.1	6.7	6.0	5.5	1.6	66	6.1 \pm 0.1 ^c	—
ts in Vero and HuH-7 cells	rDEN4 Δ 30	6.3	6.1	6.1	5.7	0.6	6.9	6.3	5.9	4.7	2.2	64	5.6 \pm 0.1 ^c	0.5
	695	6.2	6.0	5.2	<u>2.6</u> ^e	3.6	6.5	5.5	3.8	<u><1.6</u>	>4.9	6	3.0 \pm 0.2	3.2
ts in only HuH-7 cells	816	6.8	6.4	5.8	<u>3.9</u>	2.9	7.5	6.2	5.5	<u>3.1</u>	4.4	6	3.3 \pm 0.4	2.9
	773	7.4	6.6	6.0	<u>3.1</u>	4.3	7.7	6.1	5.2	<u>3.1</u>	4.6	12	3.7 \pm 0.1	2.6
	489	7.3	6.6	6.1	<u>3.3</u>	4.0	7.3	6.7	5.4	<u>3.0</u>	4.3	6	4.5 \pm 0.5	2.3
	173	7.0	6.1	<u>3.2</u>	<u>2.9</u>	4.1	7.0	<u>3.2</u>	<u>3.0</u>	<u>2.1</u>	4.9	18	4.7 \pm 0.4	2.2
	509	6.2	5.8	5.5	<u>3.4</u>	2.8	6.5	6.1	4.5	<u><1.6</u>	>4.9	6	4.9 \pm 0.3	1.9
	938	7.1	6.5	5.6	<u>3.1</u>	4.0	7.2	6.4	5.6	<u>3.1</u>	4.1	6	5.1 \pm 0.2	1.7
	1033	6.7	6.0	5.9	<u>4.1</u>	2.6	6.9	5.6	4.7	<u><1.6</u>	>5.3	12	4.7 \pm 0.2	1.7
	239	7.6	6.8	5.6	<u>3.3</u>	4.3	7.6	6.7	4.7	<u>2.5</u>	5.1	12	4.7 \pm 0.3	1.5
	793	6.5	5.8	5.3	<u>4.0</u>	2.5	7.2	6.8	5.6	<u><1.6</u>	>5.6	6	5.4 \pm 0.3	1.4
	759	7.2	6.9	6.4	<u>4.7</u>	2.5	7.5	6.8	6.3	<u>3.1</u>	4.4	12	5.1 \pm 0.1	1.4
	718	6.1	5.9	5.3	<u>3.5</u>	2.6	7.0	6.5	5.7	<u>1.7</u>	5.3	12	5.0 \pm 0.3	1.4
	473	6.7	6.3	5.4	<u>2.0</u>	4.7	7.2	6.7	<u>3.7</u>	<u>1.9</u>	5.3	12	5.1 \pm 0.3	1.2
	686	7.0	6.7	6.7	6.4	0.6	7.3	6.8	6.4	<u>2.2</u>	5.1	12	2.7 \pm 0.2	3.8
	967	6.8	6.4	6.4	5.1	1.7	6.8	6.4	5.4	<u><1.6</u>	>5.2	6	3.6 \pm 0.2	2.9
	992	7.3	7.1	6.8	5.9	1.4	7.4	6.9	5.0	<u><1.6</u>	>5.8	6	3.8 \pm 0.1	2.7
571	6.9	7.0	6.4	4.6	2.3	7.0	6.3	5.2	<u><1.6</u>	>5.4	6	4.4 \pm 0.4	2.4	
605	7.6	7.5	7.1	6.9	0.7	7.8	7.2	6.8	<u><1.6</u>	>6.2	12	4.5 \pm 0.4	2.1	
631	7.1	6.9	6.8	5.0	2.1	7.3	7.1	6.5	<u><1.6</u>	>5.7	12	4.8 \pm 0.3	1.9	
1175	7.4	7.1	6.9	5.3	2.1	7.6	6.5	4.7	<u>3.3</u>	4.3	12	4.7 \pm 0.2	1.7	

^aReduction in titer (\log_{10} PFU/ml) at 39 $^{\circ}$ C. compared to titer at permissive temperature (35 $^{\circ}$ C.).

^bGroups of 6 suckling mice were inoculated i.c. with 10⁴ PFU virus in a 30 μ l inoculum. Brains were removed 5 days later, homogenized, and titered in Vero cells.

^cAverage of 11 experiments with a total of 64 to 66 mice per group.

^dDetermined by comparing mean viral titers of mice inoculated with mutant virus and the 2A-13 wt control in the same experiment (n = 6 or 12).

^eUnderlined values indicate a 2.5 or 3.5 \log_{10} PFU/ml reduction in titer in Vero cells or HuH-7 cells, respectively, at indicated temp when compared to titer at permissive temp (35 $^{\circ}$ C.).

TABLE 3

Nucleotide and amino acid differences of the 5-FU mutant viruses which are ts in both Vero and HuH-7 cells.							
Virus	Nucleotide position	Gene/region	Mutations in UTR or coding region that result in an amino acid substitution		Mutations in coding region that do not result in an amino acid substitution		
			Nucleotide change	Amino Acid change ^b	Nucleotide position	Gene	Nucleotide change
173 ^a	7163	NS4B	A > C	L2354F	10217	NS5	A > U
	7849	NS5	A > U	N2583I			
	8872	NS5	A > G	K2924R			
239 ^a	4995	NS3	U > C	S1632P	7511	NS4B	G > A
					10070	NS5	U > C
473 ^a	4480	NS2B	U > C	V1460A	7589	NS5	G > A
	4995	NS3	U > C	S1632P	10070	NS5	U > C
489 ^a	4995	NS3	U > C	S1632P	2232	E	U > C
					3737	NS2A	C > U
509 ^a	4266	NS2B	A > G	S1389G			
	8092	NS5	A > G	E2664G			
695	40	5' UTR	U > C	n/a	1391	E	A > G
	1455	E	G > U	V452F			
	6106	NS3	A > G	E2002G			
	7546	NS4B	C > U	A2482V			
718	2280	E	U > C	F727L			
	4059	NS2A	A > G	I1320V			
	4995	NS3	U > C	S1632P			
	7630	NS5	A > G	K2510R			
759 ^a	8281	NS5	U > C	L2727S			
	4995	NS3	U > C	S1632P			
773 ^a	8020	NS5	A > U	N2640I			
	4995	NS3	U > C	S1632P			

TABLE 3-continued

Nucleotide and amino acid differences of the 5-FU mutant viruses which are ts in both Vero and HuH-7 cells.							
Virus	Mutations in UTR or coding region that result in an amino acid substitution				Mutations in coding region that do not result in an amino acid substitution		
	Nucleotide position	Gene/ region	Nucleotide change	Amino Acid change ^b	Nucleotide position	Gene	Nucleotide change
793	1776	E	G > A	A559T	5771	NS3	U > C
	2596	NS1	G > A	R832K	7793	NS5	U > A
	2677	NS1	A > G	D859G			
816 ^a	4387	NS2B	C > U	S1429F			
	4995	NS3	U > C	S1632P	6632	NS4A	G > A
	7174	NS4B	C > U	A2358V	6695	NS4A	G > A
938 ^a	3442	NS1	A > G	E1114G	747	prM	U > C
	4995	NS3	U > C	S1632P	4196	NS2b	U > C
1033 ^a	10275	3' UTR	A > U	n/a	6155	NS3	G > A
	4907	NS3	A > U	L1602F	548	prM	C > U
	8730	NS5	A > C	N2877H			
	9977	NS5	G > A	M3292I			

^aViruses that contain mutation(s) resulting in an a.a. substitution in only a NS gene(s) and/or nucleotide substitutions in the UTRs are indicated; i.e. no a.a. substitutions are present in the structural proteins (C-prM-E).

^bAmino acid position in DEN4 polyprotein beginning with the methionine residue of the C protein (nt 102-104) as residue #1. Wild-type amino acid on left of amino acid position; mutant amino acid on right.

TABLE 4

Nucleotide and amino acid differences of the 5-FU mutant viruses which are ts in only HuH-7 cells.							
Virus	Mutations in UTR or coding region that result in an amino acid substitution				Mutations in coding region that do not result in an amino acid substitution		
	Nucleotide position	Gene/ region	Nucleotide change	Amino acid change ^b	Nucleotide position	Gene	Nucleotide change
571	586	prM	U > C	V162A	6413	NS4A	U > C
	7163	NS4B	A > U	L2354F			
605	7947	NS5	G > A	G2616R			
	1455	E	G > U	V452F	none		
631	7546	NS4B	C > U	A2482V			
	595	prM	A > G	K165R	1175	E	G > A
	6259	NS3	U > C	V2053A	5174	NS3	A > G
686 ^a	7546	NS4B	C > U	A2482V			
	3575	NS2A	G > A	M1158I	4604	NS3	A > G
	4062	NS2A	A > G	T1321A	7937	NS5	A > G
967	7163	NS4B	A > U	L2354F			
	2094	E	G > C	A665P	4616	NS3	C > U
	2416	E	U > C	V772A			
	7162	NS4B	U > C	L2354S			
992 ^a	7881	NS5	G > A	G2594S			
	5695	NS3	A > G	D1865G	3542	NS2A	A > G
1175 ^a	7162	NS4B	U > C	L2354S			
	7153	NS4B	U > C	V2351A	6167	NS3	U > C
	10186	NS5	U > C	I3362T	10184	NS5	G > A
	10275	3' UTR	A > U	n/a			

^aViruses that contain mutation(s) resulting in an a.a. substitution in only a NS gene(s) and/or nucleotide substitutions in the UTRs are indicated; i.e. no a.a. substitutions are present in the structural proteins.

^bAmino acid position in DEN4 polyprotein beginning with the methionine residue of the C protein (nt 102-104) as residue #1. Wild-type amino acid on left of amino acid position; mutant amino acid on right.

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TABLE 5

Mutations which are represented in multiple 5-FU mutant DEN4 viruses.				
Nucleotide position	Gene/ region	Nucleotide change	Amino acid change	Number of viruses with "sister" mutations
1455	E	G > U	val > phe	2
4995	NS3	U > C	ser > pro	8
7162	NS4B	U > C	leu > ser	2
7163	NS4B	A > U or C	leu > phe	3

TABLE 5-continued

Mutations which are represented in multiple 5-FU mutant DEN4 viruses.				
Nucleotide position	Gene/ region	Nucleotide change	Amino acid change	Number of viruses with "sister" mutations
7546	NS4B	C > U	ala > val	3
10275	3' UTR	A > U	n/a ^a	2

^anot applicable

TABLE 8

Viruses with both ts and sp phenotypes are more restricted in replication in mouse brain than those with only a ts phenotype.

Cell culture phenotype	Number of viruses	Mean log ₁₀ reduction in virus titer from controls ^{b,c}	5
ts ^a	20	2.1 ± 0.2	
sp	6	3.0 ± 0.6	
ts/sp	16	3.5 ± 0.3	

^a20 ts mutant viruses without an sp phenotype were previously described (Example 1).

^bDetermined by comparing mean viral titers of groups of mice inoculated with mutant virus and concurrent 2A-13 parallel-passaged control virus.

^cSignificant difference between ts group and ts/sp group, Tukey-Kramer test (P < 0.05)

TABLE 9

Nucleotide and amino acid differences of the 5-FU mutant DEN4 viruses which produce small plaques in both Vero and HuH-7 cells.

Virus	Mutations in UTR or in coding regions that result in an amino acid substitution				Mutations in coding regions that do not result in an amino acid substitution		
	Nucleotide position	Gene/region	Nucleotide change	Amino acid change ^b	Nucleotide position	Gene	Nucleotide change
569	826	prM	G > A	R242K	1946	E	C > U
	832	prM	C > U	P244L			
	7546	NS4B	C > U	A2482V			
	10275	3' UTR	A > U	n/a			
	10279	3' UTR	A > U	n/a			
574	1455	E	G > U	V452F	1349	E	C > U
	1963	E	U > C	V621A			
	3880	NS2A	A > G	K1260R			
	7546	NS4B	C > U	A2482V			
	7615	NS5	A > G	N2505S			
761	10413	3' UTR	A > G	n/a	none		
	424	C	U > C	I108T			
	2280	E	U > C	F727L			
	7131	NS4B	A > G	T2344A			
	7486	NS4B	A > G	N2462S			
1189a	3303	NS1	A > G	R1068G	6719	NS4A	U > C
	4812	NS3	G > A	V1571I			
	5097	NS3	G > A	D1666N			
	7182	NS4B	G > A	G2361S			
1269	2112	E	U > C	F671L	542	prM	C > U
	3256	NS1	G > A	G1052E			
	3993	NS2A	U > C	F1298L			
	7183	NS4B	G > U	G2361V			

^aVirus contains missense mutations in only the non-structural genes.

^bAmino acid position in DEN4 polyprotein beginning with the methionine residue of the C protein (nt 102-104). Wild type amino acid on left of amino acid position; mutant amino acid on right.

TABLE 10

Nucleotide and amino acid differences of the 5-FU mutant DEN4 viruses which produce small plaques in only HuH-7 cells.

Virus	Mutations in UTR or in coding regions that result in an amino acid substitution				Mutations in coding regions that do not result in an amino acid substitution		
	Nucleotide position	Gene/region	Nucleotide change	Amino acid change ^b	Nucleotide position	Gene	Nucleotide change
311	1519	E	A > G	N473S	6761	NS4A	C > U
	2305	E	G > A	R735K			
	4896	NS3	G > U	A1599S			
326	1587	E	C > U	P496S	1523	E	G > A
	7546	NS4B	C > U	A2482V			
506					10070	NS5	U > C
	1455	E	G > U	V452F	3887	NS2A	A > G
	1902	E	G > A	V601M			
	7546	NS4B	C > U	A2482V			
	10275	3' UTR	A > U	n/a			
				5789			

TABLE 10-continued

Nucleotide and amino acid differences of the 5-FU mutant DEN4 viruses which produce small plaques in only HuH-7 cells.							
Virus	Mutations in UTR or in coding regions that result in an amino acid substitution				Mutations in coding regions that do not result in an amino acid substitution		
	Nucleotide position	Gene/region	Nucleotide change	Amino acid change ^b	Nucleotide position	Gene	Nucleotide change
529	777	prM	U > C	S226P	none		
	4641	NS3	A > G	I1514V			
	7153	NS4B	U > C	V2351A			
	8245	NS5	U > C	I2715T			
	10279	3' UTR	A > C	n/a			
738 ^a	3540	NS2A	G > A	E1147K	none		
	7162	NS4B	U > C	L2354S			
922 ^a	4306	NS2B	A > G	N1402S	7736	NS5	G > A
	5872	NS3	C > U	T1924I			
	7163	NS4B	A > U	L2354F			
	10279	3' UTR	A > C	n/a			
952	1449	E	G > U	V450L	none		
	1455	E	G > U	V452F			
	7546	NS4B	C > U	A2482V			
	7957	NS5	U > C	V2619A			
	9543	NS5	A > G	I3148V			
1012	1542	E	A > G	K481E	953	E	A > G
	7162	NS4B	U > C	L2354S	1205	E	G > A
1021	10542	3' UTR	A > G	n/a	4425	NS2B	U > C
	2314	E	U > C	I738T	665	prM	C > A
	3205	NS1	C > U	A1035V	5750	NS3	C > U
1023	4029	NS2A	U > C	C1310R	9959	NS5	C > U
	7163	NS4B	A > C	L2354F			
	10275	3' UTR	A > U	n/a			
	10279	3' UTR	A > U	n/a			
	2283	E	G > A	G728R	1001	E	C > U
	7182	NS4B	G > A	G2361S	1958	E	A > G
1029					3873	NS2a	U > C
	850	prM	C > U	A250V	8486	NS5	C > U
	3087	NS1	A > G	T996A	3867	NS2a	C > U
	4891	NS3	U > C	I1597T			
	2650	NS1	A > G	N850S	6326	NS3	C > U
1081 ^a	7163	NS4B	A > U	L2354F	9146	NS5	C > U
	3702	NS2A	G > A	A1201T	3353	NS1	A > G
1083 ^a	7153	NS4B	U > C	V2351A	6155	NS3	G > A
	10634	3' UTR	U > C	n/a			
1096	892	prM	G > A	R264Q	665	prM	C > A
	7163	NS4B	A > C	L2354F	4427	NS2b	G > A
	8659	NS5	C > U	P2853L			
1104	1692	E	G > A	V531M	none		
	5779	NS3	C > U	A1893V			
1114	7546	NS4B	C > U	A2482V			
	709	prM	A > G	K203R	1076	E	U > C
	3693	NS2A	A > G	I1198V	1182	E	C > U
	4614	NS3	U > C	F1505L	5690	NS3	C > U
1136 ^a	7546	NS4B	C > U	A2482V			
	9942	NS5	A > G	T3281A			
	3771	NS2A	A > G	R1224G	5621	NS3	A > G
	4891	NS3	U > C	I1597T			
	10275	3' UTR	A > U	n/a			

^aViruses that contain missense mutations in only the non-structural genes and/or mutations in the UTRs.

^bAmino acid position in DEN4 polyprotein beginning with the methionine residue of the C protein (nt 102-104). Wild type amino acid on left of amino acid position; mutant amino acid on right.

TABLE 11

Putative Vero cell adaptation mutations derived from the full set of 5-FU mutant viruses.				
5-FU mutant viruses				
Nucleotide position	Gene/region (a.a. #) ^b	Nucleotide change	Amino acid change	No. of viruses with the mutation
1455	E (452)	G > U	Val > Phe	5
2280	E (727)	U > C	Phe > Leu	2
4891	NS3 (1597)	U > C	Ile > Thr	2

TABLE 11-continued

Putative Vero cell adaptation mutations derived from the full set of 5-FU mutant viruses.				
5-FU mutant viruses				
Nucleotide position	Gene/region (a.a. #) ^b	Nucleotide change	Amino acid change	No. of viruses with the mutation
4995	NS3 (1599)	U > C	Ser > Pro	8
7153	NS4B (2351)	U > C	Val > Ala	3
7162	NS4B (2354)	U > C	Leu > Ser	4

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TABLE 11-continued

Putative Vero cell adaptation mutations derived from the full set of 5-FU mutant viruses.				
Nucleotide position	Gene/region (a.a. #) ^b	5-FU mutant viruses		
		Nucleotide change	Amino acid change	No. of viruses with the mutation
7163	NS4B (2354)	A > U or C	Leu > Phe	7
7182	NS4B (2361)	G > A	Gly > Ser	2
7546	NS4B (2482)	C > U	Ala > Val	10
7630	NS5 (2510)	A > G	Lys > Arg	1

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TABLE 11-continued

Putative Vero cell adaptation mutations derived from the full set of 5-FU mutant viruses.				
Nucleotide position	Gene/region (a.a. #) ^b	5-FU mutant viruses		
		Nucleotide change	Amino acid change	No. of viruses with the mutation
10275	3' UTR	A > U	n/a ^a	6
10279	3' UTR	A > C	n/a	4

^anot applicable
^bAmino acid position in DEN4 polyprotein beginning with the methionine residue of the C protein (nt 102-104) as residue #1.

TABLE 12

Mutagenic oligonucleotides used to generate recombinant DEN4 viruses containing single 5-FU mutations.							
SEQ ID NO.	Recombinant virus (rDEN4-)	Nucleotide change	Amino acid change	Gene	pUC clone	RE site ^a	Oligonucleotide ^b
23	40	U > C	n/a	5' UTR	pUC-NheI	BsaWI	CAGTTCCAAAcCGGAAGCTTG
24	2650	A > G	Asn > Ser	NS1	pUC-NS1	BsiWI	CCAACGAGCTAtcGTTACTCTCTGGG
25	3303	A > G	Arg > Gly	NS1	pUC-NS1	StyI	GATTGTGACCATgGcGGCCCATCTTTG
26	3442	A > G	Glu > Gly	NS1	pUC-NS1	BlpI	GGAGATTAGGCCgcTGAGcGgtAAAGAAGAG
27	3540	G > A	Glu > Lys	NS2A	pUC-NS1	BsmI	GTTTGTGGAAaAATGtcTGAGGAGAA
28	3575	G > A	Met > Ile	NS2A	pUC-NS1	SspI	CTAGGAAACACATaATATTAGTTGTGG
29	3702	G > A	Ala > Thr	NS2A	pUC-NS2A	BglI	CAGATCCACCTaCCATaATGGCAGTG
30	3771	A > G	Arg > Gly	NS2A	pUC-NS2A	AvaI	GGAAACTCACcTCggGAGAGACAGC
31	4059	A > G	Ile > Val	NS2A	pUC-NS2A	BstEII	TTGGGTAGAggTcACcGCACTCATCC
32	4062	A > G	Thr > Ala	NS2A	pUC-NS2A	BsrBI	GTAGAAATAgCcGctCTCATCCTAG
33	4266	A > G	Ser > Gly	NS2B	pUC-NS2A	SnaBI	GGCGGCTTACGTaATGgGaGGTAGCTCAGC
34	4306	A > G	Asn > Ser	NS2B	pUC-NS2A	AlwNI	CTAGAGAAGGCaGcttctGTGCAGTGG
35	4480	U > C	Val > Ala	NS2B	pUC-NS2A	MscI	CCTTGGCCaTTCAGcaACAATGAC
36	4812	G > A	Val > Ile	NS3	pUC-NS2A	ApoI	GACGTTCAaaTttTaGCCATAGAACC
37	4891	U > C	Ile > Thr	NS3	pUC-NS2A	KasI	CTGGAGAAAcgGGcGCcGTAACATTAG
38	4896	G > U	Ala > Ser	NS3	pUC-NS2A	BstEII	GAAATTGGAtCgGTAACcTTAGATTTT
39	4907	A > U	Leu > Phe	NS3	pUC-NS2A	AclI	GGAGCAGTAACqTTtGATTTCAAACCC
40	4995	U > C	Ser > Pro	NS3	pUC-NS2A	BsaJI	GTTACCAAAcCtGGgGATTACGTC
41	5097	G > A	Asp > Asn	NS3	pUC-NS3	BspHI	GATTAACtATcATGaACTTACACCC
42	5695	A > G	Asp > Gly	NS3	pUC-NS3	BanI	GGAAAACCTTTGgcACcGAGTATCC
43	5872	C > U	Thr > Ile	NS3	pUC-NS3	BsrFI	TCCAGTGAtaCCqGctAGCGCTGCTC
44	6106	A > G	Glu > Gly	NS3	pUC-NS3	MscI	GCCTCAGAGGtGgcCAAAGGAAG
45	6259	U > C	Val > Ala	NS3	pUC-NS3	BglIII	ACATGGAGGcaGAqATcTGGACTAGA
46	7153	U > C	Val > Ala	NS4B	pUC-NS4A	MscI	AAAGCATGgCcAAGGATGCTGTC
47	7162	U > C	Leu > Ser	NS4B	pUC-NS4A	BlpI	GCATAATGGACqctAAGCATGACTAAGG
48	7163	A > C	Leu > Phe	NS4B	pUC-NS4A	ApaLI	TTATTGCATAgTGcACgAAAAGCATG
49	7174	C > U	Ala > Val	NS4B	pUC-NS4A	BsaAI	GGGCTATTATTaCqTAATGGAC
50	7182	G > A	Gly > Ser	NS4B	pUC-NS4A	n/a	CTGCAATCCTGGtgaTATTATTGC

TABLE 12-continued

Mutagenic oligonucleotides used to generate recombinant DEN4 viruses containing single 5-FU mutations.							
SEQ ID NO.	Recombinant virus (rDEN4-)	Nucleotide change	Amino acid change	Gene	pUC clone	RE site ^a	Oligonucleotide ^b
51	7546	C > U	Ala > Val	NS4B	pUC-NSSA	AclI	CTCATAAAGAA <u>AcGtt</u> CAAACCTT
52	7630	A > G	Lys > Arg	NS5	pUC-NSSA	HgaI	CATTAGACAG <u>Acgc</u> GAGTTTGAAG
53	7849	A > U	Asn > Ile	NS5	pUC-NSSA	HgaI	TGGCGAC <u>Cq</u> CTCAAGAtaGTGACTGAAG
54	8020	A > U	Asn > Ile	NS5	pUC-NSSA	ClaI	GAGTCATCa <u>Tcq</u> AtaCCAACAATAG
55	8092	A > G	Glu > Gly	NS5	pUC-NSSA	EcoRI	CTTCAAACCTG <u>Gc</u> TTCTGCATCAAAG
56	8281	U > C	Leu > Ser	NS5	pUC-NSSB	XmnI	CAAAGATGTTGagcAACAGGTTCAACAAC
57	8730	A > C	Asn > His	NS5	pUC-NSSB	AvaI	GGAAAGAAGAAAc <u>Ac</u> CCqAGACTGTGC
58	8872	A > G	Lys > Arg	NS5	pUC-NSSB	PvuI	GGGAACGGT <u>Cg</u> AtcgAGAAAGGGC
59	9977	G > A	Met > Ile	NS5	pUC-NSSC	SfcI	CCAGTGGATt <u>Act</u> ACaGAAGATATGCTC
60	10186	U > C	Ile > Thr	NS5	pUC-NSSC	AgeI	CAGGAACCTG <u>Ac</u> CGGtAAAGAGGAATACG
61	10275	A > U	n/a	3' UTR	pUC-NSSC	n/a	CTGTAATTACCAACAtCAAACACCAAAG
62	10279	A > C	n/a	3' UTR	pUC-NSSC	n/a	CCAACAACAAcCACCAAAGGCTATTG
63	10634	U > C	n/a	3' UTR	pUC-3' UTR	n/a	GGATTGGTGTtGtGATCCAACAGG

^aPrimers were engineered which introduced (underline) or ablated (hatched line) translationally-silent restriction enzyme sites.

^bLowercase letters indicate nt changes and bold letters indicate the site of the 5-FU mutation, which in some oligonucleotides differs from the original nucleotide substitution change in order to create a unique restriction enzyme site. The change preserves the codon for the amino acid substitution.

TABLE 13

sp, ts and mouse attenuation phenotypes of rDEN4 mutant viruses encoding single mutations identified in six sp 5-FU mutant viruses.														
5-FU mu-	Gene/region	Mean virus titer							Replication in suckling mice ^b		Replication in HuH-7-SCID mice ^d			
		(log ₁₀ PFU/ml) at indicated temp (° C.)			Mean virus titer ± SE	Mean log ₁₀ -unit reduction from	Mean peak virus titer ± SE (log ₁₀ PFU/ml)	Mean log ₁₀ -unit reduction						
tant	containing	Vero cells		HuH-7 cells			(log ₁₀ PFU/	reduction from	PFU/ml	from value				
virus	Virus	35	39	Δ ^a	35	39	Δ	n	g brain)	value for wt ^c	n	serum)	for wt ^c	
	2A-13 rDEN4	7.6	7.1	0.5	7.8	6.6	1.2	30	6.5 ± 0.1	—	29	6.8 ± 0.2	—	
	rDEN4Δ30	7.6	6.8	0.8	8.0	6.7	1.3	54	5.8 ± 0.1	—	32	6.3 ± 0.2	—	
738	parent	7.6	6.9	0.7	7.7	5.6	2.1	30	5.6 ± 0.1	0.2	18	5.4 ± 0.2	0.9	
	rDEN4-3540 NS2A	6.5	5.7	0.8	^x 6.9	<u>3.1</u> ^e	3.8	12	4.4 ± 0.4	2.3	9	5.4 ± 0.7	1.9	
	rDEN4-7162 NS4B	6.9	5.1	1.8	7.4	<u>3.7</u>	3.7	12	4.1 ± 0.3	1.7	5	6.1 ± 0.3	(+)0.1	
922	parent	7.2	6.8	0.4	7.4	6.6	0.8	8	5.6 ± 0.3	0.3	5	6.8 ± 0.6	0.3	
	rDEN4-4306 NS2B	7.3	<u>3.8</u>	3.5	^x 7.4	<u>3.0</u>	4.4	12	3.5 ± 0.1	2.9	6	6.2 ± 0.2	0.4	
	rDEN4-5872 NS3	^x 5.0	<u>2.2</u>	2.8	^x 5.6	<u><1.6</u>	>4.0	12	1.7 ± 0.1	4.1	5	5.2 ± 0.6	1.1	
	rDEN4-7163 NS4B	5.7	<u>2.5</u>	3.2	^x 6.5	<u><1.6</u>	>4.9	12	4.5 ± 0.3	1.3	5	6.2 ± 0.5	0.1	
	rDEN4-10279 3' UTR	7.8	7.2	0.6	8.0	7.4	0.6	6	6.2 ± 0.2	(+)0.1	6	5.8 ± 0.6	(+)0.2	
1081	parent	6.9	5.7	1.2	7.7	5.7	2.0	6	4.8 ± 0.2	0.7	4	6.7 ± 0.2	0.4	
	rDEN4-2650 NS1	6.9	<u>3.9</u>	3.0	^x 5.8	<u>1.9</u>	3.9	12	2.6 ± 0.2	3.9	4	4.2 ± 0.5	2.4	
	rDEN4-7163 NS4B	5.1	3.0	2.1	^x 5.5	2.8	2.7	12	3.0 ± 0.3	2.8	6	4.7 ± 0.5	2.2	
1083	parent	7.8	7.2	0.6	8.0	7.4	0.6	6	6.2 ± 0.2	(+)0.1	6	5.8 ± 0.6	(+)0.2	
	rDEN4-3702 NS2A	7.4	5.8	1.6	^x 7.4	<u><1.6</u>	≥5.8	12	4.5 ± 0.4	2.0	9	4.4 ± 0.3	2.9	
	rDEN4-7153 NS4B	6.8	5.6	1.2	7.6	4.7	2.9	18	4.9 ± 0.3	0.9	7	6.3 ± 0.3	0.2	
	rDEN4-10634 3' UTR	7.7	7.2	0.5	8.0	6.9	1.1	6	5.7 ± 0.1	0.2	4	5.9 ± 0.7	0.1	
1136	parent	4.9	<u>1.6</u>	3.3	^x 5.7	<u><1.6</u>	≥4.1	12	2.4 ± 0.3	3.4	7	3.3 ± 0.4	3.6	
	rDEN4-3771 NS2A	5.1	<u><1.6</u>	≥3.5	^x 5.7	<u><1.6</u>	≥4.1	6	2.9 ± 0.3	4.5	7	4.5 ± 0.4	1.2	
	rDEN4-4891 NS3	7.0	4.6	2.4	^x 7.6	<u>3.7</u>	3.9	12	2.6 ± 0.4	3.2	4	6.4 ± 0.2	(+)0.1	
	rDEN4-10275 3' UTR	7.1	<u><1.6</u>	>5.5	^x 7.4	<u><1.6</u>	>5.8	12	2.5 ± 0.3	3.5	6	6.0 ± 0.5	0.3	
	rDEN4-10275 3' UTR	6.9	5.8	1.1	7.1	5.2	1.9	6	5.0 ± 0.3	0.5	4	6.7 ± 0.3	0.4	

TABLE 15

sp, ts and mouse attenuation phenotypes of rDEN4 mutant viruses encoding single mutations identified in 3 HuH-7 cell-specific ts 5-FU mutant viruses.																
5-FU mutant viruses	rDEN4-Mutation (nt position)	Gene/region	Mean virus titer (log ₁₀ PFU/ml) at indicated temp (° C.)										Replication in 7-day mice ^b		Replication in HuH-7-SCID mice ^b	
			Vero cells					HuH-7 cells					Mean log ₁₀ reduction from wt ^c (log ₁₀ PFU/g brain) ₁₀	n	Mean log ₁₀ reduction from wt ^c (log ₁₀ PFU/ml serum)	
			35	37	39	39	Δ ^a	35	37	38	39	Δ				n
686	parent		7.0	6.7	6.7	6.4	0.6	7.3	6.8	6.4	<u>2.2</u>	5.1	12	3.8	6	1.2
	3575	NS2A	6.9	6.9	7.1	7.0	0.1	7.9	6.8	6.9	4.9	3.0	12	2.3		nd ^e
	4062	NS2A	6.8	6.6	6.3	4.7	2.1	6.9	6.8	7.0	<u><1.6</u>	>5.3	12	2.2		nd
	7163	NS4B	7.8	7.7	7.6	7.2	0.6	8.0	7.7	7.5	7.4	0.6	6	(+)0.1		nd
992	parent		7.3	7.1	6.8	5.9	1.4	7.4	6.9	5.0	<u><1.6</u>	>5.8	6	2.7	7	1.3
	5695	NS3	5.6	4.7	4.7	3.8	1.8	6.3	5.1	3.7	<u><1.6</u>	>4.7	6	2.8		nd
	7162	NS4B	7.2	7.3	6.6	6.8	0.4	7.4	7.3	7.3	6.6	0.8	8	0.3		nd
1175	parent		7.4	7.1	6.9	5.3	2.1	7.6	6.5	4.7	<u>3.3</u>	4.3	12	1.7	5	1.0
	7153	NS4B	7.7	7.7	7.6	7.2	0.5	8.0	7.8	7.5	6.9	1.1	6	0.2		nd
	10186	NS5	4.3	3.7	2.4	<u><1.6</u>	>2.7	5.1	<u><1.6</u>	<u><1.6</u>	<u><1.6</u>	>3.5	6	3.4		nd
	10275	3' UTR	6.9	6.4	6.4	5.8	1.1	7.1	6.8	7.1	5.2	1.9	6	0.5		nd

^aReduction in titer (log₁₀PFU/ml) at 39° C. compared to permissive temperature (35° C.).

^bGroups of 6 suckling mice were inoculated i.c. with 10⁴ PFU virus. Brains were removed 5 days later, homogenized, and titered in Vero cells.

^cDetermined by comparing mean viral titers of mice inoculated with mutant virus and concurrent 2A-13 or rDEN4 wt control.

^dUnderlined values indicate a 2.5 or 3.5 log₁₀PFU/ml reduction in titer in Vero cells or HuH-7 cells, respectively, at indicated temp when compared to permissive temp (35° C.).

TABLE 16

Temperature-sensitive (ts) and mouse brain attenuation (att) phenotypes of additional rDEN4 viruses encoding single 5-FU mutations.																
5-FU mutant virus	Virus	Gene/region containing mutation	Mean virus titer (log ₁₀ PFU/ml) at indicated temp (° C.)										Replication in suckling mice ^b			
			Vero cells					HuH-7 cells					SE (log ₁₀ PFU/g brain)	Mean log ₁₀ -unit reduction from value for wt ^c		
			35	37	38	39	Δ ^a	35	37	38	39	Δ			n	
695	rDEN4-40	5' UTR	7.4	7.2	6.7	6.2	1.2	7.6	7.5	7.1	5.8	1.8		nd ^f		nd
718	rDEN4-4059	NS2A	7.0	6.7	6.4	6.2	0.8	7.7	7.1	7.0	6.6	1.1		nd		nd
311	rDEN4-4896	NS3	7.0	6.1	5.9	<u>4.2</u>	2.8	6.9 ^x	6.0	5.6	<u>3.3</u>	3.6	6	4.1 ± 0.4		2.0**
695	rDEN4-6106	NS3	6.8	6.3	5.9	<u>3.9</u>	2.9	7.1	6.0	5.2	<u>3.4</u>	3.7		nd		nd
631	rDEN4-6259	NS3	7.0	6.1	5.8	5.0	2.0	7.5	6.6	5.7	4.2	3.3	6	2.2 ± 0.2		3.9**
695 ^e	rDEN4-7546	NS4B	7.5	7.6	7.4	6.6	0.9	7.7	7.6	7.3	5.7	2.0		nd		nd
718	rDEN4-7630	NS5	7.0	6.9	6.9	6.4	0.6	7.4	7.4	7.2	6.8	0.6	6	5.0 ± 0.3		0.5
718	rDEN4-8281	NS5	6.4	6.6	6.7	5.4	1.0	7.6	7.6	7.0	5.1	2.5	6	5.0 ± 0.5		1.1

^aReduction in titer (log₁₀PFU/ml) at 39° C. compared to titer at permissive temperature (35° C.).

^b6 mice were inoculated i.c. with 10⁴ PFU virus in 30 μl inoculum. Brains were removed 5 days later, homogenized, and titered on Vero cells. Limit of detection is 2.0 log₁₀PFU/g.

^cDetermined by comparing mean viral titers of mice inoculated with sample virus and wt rDEN4 control.

^dUnderlined values indicate a 2.5 or 3.5 log₁₀PFU/ml reduction in titer in Vero cells or HuH-7 cells, respectively, at indicated temperature when compared to permissive temperature (35° C.).

^eThe 7546 mutation is also present in nine other 5-FU mutant viruses.

^xSmall plaque size at 35° C.; small plaques have a diameter of <0.4 mm compared to wt plaque diameter of 0.75 to 1.0 mm in HuH-7 cells.

^fnot determined

**The att phenotype is defined as a reduction of >1.5 log₁₀PFU/g compared to wt virus.

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TABLE 17

Growth of wt DEN-4 2A-13 in SCID mice transplanted with HuH-7 cells. ^a						
Dose (log ₁₀ PFU/ml)	Mouse #	Virus titer				
		log ₁₀ PFU/ml serum		log ₁₀ PFU/g tissue		
		day 3	day 5	Brain	Liver	Tumor
4	87	2.7	5.9	2.0	6.9	8.0
	88	2.0	5.9	3.8	3.3	8.0
	89	<1.7	6.2	2.7	3.6	8.0
	90	1.7	3.5	3.2	3.0	7.0
	5	84	<1.7	7.2	3.2	4.0
	85	1.7	6.6	3.6	6.3	5.8

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TABLE 17-continued

Growth of wt DEN-4 2A-13 in SCID mice transplanted with HuH-7 cells. ^a						
Dose (log ₁₀ PFU/ml)	Mouse #	Virus titer				
		log ₁₀ PFU/ml serum		log ₁₀ PFU/g tissue		
		day 3	day 5	Brain	Liver	Tumor
6	91	4.4	8.3	6.0	7.3	8.0
	92	4.2	7.7	3.3	6.9	7.3
	93	4.0	6.6	3.3	5.7	8.4
	94	4.3	8.1	5.8	7.8	7.5

^aSCID mice were injected i.p. with 10⁷ HuH-7 human hepatoma cells. Approximately 8 weeks later, groups of tumor-bearing SCID-HuH-7 mice were inoculated with virus directly into the tumor. Serum and tissues were collected on day 5, processed, and titered in Vero cells.

TABLE 18

Combination of ts mutations, NS3 4995 and NS5 7849, in rDEN4 results in an additive ts phenotype.												
Virus	Mean virus titer (log ₁₀ PFU/ml)										Replication in suckling mice ^b	
	at indicated temp (° C.)										Mean virus titer ± SE (log ₁₀ PFU/g brain)	Mean log ₁₀ reduction from wt ^c
	Vero cells					HuH-7 cells						
	35	37	38	39	Δ ^a	35	37	38	39	Δ		
2A-13 wt	7.1	7.1	6.9	6.8	0.3	7.4	7.3	6.7	6.4	1.0	6.9 ± 0.09	—
rDEN4 wt	7.0	6.8	6.6	6.4	0.6	7.5	7.3	6.7	6.4	1.1	6.5 ± 0.11	—
rDEN4Δ30	7.0	6.7	6.2	6.2	0.8	7.5	7.0	6.5	5.1	2.4	5.9 ± 0.21	0.6
rDEN4-4995	5.7	4.9	3.6	<u><1.6^d</u>	>4.1	6.4	5.7	4.0	<u><1.6</u>	>4.8	3.4 ± 0.10	3.1
rDEN4-7849	7.0	6.7	<u>3.7</u>	<u>2.1</u>	4.9	7.7	5.5	<u>3.6</u>	<u>2.4</u>	5.3	2.6 ± 0.29	3.9
rDEN4-4995-7849	5.9	<u>2.8</u>	<u><1.6</u>	<u><1.6</u>	>4.3	5.6	2.4	<u><1.6</u>	<u><1.6</u>	>4.0	2.3 ± 0.20	4.2

^aReduction in titer (log₁₀PFU/ml) at 39° C. compared to titer at permissive temperature (35° C.).

^bGroups of 6 suckling mice were inoculated i.c. with 10⁴ PFU virus. Brains were removed 5 days later, homogenized, and titered in Vero cells. The limit of detection is 2.0 log₁₀PFU/g.

^cDetermined by comparing mean viral titers of mice inoculated with sample virus and rDEN4 wt control.

^dUnderlined values indicate a 2.5 or 3.5 log₁₀PFU/ml reduction in titer in Vero cells or HuH-7 cells, respectively, at indicated temperature when compared to permissive temperature.

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TABLE 19

The 5-FU mutations are compatible with the Δ30 mutation for replication in the brain of suckling mice.

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Virus	No. of mice/group	Mean virus titer ± SE (log ₁₀ PFU/g brain) ^a	Mean log ₁₀ -
			unit reduction from wt ^b
rDEN4	12	6.0 ± 0.1	—
rDEN4Δ30	12	5.3 ± 0.1	0.7
rDEN4-2650 ^c	12	3.7 ± 0.2	2.3
rDEN4Δ30-2650	12	3.9 ± 0.1	2.1
rDEN4-4995 ^d	6	3.5 ± 0.2	2.5
55 rDEN4Δ30-4995	6	2.7 ± 0.4	3.3
rDEN4-8092 ^d	12	2.0 ± 0.1	4.0
rDEN4Δ30-8092	6	3.2 ± 0.2	2.8
rDEN4-10634 ^c	12	3.8 ± 0.1	2.2
rDEN4Δ30-10634	12	3.6 ± 0.1	2.4

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^aGroups of 6 suckling mice were inoculated i.c. with 10⁴ PFU of virus. Brains were removed 5 days later, homogenized, and titered in Vero cells.

^bComparison of mean virus titers of mice inoculated with mutant virus and rDEN4 control.

^cMutation restricts growth in both mouse brain and HuH-7-SCID mice.

65 ^dMutation restricts growth in mouse brain only. The 8092 mutation has not been tested in SCID-HuH7 mice.

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TABLE 22

Combination of paired charge-cluster-to-alanine mutations into double-pair mutant viruses.		
Mutation Pair 1	Mutation Pair 2	Recovered
23-24	200-201	Yes
23-24	356-357	Yes
23-24	396-397	Yes
23-24	523-524	Yes
23-24	827-828	No
157-158	200-201	No
157-158	356-357	No

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TABLE 22-continued

Combination of paired charge-cluster-to-alanine mutations into double-pair mutant viruses.		
Mutation Pair 1	Mutation Pair 2	Recovered
157-158	396-397	No
157-158	523-524	Yes
157-158	827-828	No
827-828	200-201	No
827-828	356-357	No
827-828	396-397	Yes
827-828	523-524	No

TABLE 23

Temperature-sensitive and mouse brain attenuation phenotypes of double charge-cluster-to-alanine mutants of the NS5 gene of rDEN4.

Mutation ^a	AA Pair	# nt changed	Mean virus titer (log ₁₀ PFU/ml) at indicated temperature (° C.) ^b											Replication in suckling mice ^d			
			Charged	# nt	Vero Cells					HuH-7 cells					n	Mean virus titer ± SE (log ₁₀ PFU/g brain)	Mean log reduction from wt ^e
					35	37	38	39	Δ ^c	35	37	38	39	Δ			
					35	37	38	39	Δ	35	37	38	39	Δ			
wt	n/a	0	8.1	8.1	7.9	7.6	0.5	8.3	8.0	7.5	7.5	0.8	48	6.0 ± 0.16	—		
Δ30	n/a	30	6.3	6.1	6.1	5.7	0.6	6.9	6.3	5.9	4.7	2.2	42	5.4 ± 0.22	0.6		
23-24	K E	3	6.7	6.6	6.0	6.5	0.2	7.1	7.3	5.6	<u><1.7</u>	>5.4	18	4.7 ± 0.09	1.5		
200-201	K H	4	5.3	4.6	5.3	4.1	1.2	5.6	4.9	3.7	<u><1.7</u>	>3.9	12	5.5 ± 0.45	0.8		
23-24; 200-201	K E, K H	7	7.1	6.5	6.6	<u><1.7</u>	>5.4	7.8	7.3	<u><1.7</u>	<u><1.7</u>	>6.1	6	5.8 ± 0.16	0.6		
23-24	K E	3	6.7	6.6	6.0	6.5	0.2	7.1	7.3	5.6	<u><1.7</u>	>5.4	18	4.7 ± 0.09	1.5		
356-357	K E	3	7.7	7.6	7.0	7.0	0.7	8.0	7.3	6.4	<u><1.7</u>	>6.3	6	3.5 ± 0.58	2.0		
23-24; 356-357	K E, K E	6															
23-24	K E	3	6.7	6.6	6.0	6.5	0.2	7.1	7.3	5.6	<u><1.7</u>	>5.4	18	4.7 ± 0.09	1.5		
396-397	R E	4	7.0	7.3	6.5	5.5	1.5	7.5	7.6	7.5	<u><1.7</u>	>5.8	18	5.4 ± 0.35	1.1		
23-24; 396-397	K E, R E	7	6.3	4.9	<u><1.7</u>	<u><1.7</u>	>4.6	7.1	6.0	5.6	<u><1.7</u>	>5.4	6	3.7 ± 0.44	2.7		
157-158	E E	3	6.5	7.2	5.1	5.1	1.4	7.6	7.4	5.9	<u><1.7</u>	>5.9	6	2.8 ± 0.31	2.7		
396-397	R E	4	7.0	7.3	6.5	5.5	1.5	7.5	7.6	7.5	<u><1.7</u>	>5.8	18	5.4 ± 0.35	1.1		
157-158; 396-397	E E, R E	7											6	2.0 ± 0.12	4.8		
157-158	E E	3	6.5	7.2	5.1	5.1	1.4	7.6	7.4	5.9	<u><1.7</u>	>5.9	6	2.8 ± 0.31	2.7		
523-524	D K	4	6.6	6.3	6.3	5.8	0.8	7.1	6.6	<u><1.7</u>	<u><1.7</u>	>5.4	6	4.2 ± 0.47	1.3		
157-158; 523-524	E E, D K	7	5.6	3.9	<u><1.7</u>	<u><1.7</u>	>3.9	6.3	4.1	<u><1.7</u>	<u><1.7</u>	>4.6					
396-397	R E	4	7.0	7.3	6.5	5.5	1.5	7.5	7.6	7.5	<u><1.7</u>	>5.8	6	4.8 ± 0.54	1.6		
827-828	D K	4	6.9	6.3	6.3	5.9	1.0	7.5	6.9	5.0	<u><1.7</u>	>5.8	6	3.6 ± 0.76	2.3		
396-397; 827-828	R E, D K	8	7.0	6.5	6.0	<u><1.7</u>	5.3	>6.7	5.7	<u><1.7</u>	<u><1.7</u>	>5.0	6	4.7 ± 0.10	1.2		

^aPositions of the amino acid pair mutated to an alanine pair; numbering starts at the amino terminus of the NS5 protein.

^bUnderlined values indicate a 2.5 or 3.5 log₁₀PFU/ml reduction in titer in Vero or HuH-7 cells respectively, at the indicated temperatures when compared to permissive temperature (35° C.).

^cReduction in titer (log₁₀PFU/ml) at 39° C. compared to permissive temperature (35° C.).

^dGroups of six suckling mice were inoculated i.c. with 4.0 log₁₀PFU virus in a 30 μl inoculum. Brains were removed 5 days later, homogenized, and titered in Vero cells.

^eDetermined by comparing mean viral titers in mice inoculated with sample virus and concurrent wt controls (n = 6); reductions ≥1.5 are listed in boldface.

TABLE 24

SCID-HuH-7 attenuation phenotypes of double charge-cluster-to-alanine mutants of the NS5 gene of rDEN4.				
Mutation ^a	Charged AA Pair	Replication in SCID-HuH-7 mice ^b		
		n	Mean peak virus titer ± SE (log ₁₀ PFU/ml serum)	Mean log reduction from wt ^c
wt	n/a	21	5.4 ± 0.4	—
Δ30	n/a	4	3.7 ± 0.6	2.5
23-24	KE	19	4.7 ± 0.5	1.3
200-201	K H	12	3.7 ± 0.2	2.6
23-24; 200-201	K E, K H	13	3.4 ± 0.1	2.9
23-24	KE	19	4.7 ± 0.5	1.3
356-357	K E	10	6.3 ± 0.7	(+) 1.1
23-24; 356-357	K E, K E	4	3.6 ± 0.3	2.3
23-24	KE	19	4.7 ± 0.5	1.3
396-397	R E	12	4.4 ± 1.3	1.2
23-24; 396-397	K E, R E	10	3.4 ± 0.5	3.3
157-158	EE	6	4.6 ± 0.6	1.3
396-397	R E	12	4.4 ± 1.3	1.2

TABLE 24-continued

SCID-HuH-7 attenuation phenotypes of double charge-cluster-to-alanine mutants of the NS5 gene of rDEN4.				
Mutation ^a	Charged AA Pair	Replication in SCID-HuH-7 mice ^b		
		n	Mean peak virus titer ± SE (log ₁₀ PFU/ml serum)	Mean log reduction from wt ^c
157-158; 396-397	E E, R E	6	2.2 ± 0.2	3.6
157-158	E E	6	4.6 ± 0.6	1.3
523-524	D K	5	5.3 ± 0.7	0.6
157-158; 523-524	E E, D K	3	5.1 ± 0.6	0.8
396-397	R E	12	4.4 ± 1.3	1.2
827-828	D K	5	2.9 ± 0.2	1.6
396-397; 827-828	R E, D K	4	4.1 ± 0.7	0.4

^aPositions of the amino acid pair mutated to an alanine pair; numbering starts at the amino terminus of the NS5 protein.
^bGroups of SCID-HuH-7 mice were inoculated directly into the tumor with 10⁴ PFU of virus. Serum was collected on days 6 and 7 and titered in Vero cells.
^cComparison of mean virus titers of mice inoculated with mutant virus and concurrent DEN4 control. Bold denotes a ≥100-fold decrease in replication. A (+) sign indicates an increase in replication relative to wt.

TABLE 25

Phenotypes (temperature sensitivity, plaque size and replication in mouse brain and SCID-HuH-7 mice) of wt DEN4 and viruses containing the Δ30 and 7129 mutations.														
Virus ID	Mutation ^a	Mean virus titer (log ₁₀ PFU/ml) at indicated temperature (° C.)							Replication in suckling mouse brain ^c			Replication in SCID-HuH-7 mice ^e		
		VERO			HUH7			C6/36	n	Mean virus titer ± SE (log ₁₀ PFU/g brain)	Mean log reduction from wt ^d	n	Mean peak virus titer ± SE (log ₁₀ PFU/ml serum) ^f	Mean log reduction from wt ^d
		35	39	Δ ^b	35	39	Δ							
1-TD- 1A	wt	7.3	6.8	0.5	8	6.8	1.2	8.3	36	6.1 ± 0.21	—	21	5.4 ± 0.4	—
p4Δ30	Δ30	6.6	6.5	0.1	7.4	6.4	1.0	42	5.4 ± 0.22	0.6	4	3.7 ± 0.6	2.5	
5-1A1	C7129U	6.7	6.5	0.2	7.5	6	1.5	7.6*	6	6.2 ± 0.30	0.0			
rDEN4-7129-1A	C7129U	7.3	7.0	0.3	7.6	6.3	1.3	7.5*	6	7.2 ± 0.12	(-)0.4	4	5.4 ± 0.8	(-)0.8
rDEN4Δ30-7129	C7129U + Δ30	7.0						7.1*						

^aPosition and identity of the mutated nucleotides.

^bReduction in titer (log₁₀PFU/ml) at 39° C. compared to permissive temperature (35° C.).

^cGroups of six suckling mice were inoculated i.c. with 4.0 log₁₀PFU virus in a 30 μl inoculum. The brain was removed 5 days later, homogenized, and titered in Vero cells.

^dDetermined by comparing mean viral titers in mice inoculated with sample virus and concurrent wt controls (n = 6). The attenuation phenotype is defined as a ≥50- or ≥100-fold decrease in replication in suckling or SCID-HuH-7 mice, respectively. A (-) sign indicates an increase in replication relative to the wt control.

^eGroups of SCID-HuH-7 mice were inoculated directly into the tumor with 10⁴ PFU virus. Serum was collected on days 6 and 7 and titered in Vero cells.

*Small plaque size.

TABLE 26

The 5-fluorouracil 5-1A1 small plaque mutant demonstrates a restriction of midgut infection following oral infection of <i>Aedes aegypti</i> mosquitoes.					
Virus tested	Dose ingested (log ₁₀ PFU) ^a	No. mosquitoes tested	Midgut-only infection ^b	Disseminated infection ^c	Total no. infected ^{d,e}
wtDEN4	4.5	19	1 (5%)	17 (89%)	18 (95%)
(2A-13)	3.5	26	9 (35%)	7 (27%)	16 (62%)
	2.5	28	1 (4%)	0	1 (4%)
				OID ₅₀ = 3.9	OID ₅₀ = 3.3
5-1A1	3.5	34	4 (12%)	2 (6%)	6 (18%)
	2.5	9	0	1 (11%)	1 (11%)
	1.5	23	0	0	0
					OID ₅₀ ≥ 3.9

^aAmount of virus ingested, assuming a 2 μl bloodmeal.

^bNumber (percentage) of mosquitoes with detectable dengue virus antigen in midgut tissue, but no detectable dengue virus antigen in head; mosquitoes were assayed 21 days post-feed, and dengue virus antigen was identified by IFA.

^cNumber (percentage) of mosquitoes with detectable dengue virus antigen in both midgut and head tissue.

^dTotal number (percentage) of mosquitoes with detectable dengue virus antigen.

^eThe proportion of total infections caused by wild type DEN4 was significantly higher than the proportion caused by 5-1A1 (logistic regression, N = 426, P < 0.0001). There were too few disseminated infection caused by 5-1A1 to permit statistical analysis.

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TABLE 27

The 5-fluorouracil 5-1A1 small plaque mutant demonstrates a restriction of infection following intrathoracic inoculation of *Toxorhynchites splendens* mosquitoes.

Virus tested	Dose ingested (log ₁₀ PFU) ^a	No. mosquitoes tested	No (%) infected ^c
wtDEN4	4.0	5	5 (100)
(2A-13)	3.0	4	4 (100)
	2.0	4	1 (25)
			MID ₅₀ = 2.3 log ₁₀ PFU
5-1A1	3.0	9	0
	2.0	7	1 (14)
	1.0	7	0
			MID ₅₀ > 3.0 log ₁₀ PFU

^aAmount of virus inoculated in a 0.22 μl inoculum.^bNumber (percentage) of mosquitoes with detectable dengue virus antigen in head tissue; mosquitoes were assayed 14 days post-inoculation, and dengue virus antigen was identified by IFA.^cThe proportion of infections caused by wild type DEN4 was significantly higher than the proportion caused by 5-1A1 (logistic regression, N = 36, P < 0.01).

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TABLE 30-continued

Infectivity of wt DEN4 and 3' UTR mutants for *Toxorhynchites splendens* via intrathoracic inoculation.

Virus	Dose (log ₁₀ PFU) ^a	No. mosquitoes tested	% Infected ^b	MID ₅₀ (log ₁₀ PFU)
rDEN4Δ10508-10530	4.4	8	0	
10530	3.4	9	11	
	2.4	4	0	

^aAmount of virus inoculated in a 0.22 μl inoculum.^bPercentage of mosquitoes with detectable dengue virus antigen in head tissue; mosquitoes were assayed 14 days post-inoculation, and dengue virus antigen was identified by IFA.

TABLE 28

Mutagenesis primers for the deletion or swap of sequences in DEN4 showing conserved differences from tick-borne flaviviruses.

DEN4 nucleotides ¹	Type of mutation ²	Mutagenesis Primer ³	SEQ ID NO
10508-10530	Δ	CTGGTGAAGCCCAACACAAAAAC	64
10508-10530	swap	CTGGTGAAGGAAGAGAGAAATTGGCAACTCCCCAACACAAAAAC	65
10535-10544	Δ	AGACCCCCCAAGCATATTGAC	66
10535-10544	swap	AGACCCCCCAATATTTCTCCTCCTATAGCATATTGAC	67
10541-10544	Δ	CCCAACACAAAGCATATTGAC	68

¹Nucleotides numbered 5' to 3', in the opposite direction from FIG. 5.3²Δ: deletion of specified DEN4 nucleotides; swap: exchange of specified DEN4 nucleotides with homologous sequence from Langat³no swap mutation was made for nucleotides 10541-10544

TABLE 29

Virus titer and plaque size of 3' UTR mutant viruses in Vero and C6/36 cells.

Virus	Vero		C6/36	
	Titer (log ₁₀ PFU/ml)	Plaque size ¹	Titer (log ₁₀ PFU/ml)	Plaque size
rDEN4Δ10508-10530	8.1	wt	7.5	wt
rDEN4swap10508-10530	5.4	sp	6.6	wt
rDEN4Δ10535-10544	5.8	wt	7.0	sp
rDEN4swap10535-10544	7.0	wt	7.3	wt
rDEN4Δ10541-10544	6.4	wt	>7.0	wt

¹Plaque size is designated as equivalent to wild type (wt) or ≥50% of wild type (sp) on the designated cell type.

TABLE 30

Infectivity of wt DEN4 and 3' UTR mutants for *Toxorhynchites splendens* via intrathoracic inoculation.

Virus	Dose (log ₁₀ PFU) ^a	No. mosquitoes tested	% Infected ^b	MID ₅₀ (log ₁₀ PFU)
rDEN4 wt	3.3	6	83	2.3
	2.3	7	57	
	1.3	6	0	
	0.3	6	0	

TABLE 31

Infectivity of 3' UTR swap mutant viruses for *Aedes aegypti* fed on an infectious bloodmeal.

Virus Tested	Dose ingested (log ₁₀ PFU) ^a	No. Mosquitoes Tested	Total No. Infected ^{b,c}	Disseminated Infections ^{c,d}
rDEN4	3.8	18	11 (61%)	4 (22%)
	2.8	15	5 (33%)	1 (6%)
	1.8	15	0	0
			OID ₅₀ = 3.4	OID ₅₀ = ≥4.2
rDEN4swap	3.8	25	5 (20%)	2 (8%)
10535-10544	2.8	25	0	0
	1.8	20	0	0
			OID ₅₀ =	≥4.2

^aAmount of virus ingested, assuming a 2 μl bloodmeal.^bNumber (%) of mosquitoes with detectable dengue virus antigen in the midgut tissue; mosquitoes were assayed either 14 d post-feed and dengue virus antigen was identified by IFA.^cAt a dose of 3.8 log₁₀PFU, rDEN4swap 10535-10544 infected significantly fewer mosquitoes at the midgut than wt rDEN4 (Fisher's exact test, N = 43, P < 0.01), although disseminated infections were not significantly different (Fisher's exact test, N = 43, P = 0.38).^dNumber (%) of mosquitoes with detectable dengue virus antigen in the head tissue.

TABLE 32

Putative Vero cell adaptation mutations derived from the set of 5-FU mutant viruses and other DEN4 viruses passaged in Vero cells.							
Nucleotide position	Gene/region (a.a. #) ^b	5-FU mutant viruses			Other DEN viruses passaged in Vero cells		
		Nucleotide change	Amino acid change	No. of viruses with the mutation	Virus	Nucleotide change	Amino acid change
1455	E (452)	G > U	val > phe	5			
2280 ^{1,2,3}	E (727)	U > C	phe > leu	2			
4891 ^{2,3}	NS3 (1597)	U > C	ile > thr	2			
4995 ^{1,2}	NS3 (1599)	U > C	ser > pro	8			
7153	NS4B (2351)	U > C	val > ala	3	2AΔ30	U > C	val > ala
7162	NS4B (2354)	U > C	leu > ser	4	2A-1	U > C	leu > ser
7163	NS4B (2354)	A > U or C	leu > phe	7	rDEN4Δ30	A > U	leu > phe
					2A-13-1A1	A > U	leu > phe
7182 ^{1,2,3}	NS4B (2361)	G > A	gly > ser	2			
7546	NS4B (2482)	C > U	ala > val	10			
76303	NS5 (2510)	A > G	lys > arg	1	814669	A > G	lys > arg
10275	3' UTR	A > U	n/a ^c	6			
10279	3' UTR	A > C	n/a	4			

^aConservation with DEN1, DEN2, or DEN3 is designated by superscript Lack of conservation is designated by no superscript.

^bAmino acid position in DEN4 polypeptide beginning with the methionine residue of the C protein (nt 102-104) as residue #1.

^cnot applicable

TABLE 33

Sequence analysis of rDEN2/4A30 clone 27(p4)-2-2A2.			
		Mutation	
Nucleotide	Gene	Nucleotide	Amino acid
743	M anchor	G > A	Gly > Glu
1493	E	C > U	Ser > Phe
7544*	NS4B	C > U	Ala > Val

*Same as DEN4 nucleotide position 7546

TABLE 34

Sequence analysis of rDEN2/4A30 clone 27(p3)-2-1A1.			
		Mutation	
Nucleotide	Gene	Nucleotide	Amino acid
1345	E	U > C	Tyr > His
4885*	NS3	G > A	Glu > Lys
8297	NS5	G > A	Arg > Lys

*Codon adjacent to 5-FU mutation 4891

TABLE 35

Recombinant virus rDEN2/4A30 bearing Vero adaptation mutations can be recovery and titered on Vero cells.			
Virus	Virus titer in indicated cell line ¹ (log ₁₀ PFU/ml)		Virus titer following recovery in Vero cells (log ₁₀ PFU/ml)
	C6/36	Vero	
rDEN2/4A30 wt	5.2	1.7	<0.7
rDEN2/4A30-7153	5.4	5.2	<0.7
rDEN2/4A30-7162	5.4	5.3	nd ²
rDEN2/4A30-7182	4.7	4.9	2.3
rDEN2/4A30-7630	5.3	4.8	1.3
rDEN2/4A30-7153-7163	5.1	4.7	nd

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TABLE 35-continued

Recombinant virus rDEN2/4A30 bearing Vero adaptation mutations can be recovery and titered on Vero cells.			
Virus	Virus titer in indicated cell line ¹ (log ₁₀ PFU/ml)		Virus titer following recovery in Vero cells (log ₁₀ PFU/ml)
	C6/36	Vero	
rDEN2/4A30-7153-7182	4.1	3.2	nd
rDEN2/4A30-7546-7630	5.2	5.2	nd

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¹Virus recovered following transfection of C6/36 mosquito cells was terminally diluted once in C6/36 cells and titered simultaneously in C6/36 cells and Vero cells.

²not determined

TABLE 36

Putative Vero cell adaptation mutations of dengue type 4 virus and the corresponding wildtype amino acid residue in other dengue viruses.						
Mutation	Amino acid position ^a	Mutant residue	Amino acid in indicated wt dengue virus ^b			
			DEN4	DEN1	DEN2	DEN3
1455	452	F	V	I	A	A
2280	727	L	<u>F</u> ^c	<u>F</u>	<u>F</u>	<u>F</u>
4891	1597	T	<u>I</u>	V	<u>I</u>	<u>I</u>
4995	1632	P	<u>S</u>	<u>S</u>	<u>S</u>	N
7129	2343	L	<u>P</u>	<u>P</u>	<u>P</u>	<u>P</u>
7153	2351	A	V	F	F	L
7162	2354	S	L	V	V	V
7163	2354	F	L	V	V	V
7182	2361	S	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>
7546	2482	V	A	L	T	V
7630	2510	R	K	S	S	K

^aAmino acid position is given for the polypeptide of DEN4

^bDEN4 = rDEN4 (GenBankAF326825); DEN1 = Western pacific (GenBank DVU88535); DEN2 = New Guinea C (GenBankAF038403); DEN3 = H87 (GenBank M93130)

^cUnderlined nucleotides are shared between DEN4 and one or more additional DEN types.

TABLE 37

Mutations known to attenuate dengue type 4 virus and the corresponding wildtype amino acid residue in other dengue virus.							
Mutation	Amino acid position ^a	Mutant residue	Amino acid in indicated wt dengue virus ^b				
			DEN4	DEN1	DEN2	DEN3	
5-FU mutations	2650	850	S	<u>N</u> ^d	<u>N</u>	<u>N</u>	<u>N</u>
	3442	1114	G	<u>E</u>	<u>E</u>	<u>E</u>	<u>E</u>
	3540	1147	K	<u>E</u>	<u>E</u>	<u>E</u>	<u>E</u>
	3575	1158	I	<u>M</u>	<u>L</u>	<u>A</u>	<u>M</u>
	3771	1224	G	<u>R</u>	<u>R</u>	<u>K</u>	<u>R</u>
	4062	1321	A	<u>T</u>	<u>L</u>	<u>A</u>	<u>T</u>
	4306	1402	S	<u>N</u>	<u>E</u>	<u>D</u>	<u>D</u>
	4891	1597	T	<u>I</u>	<u>V</u>	<u>I</u>	<u>I</u>
	4896	1599	S	<u>A</u>	<u>A</u>	<u>A</u>	<u>A</u>
	4907	1602	F	<u>L</u>	<u>L</u>	<u>L</u>	<u>L</u>
	4995	1632	P	<u>S</u>	<u>S</u>	<u>S</u>	<u>N</u>
	5097	1666	N	<u>D</u>	<u>D</u>	<u>D</u>	<u>D</u>
	5695	1865	G	<u>D</u>	<u>D</u>	<u>D</u>	<u>D</u>
	6259	2053	A	<u>V</u>	<u>V</u>	<u>V</u>	<u>V</u>
	7129 ^c	2343	L	<u>P</u>	<u>P</u>	<u>P</u>	<u>P</u>
	7849	2583	I	<u>N</u>	<u>K</u>	<u>N</u>	<u>K</u>
	8092	2664	G	<u>E</u>	<u>Q</u>	<u>Q</u>	<u>Q</u>
	10186	3362	T	<u>I</u>	<u>I</u>	<u>I</u>	<u>I</u>
	10634	3' UTR	—	—	—	—	—
	Charge-cluster-to-alanine mutations	22, 23	2509, 2510	AA	<u>RK</u>	<u>KS</u>	<u>KS</u>
23, 24		2510, 2511	AA	<u>KE</u>	<u>SE</u>	<u>SE</u>	<u>KE</u>
157, 158		2644, 2645	AA	<u>EE</u>	<u>EE</u>	<u>EA</u>	<u>EE</u>
200, 201		2687, 2688	AA	<u>KH</u>	<u>KH</u>	<u>KY</u>	<u>KH</u>
356, 357		2843, 2844	AA	<u>KE</u>	<u>KE</u>	<u>KE</u>	<u>KE</u>
387, 388		2874, 2875	AA	<u>KK</u>	<u>RN</u>	<u>KK</u>	<u>RN</u>
436, 437		2923, 2924	AA	<u>DK</u>	<u>HR</u>	<u>DK</u>	<u>DK</u>
524, 525		3011, 3012	AA	<u>KK</u>	<u>KI</u>	<u>KK</u>	<u>KI</u>
525, 526		3012, 3013	AA	<u>KD</u>	<u>IP</u>	<u>KE</u>	<u>IP</u>
642, 643		3129, 3130	AA	<u>ER</u>	<u>ER</u>	<u>IA</u>	<u>KK</u>
654, 655		3141, 3142	AA	<u>DR</u>	<u>ER</u>	<u>ER</u>	<u>ER</u>
808, 809		3295, 3296	AA	<u>ED</u>	<u>ED</u>	<u>ED</u>	<u>ED</u>
827, 828		3314, 3315	AA	<u>DK</u>	<u>DK</u>	<u>DK</u>	<u>DK</u>
877, 878		3364, 3365	AA	<u>KE</u>	<u>NE</u>	<u>NE</u>	<u>NE</u>
878, 879	3365, 3366	AA	<u>EE</u>	<u>EN</u>	<u>EE</u>	<u>EE</u>	

^aAmino acid position is given for the polyprotein of DEN4

^bDEN4 = rDEN4 (GenBank AF326825); DEN1 = Western pacific (GenBank U88535); DEN2 = New Guinea C (GenBank AF038403); DEN3 = H87 (GenBank M93130)

^cThis mutation results in decreased replication of DEN4 in mosquitoes.

^dUnderlined nucleotides are shared between DEN4 and one or more additional DEN types.

APPENDIX 1

25

Sequence of Recombinant Dengue Type 4 Virus
Strain 2A

LOCUS AF375822 10649 bp ss-RNA linear VRL 19 SEP. 2001
 DEFINITION Dengue virus type 4 recombinant clone 2A, complete genome.
 ACCESSION AF375822
 VERSION AF375822.1 GI: 14269097
 KEYWORDS .
 SOURCE Dengue virus type 4.
 ORGANISM Dengue virus type 4
 Viruses; ssRNA positive-strand viruses, no DNA stage;
 Flaviviridae; Flavivirus; Dengue virus group.
 REFERENCE 1 (bases 1 to 10649)
 AUTHORS Blaney, J. E. Jr., Johnson, D. H., Firestone, C. Y., Hanson, C. T.,
 Murphy, B. R. and Whitehead, S. S.
 TITLE Chemical Mutagenesis of Dengue Virus Type 4 Yields Mutant Viruses
 Which Are Temperature Sensitive in Vero Cells or Human Liver Cells
 and Attenuated in Mice
 JOURNAL J. Virol. 75 (20), 9731-9740 (2001)
 MEDLINE 21443968
 PUBMED 11559806
 REFERENCE 2 (bases 1 to 10649)
 AUTHORS Blaney, J. E. Jr., Johnson, D. H., Firestone, C. Y., Hanson, C. T.,
 Murphy, B. R. and Whitehead, S. S.
 TITLE Direct Submission
 JOURNAL Submitted (02 MAY 2001) LID, NIAID, 7 Center Drive, Bethesda, MD
 20892, USA
 FEATURES Location/Qualifiers
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 /organism = "Dengue virus type 4"
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 /note = "anchC"
 /product = "anchored capsid protein"
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 /note = "virC"
 /product = "virion capsid protein"
 CDS 102 . . . 10265
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 /translation = "MNQRKKVVRPPFNMLKRERNRVSTPQGLVKRFSTGLFSGKGPLR
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- continued

TLLCLIPTVMAFSLSTRDGEPLMIVAKHERGRPLLFKTTTEGINKCTLIAMDLGEMCED
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 RAETWMSSEGAWKHAQRVESWILRNPGFALLAGFMAYMIGQTGIQRTVFFVLMMLVAP
 SYGMRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQ GKPTLDFELTKT TAKEVAL
 LRTYCI EASISNITTATRCPTQGE PYLKEEQDQQYICRRDVVDRGWNGCGLFGKGGV
 VTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMI TPRS P SV
 EVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPWPWTAGADTSEV
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 RMEKLRKMSYTMCSGKFSIDKEMAETQHGT TVVKVYEGAGAPCKVPIEIRDVNKE
 KVVGR IISSTPLAENTNSVTNIELEPPFGDSYIVIGVNSALTLHWFRKSSIGK MFE
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 LVLWIGTNSRNTSMAMTCIAVGGITLFLGFTVQADMGCVVSWSGKELKCGSGIFVVDN
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 GHDLTVVAGDVKGVLTKGKRALTPPVSDLKYSWKTWGKAKIFTPEARNSTFLIDGPD
 SECPNERRAWSLEVEDYGFGMFTNIWMKFREGSSEVCDHRLMSAAIKDQKAVHAD
 GYWIESSKNQWQIEKASLIEVKTC LWPKHTLWNSGVLESQMLIPKSYAGPFSQHNY
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 VFKMSPGYVLGVFLRKLTSRETALM VIGMAMTTVLSIPHDLMELIDGISLGLIILKIV
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 GLLLLAAYVMGSSADLSLEKAAANVQWDEMADITGSP IIEVKQDEGDSFSIRDVEET
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 GVVYRIMQRGLPGKTQVGVGIHMEGVFHTMWHVTRGSVICHETGRLEPSWADVRNDMIS
 YGGWRLGDKWKEEDVQVLAIEPGKNPKHVQTKPGLFKTLTGEIGAVTLDFKPGTSG
 SPIINRKGKVI GLYNGVVTKSGDYVSAITQAERIGEPDYEVEDEIFRKKRLTIMDLH
 PGAGKTKRILPSIVREALKRRRLTLILAPTRVVAEMEEALRGLPIRYQTPAVKSEHT
 GREIVDLMCHATFTTRLLSSTRV PNYNLI VMDEAHFTDPSSVAARGYISTRVEMGEAA
 AIFMTATPPGATDPFPQSN SPIEDIEREIPERSWNTGPDWITDYQGKT VWFVPSIKAG
 NDIANCLRKSGKKVIQLSRKTFDEYPKTKLTDWDFVVTDDISEMGANFRAGRVIDPR
 RCLKPVILPDGPERVILAGPIPVTPASAAQRGRIGRNPAQEDDQYVFSGDPLKND
 HAHWTEAKMLLDNIYTPGIIPTLFGPSREKTQAIDGEPRLRGEQRKTFVELMRRGDL
 PVWLSYKVASAGISYKDREWCFTGERNNQILEENMEVEIWTREGEKKLRPRWLDARV
 YADPMALKDFKEFASGRKSITLDILTEIASLPTYLSRAKLALDNIVMLHTTERGGRA
 YQHALLNELPSSLETMLLVALLGAMTAGIFLFFMQGKGIGKLSMGLITIAVASGLLWVA
 EIQQQWIAASIILEFFLMVLLIPEPEKQRTPODNQLIYVILTILTIIGLIAANEMGLI
 EKTKTDFGFYQVKTEETILDVDLRPASAWTLYAVATTILTPMLRHTIENTSANLSLAA
 IANQA AVL MGLGKGWPLHRMDLGVPLLAMGCYSQVNPTTLTASLVMLLVHYAII CGPL
 QAKATREAQKRTAAGIMKNPTVDGITVIDLEPISYDPKFEKQLGQVMLLVLCAGQLLL

While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention. All figures, tables, and appendices, as well as patents, applications, and publications, referred to above, are hereby incorporated by reference.

 SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 70

<210> SEQ ID NO 1

<211> LENGTH: 900

<212> TYPE: PRT

<213> ORGANISM: Dengue 4 virus

<400> SEQUENCE: 1

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

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Met	Val	Thr	Gln	Leu	Ala	Met	Thr	Asp	Thr	Thr	Pro	Phe	Gly	Gln	Gln
			340					345					350		
Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	Thr	Pro	Gln	Pro	Lys	Pro
		355					360					365			
Gly	Thr	Arg	Met	Val	Met	Thr	Thr	Thr	Ala	Asn	Trp	Leu	Trp	Ala	Leu
	370					375					380				
Leu	Gly	Lys	Lys	Lys	Asn	Pro	Arg	Leu	Cys	Thr	Arg	Glu	Glu	Phe	Ile
385					390					395					400
Ser	Lys	Val	Arg	Ser	Asn	Ala	Ala	Ile	Gly	Ala	Val	Phe	Gln	Glu	Glu
				405					410					415	
Gln	Gly	Trp	Thr	Ser	Ala	Ser	Glu	Ala	Val	Asn	Asp	Ser	Arg	Phe	Trp
			420					425						430	
Glu	Leu	Val	Asp	Lys	Glu	Arg	Ala	Leu	His	Gln	Glu	Gly	Lys	Cys	Glu
		435					440					445			
Ser	Cys	Val	Tyr	Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Leu	Gly	Glu
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Phe	Gly	Arg	Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly
465					470					475					480
Ala	Arg	Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His
				485					490					495	
Trp	Phe	Gly	Arg	Glu	Asn	Ser	Trp	Ser	Gly	Val	Glu	Gly	Glu	Gly	Leu
			500					505						510	
His	Arg	Leu	Gly	Tyr	Ile	Leu	Glu	Glu	Ile	Asp	Lys	Lys	Asp	Gly	Asp
		515					520						525		
Leu	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile	Thr	Glu
	530					535						540			
Asp	Asp	Leu	Gln	Asn	Glu	Glu	Leu	Ile	Thr	Glu	Gln	Met	Ala	Pro	His
545					550					555					560
His	Lys	Ile	Leu	Ala	Lys	Ala	Ile	Phe	Lys	Leu	Thr	Tyr	Gln	Asn	Lys
				565					570					575	
Val	Val	Lys	Val	Leu	Arg	Pro	Thr	Pro	Arg	Gly	Ala	Val	Met	Asp	Ile
			580					585						590	
Ile	Ser	Arg	Lys	Asp	Gln	Arg	Gly	Ser	Gly	Gln	Val	Gly	Thr	Tyr	Gly
		595					600					605			
Leu	Asn	Thr	Phe	Thr	Asn	Met	Glu	Val	Gln	Leu	Ile	Arg	Gln	Met	Glu
						615						620			
Ala	Glu	Gly	Val	Ile	Thr	Gln	Asp	Asp	Met	Gln	Asn	Pro	Lys	Gly	Leu
	625					630				635					640
Lys	Glu	Arg	Val	Glu	Lys	Trp	Leu	Lys	Glu	Cys	Gly	Val	Asp	Arg	Leu
				645					650					655	
Lys	Arg	Met	Ala	Ile	Ser	Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Leu	Asp
			660					665					670		
Glu	Arg	Phe	Gly	Thr	Ser	Leu	Leu	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val
		675					680						685		
Arg	Lys	Asp	Ile	Pro	Gln	Trp	Glu	Pro	Ser	Lys	Gly	Trp	Lys	Asn	Trp
			690				695					700			
Gln	Glu	Val	Pro	Phe	Cys	Ser	His	His	Phe	His	Lys	Ile	Phe	Met	Lys
					710					715					720
Asp	Gly	Arg	Ser	Leu	Val	Val	Pro	Cys	Arg	Asn	Gln	Asp	Glu	Leu	Ile
				725					730					735	
Gly	Arg	Ala	Arg	Ile	Ser	Gln	Gly	Ala	Gly	Trp	Ser	Leu	Arg	Glu	Thr

-continued

740				745				750							
Ala	Cys	Leu	Gly	Lys	Ala	Tyr	Ala	Gln	Met	Trp	Ser	Leu	Met	Tyr	Phe
		755					760					765			
His	Arg	Arg	Asp	Leu	Arg	Leu	Ala	Ser	Met	Ala	Ile	Cys	Ser	Ala	Val
	770					775					780				
Pro	Thr	Glu	Trp	Phe	Pro	Thr	Ser	Arg	Thr	Thr	Trp	Ser	Ile	His	Ala
	785				790					795					800
His	His	Gln	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Lys	Val	Trp	Asn	Arg
				805					810					815	
Val	Trp	Ile	Glu	Asp	Asn	Pro	Asn	Met	Thr	Asp	Lys	Thr	Pro	Val	His
			820						825				830		
Ser	Trp	Glu	Asp	Ile	Pro	Tyr	Leu	Gly	Lys	Arg	Glu	Asp	Leu	Trp	Cys
		835					840					845			
Gly	Ser	Leu	Ile	Gly	Leu	Ser	Ser	Arg	Ala	Thr	Trp	Ala	Lys	Asn	Ile
	850					855					860				
His	Thr	Ala	Ile	Thr	Gln	Val	Arg	Asn	Leu	Ile	Gly	Lys	Glu	Glu	Tyr
	865				870					875					880
Val	Asp	Tyr	Met	Pro	Val	Met	Lys	Arg	Tyr	Ser	Ala	Pro	Ser	Glu	Ser
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<210> SEQ ID NO 2
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 <212> TYPE: DNA
 <213> ORGANISM: Dengue 4 virus

<400> SEQUENCE: 2

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acaaaaacag catattgacg ctgggaaaga ccagagatcc tgctgtctct gcaacatcaa    180
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<210> SEQ ID NO 3
 <211> LENGTH: 228
 <212> TYPE: DNA
 <213> ORGANISM: Dengue 1 virus

<400> SEQUENCE: 3

```

gactagtggg tagaggagac cctcccaag acacaacgca gcagcggggc ccaacaccag    60
gggaagctgt accctgggtg taaggactag aggttagagg agacccccg cacaacaaca    120
aacagcatat tgacgctggg agagaccaga gatcctgctg tctctacagc atcattccag    180
gcacagaacg ccaaaaaatg gaatggtgct gttgaatcaa caggttct          228

```

<210> SEQ ID NO 4
 <211> LENGTH: 230
 <212> TYPE: DNA
 <213> ORGANISM: Dengue 2 virus

<400> SEQUENCE: 4

```

gactagcggg tagaggagac cctccctta caaatcgcag caacaatggg ggcccaggt    60
gagatgaagc tgtagtctca ctggaaggac tagaggtagg aggagacccc cccaaaacaa    120
aaaacagcat attgacgctg ggaaagacca gagatcctgc tgtctcctca gcatcattcc    180
aggcacagaa cgccagaaaa tggaatggtg ctgttgaatc aacaggttct          230

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<210> SEQ ID NO 5
<211> LENGTH: 227
<212> TYPE: DNA
<213> ORGANISM: Dengue 3 virus

<400> SEQUENCE: 5
gactagtggg tagaggagac cctcccatg acacaacgca gcagcggggc cggagcactg    60
agggaaagctg tacctccttg caaaggacta gaggttatag gagaccccc gcaaacaaaa    120
acagcatatt gacgctggga gagaccagag atcctgctgt ctctcagca tcattccagg    180
cacagaacgc cagaaaatgg aatgggtgctg ttgaatcaac aggttct                227

```

```

<210> SEQ ID NO 6
<211> LENGTH: 227
<212> TYPE: DNA
<213> ORGANISM: West Nile virus

<400> SEQUENCE: 6
gactagaggt tagaggagac cccgcgtaaa aaagtgcacg gcccaacttg gctgaagctg    60
taagccaagg gaaggactag aggttagagg agaccccgctg ccaaaaacac caaaagaaac    120
agcatattga cacctgggat agactagggg atcttctgct ctgcacaacc agccacacgg    180
cacagtgcgc cgacataggt ggctgggtgg gctagaacac aggatct                227

```

```

<210> SEQ ID NO 7
<211> LENGTH: 229
<212> TYPE: DNA
<213> ORGANISM: Japanese encephalitis virus

<400> SEQUENCE: 7
gactagaggt tagaggagac cccgtggaaa caacaacatg cggcccaagc cccctcgaag    60
ctgtagagga ggtggaagga ctagagggta gaggagacc cgcatttgca tcaaacagca    120
tattgacacc tgggaataga ctgggagatc ttctgctcta tctcaacatc agctactagg    180
cacagagcgc cgaagtatgt acgtgggtgg gaggaagaac acaggatct                229

```

```

<210> SEQ ID NO 8
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Yellow fever virus

<400> SEQUENCE: 8
aacctggttt ctgggacctc ccaccccaga gtaaaaagaa cggagcctcc gctaccaccc    60
tcccacgtgg tggtagaaag acggggctca gaggttagag gagaccctcc agggaaacaaa    120
tagtgggacc atattgacgc cagggaaaga cgggagtggt tctctgcttt tctccagag    180
gtctgtgagc acagtttgct caagaataag cagaccttg gatgacaaac acaaaaccac    240
t                                                                241

```

```

<210> SEQ ID NO 9
<211> LENGTH: 249
<212> TYPE: DNA
<213> ORGANISM: Powassan virus

<400> SEQUENCE: 9
aaacgaactt tgtgagacca aaaggcctcc tggaaaggctc accaggagtt aggcggttta    60
ggagcccccg agcataactc gggaggaggg aggaagaaaa ttggcaatct tctcgggat    120

```

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```

ttttccgect cctatactaa atttccccca ggaaactggg ggggcgggtc ttgttctccc 180
tgagccacca ccatccaggc acagatagcc tgacaaggag atggtgtgtg actcggaaaa 240
acacccgct 249

```

```

<210> SEQ ID NO 10
<211> LENGTH: 250
<212> TYPE: DNA
<213> ORGANISM: Louping ill virus

```

```

<400> SEQUENCE: 10

```

```

tgcaagattt tgcgagacc cccgccccat gacaaggccg aacatggagc attaaagggg 60
ggcccccgga agcatgcttc cgggaggagg gaagagagaa attggcagct ctcttcaggg 120
tttttctctc tcctatacca aatttcccc tcgacagagg gggggcggtt cttgttctcc 180
ctgagccacc atcaccaga cacagatagt ctgacaagga ggtgatgtgt gactcggaaa 240
aacacccgct 250

```

```

<210> SEQ ID NO 11
<211> LENGTH: 250
<212> TYPE: DNA
<213> ORGANISM: Tick-borne encephalitis virus

```

```

<400> SEQUENCE: 11

```

```

tgaaaaattt tgtgagacc cctgcatcat gataaggccg aacatggtgc atgaaagggg 60
aggccccggg aagcacgctt ccgggaggag ggaagagaga aattggcagc tctcttcagg 120
atTTTTctctc ctctataca aaattcccc tcggtagagg gggggcggtt cttgttctcc 180
ctgagccacc atcaccaga cacaggtagt ctgacaagga ggtgatgtgt gactcggaaa 240
aacacccgct 250

```

```

<210> SEQ ID NO 12
<211> LENGTH: 247
<212> TYPE: DNA
<213> ORGANISM: Langat virus

```

```

<400> SEQUENCE: 12

```

```

tgtgaaactt tgtgagacc cttgcgtcca gagaaggccg aactgggctt tataaggagg 60
ccccaggggg gaaacccttg ggaggaggga agagagaaat tggcaactct cttcaggata 120
tttctctctc ctatacaaa tccccctcg tcagaggggg ggcggttctt gttctccctg 180
agccaccatc acctagacac agatagtctg aaaaggaggt gatgcgtgtc tcggaaaaac 240
accgct 247

```

```

<210> SEQ ID NO 13
<211> LENGTH: 3387
<212> TYPE: PRT
<213> ORGANISM: Dengue 4 virus strain 2A

```

```

<400> SEQUENCE: 13

```

```

Met Asn Gln Arg Lys Lys Val Val Arg Pro Pro Phe Asn Met Leu Lys
 1           5           10           15

Arg Glu Arg Asn Arg Val Ser Thr Pro Gln Gly Leu Val Lys Arg Phe
          20           25           30

Ser Thr Gly Leu Phe Ser Gly Lys Gly Pro Leu Arg Met Val Leu Ala
          35           40           45

Phe Ile Thr Phe Leu Arg Val Leu Ser Ile Pro Pro Thr Ala Gly Ile
          50           55           60

```

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

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Lys Lys Lys Thr Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro
 485 490 495
 Leu Pro Trp Thr Ala Gly Ala Asp Thr Ser Glu Val His Trp Asn Tyr
 500 505 510
 Lys Glu Arg Met Val Thr Phe Lys Val Pro His Ala Lys Arg Gln Asp
 515 520 525
 Val Thr Val Leu Gly Ser Gln Glu Gly Ala Met His Ser Ala Leu Ala
 530 535 540
 Gly Ala Thr Glu Val Asp Ser Gly Asp Gly Asn His Met Phe Ala Gly
 545 550 555 560
 His Leu Lys Cys Lys Val Arg Met Glu Lys Leu Arg Ile Lys Gly Met
 565 570 575
 Ser Tyr Thr Met Cys Ser Gly Lys Phe Ser Ile Asp Lys Glu Met Ala
 580 585 590
 Glu Thr Gln His Gly Thr Thr Val Val Lys Val Lys Tyr Glu Gly Ala
 595 600 605
 Gly Ala Pro Cys Lys Val Pro Ile Glu Ile Arg Asp Val Asn Lys Glu
 610 615 620
 Lys Val Val Gly Arg Ile Ile Ser Ser Thr Pro Leu Ala Glu Asn Thr
 625 630 635 640
 Asn Ser Val Thr Asn Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr
 645 650 655
 Ile Val Ile Gly Val Gly Asn Ser Ala Leu Thr Leu His Trp Phe Arg
 660 665 670
 Lys Gly Ser Ser Ile Gly Lys Met Phe Glu Ser Thr Tyr Arg Gly Ala
 675 680 685
 Lys Arg Met Ala Ile Leu Gly Glu Thr Ala Trp Asp Phe Gly Ser Val
 690 695 700
 Gly Gly Leu Phe Thr Ser Leu Gly Lys Ala Val His Gln Val Phe Gly
 705 710 715 720
 Ser Val Tyr Thr Thr Met Phe Gly Gly Val Ser Trp Met Ile Arg Ile
 725 730 735
 Leu Ile Gly Phe Leu Val Leu Trp Ile Gly Thr Asn Ser Arg Asn Thr
 740 745 750
 Ser Met Ala Met Thr Cys Ile Ala Val Gly Gly Ile Thr Leu Phe Leu
 755 760 765
 Gly Phe Thr Val Gln Ala Asp Met Gly Cys Val Val Ser Trp Ser Gly
 770 775 780
 Lys Glu Leu Lys Cys Gly Ser Gly Ile Phe Val Val Asp Asn Val His
 785 790 795 800
 Thr Trp Thr Glu Gln Tyr Lys Phe Gln Pro Glu Ser Pro Ala Arg Leu
 805 810 815
 Ala Ser Ala Ile Leu Asn Ala His Lys Asp Gly Val Cys Gly Ile Arg
 820 825 830
 Ser Thr Thr Arg Leu Glu Asn Val Met Trp Lys Gln Ile Thr Asn Glu
 835 840 845
 Leu Asn Tyr Val Leu Trp Glu Gly Gly His Asp Leu Thr Val Val Ala
 850 855 860
 Gly Asp Val Lys Gly Val Leu Thr Lys Gly Lys Arg Ala Leu Thr Pro
 865 870 875 880
 Pro Val Ser Asp Leu Lys Tyr Ser Trp Lys Thr Trp Gly Lys Ala Lys
 885 890 895
 Ile Phe Thr Pro Glu Ala Arg Asn Ser Thr Phe Leu Ile Asp Gly Pro

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900					905					910					
Asp	Thr	Ser	Glu	Cys	Pro	Asn	Glu	Arg	Arg	Ala	Trp	Asn	Ser	Leu	Glu
		915					920					925			
Val	Glu	Asp	Tyr	Gly	Phe	Gly	Met	Phe	Thr	Thr	Asn	Ile	Trp	Met	Lys
	930					935					940				
Phe	Arg	Glu	Gly	Ser	Ser	Glu	Val	Cys	Asp	His	Arg	Leu	Met	Ser	Ala
	945					950					955				960
Ala	Ile	Lys	Asp	Gln	Lys	Ala	Val	His	Ala	Asp	Met	Gly	Tyr	Trp	Ile
				965					970					975	
Glu	Ser	Ser	Lys	Asn	Gln	Thr	Trp	Gln	Ile	Glu	Lys	Ala	Ser	Leu	Ile
			980					985					990		
Glu	Val	Lys	Thr	Cys	Leu	Trp	Pro	Lys	Thr	His	Thr	Leu	Trp	Ser	Asn
		995					1000						1005		
Gly	Val	Leu	Glu	Ser	Gln	Met	Leu	Ile	Pro	Lys	Ser	Tyr	Ala	Gly	Pro
	1010					1015						1020			
Phe	Ser	Gln	His	Asn	Tyr	Arg	Gln	Gly	Tyr	Ala	Thr	Gln	Thr	Val	Gly
	1025			1030					1035						1040
Pro	Trp	His	Leu	Gly	Lys	Leu	Glu	Ile	Asp	Phe	Gly	Glu	Cys	Pro	Gly
				1045					1050					1055	
Thr	Thr	Val	Thr	Ile	Gln	Glu	Asp	Cys	Asp	His	Arg	Gly	Pro	Ser	Leu
			1060					1065					1070		
Arg	Thr	Thr	Thr	Ala	Ser	Gly	Lys	Leu	Val	Thr	Gln	Trp	Cys	Cys	Arg
			1075				1080						1085		
Ser	Cys	Thr	Met	Pro	Pro	Leu	Arg	Phe	Leu	Gly	Glu	Asp	Gly	Cys	Trp
	1090					1095						1100			
Tyr	Gly	Met	Glu	Ile	Arg	Pro	Leu	Ser	Glu	Lys	Glu	Glu	Asn	Met	Val
	1105					1110					1115				1120
Lys	Ser	Gln	Val	Thr	Ala	Gly	Gln	Gly	Thr	Ser	Glu	Thr	Phe	Ser	Met
				1125					1130					1135	
Gly	Leu	Leu	Cys	Leu	Thr	Leu	Phe	Val	Glu	Glu	Cys	Leu	Arg	Arg	Arg
			1140					1145					1150		
Val	Thr	Arg	Lys	His	Met	Ile	Leu	Val	Val	Val	Ile	Thr	Leu	Cys	Ala
		1155					1160						1165		
Ile	Ile	Leu	Gly	Gly	Leu	Thr	Trp	Met	Asp	Leu	Leu	Arg	Ala	Leu	Ile
	1170					1175						1180			
Met	Leu	Gly	Asp	Thr	Met	Ser	Gly	Arg	Ile	Gly	Gly	Gln	Ile	His	Leu
	1185					1190					1195				1200
Ala	Ile	Met	Ala	Val	Phe	Lys	Met	Ser	Pro	Gly	Tyr	Val	Leu	Gly	Val
				1205					1210					1215	
Phe	Leu	Arg	Lys	Leu	Thr	Ser	Arg	Glu	Thr	Ala	Leu	Met	Val	Ile	Gly
			1220					1225					1230		
Met	Ala	Met	Thr	Thr	Val	Leu	Ser	Ile	Pro	His	Asp	Leu	Met	Glu	Leu
			1235				1240					1245			
Ile	Asp	Gly	Ile	Ser	Leu	Gly	Leu	Ile	Leu	Leu	Lys	Ile	Val	Thr	Gln
	1250					1255					1260				
Phe	Asp	Asn	Thr	Gln	Val	Gly	Thr	Leu	Ala	Leu	Ser	Leu	Thr	Phe	Ile
	1265			1270					1275						1280
Arg	Ser	Thr	Met	Pro	Leu	Val	Met	Ala	Trp	Arg	Thr	Ile	Met	Ala	Val
				1285					1290					1295	
Leu	Phe	Val	Val	Thr	Leu	Ile	Pro	Leu	Cys	Arg	Thr	Ser	Cys	Leu	Gln
			1300				1305						1310		
Lys	Gln	Ser	His	Trp	Val	Glu	Ile	Thr	Ala	Leu	Ile	Leu	Gly	Ala	Gln
			1315				1320						1325		

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Ala Leu Pro Val Tyr Leu Met Thr Leu Met Lys Gly Ala Ser Arg Arg
1330 1335 1340

Ser Trp Pro Leu Asn Glu Gly Ile Met Ala Val Gly Leu Val Ser Leu
1345 1350 1355 1360

Leu Gly Ser Ala Leu Leu Lys Asn Asp Val Pro Leu Ala Gly Pro Met
1365 1370 1375

Val Ala Gly Gly Leu Leu Leu Ala Ala Tyr Val Met Ser Gly Ser Ser
1380 1385 1390

Ala Asp Leu Ser Leu Glu Lys Ala Ala Asn Val Gln Trp Asp Glu Met
1395 1400 1405

Ala Asp Ile Thr Gly Ser Ser Pro Ile Ile Glu Val Lys Gln Asp Glu
1410 1415 1420

Asp Gly Ser Phe Ser Ile Arg Asp Val Glu Glu Thr Asn Met Ile Thr
1425 1430 1435 1440

Leu Leu Val Lys Leu Ala Leu Ile Thr Val Ser Gly Leu Tyr Pro Leu
1445 1450 1455

Ala Ile Pro Val Thr Met Thr Leu Trp Tyr Met Trp Gln Val Lys Thr
1460 1465 1470

Gln Arg Ser Gly Ala Leu Trp Asp Val Pro Ser Pro Ala Ala Thr Lys
1475 1480 1485

Lys Ala Ala Leu Ser Glu Gly Val Tyr Arg Ile Met Gln Arg Gly Leu
1490 1495 1500

Phe Gly Lys Thr Gln Val Gly Val Gly Ile His Met Glu Gly Val Phe
1505 1510 1515 1520

His Thr Met Trp His Val Thr Arg Gly Ser Val Ile Cys His Glu Thr
1525 1530 1535

Gly Arg Leu Glu Pro Ser Trp Ala Asp Val Arg Asn Asp Met Ile Ser
1540 1545 1550

Tyr Gly Gly Gly Trp Arg Leu Gly Asp Lys Trp Asp Lys Glu Glu Asp
1555 1560 1565

Val Gln Val Leu Ala Ile Glu Pro Gly Lys Asn Pro Lys His Val Gln
1570 1575 1580

Thr Lys Pro Gly Leu Phe Lys Thr Leu Thr Gly Glu Ile Gly Ala Val
1585 1590 1595 1600

Thr Leu Asp Phe Lys Pro Gly Thr Ser Gly Ser Pro Ile Ile Asn Arg
1605 1610 1615

Lys Gly Lys Val Ile Gly Leu Tyr Gly Asn Gly Val Val Thr Lys Ser
1620 1625 1630

Gly Asp Tyr Val Ser Ala Ile Thr Gln Ala Glu Arg Ile Gly Glu Pro
1635 1640 1645

Asp Tyr Glu Val Asp Glu Asp Ile Phe Arg Lys Lys Arg Leu Thr Ile
1650 1655 1660

Met Asp Leu His Pro Gly Ala Gly Lys Thr Lys Arg Ile Leu Pro Ser
1665 1670 1675 1680

Ile Val Arg Glu Ala Leu Lys Arg Arg Leu Arg Thr Leu Ile Leu Ala
1685 1690 1695

Pro Thr Arg Val Val Ala Ala Glu Met Glu Glu Ala Leu Arg Gly Leu
1700 1705 1710

Pro Ile Arg Tyr Gln Thr Pro Ala Val Lys Ser Glu His Thr Gly Arg
1715 1720 1725

Glu Ile Val Asp Leu Met Cys His Ala Thr Phe Thr Thr Arg Leu Leu
1730 1735 1740

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Ser Ser Thr Arg Val Pro Asn Tyr Asn Leu Ile Val Met Asp Glu Ala
 1745 1750 1755 1760
 His Phe Thr Asp Pro Ser Ser Val Ala Ala Arg Gly Tyr Ile Ser Thr
 1765 1770 1775
 Arg Val Glu Met Gly Glu Ala Ala Ala Ile Phe Met Thr Ala Thr Pro
 1780 1785 1790
 Pro Gly Ala Thr Asp Pro Phe Pro Gln Ser Asn Ser Pro Ile Glu Asp
 1795 1800 1805
 Ile Glu Arg Glu Ile Pro Glu Arg Ser Trp Asn Thr Gly Phe Asp Trp
 1810 1815 1820
 Ile Thr Asp Tyr Gln Gly Lys Thr Val Trp Phe Val Pro Ser Ile Lys
 1825 1830 1835 1840
 Ala Gly Asn Asp Ile Ala Asn Cys Leu Arg Lys Ser Gly Lys Lys Val
 1845 1850 1855
 Ile Gln Leu Ser Arg Lys Thr Phe Asp Thr Glu Tyr Pro Lys Thr Lys
 1860 1865 1870
 Leu Thr Asp Trp Asp Phe Val Val Thr Thr Asp Ile Ser Glu Met Gly
 1875 1880 1885
 Ala Asn Phe Arg Ala Gly Arg Val Ile Asp Pro Arg Arg Cys Leu Lys
 1890 1895 1900
 Pro Val Ile Leu Pro Asp Gly Pro Glu Arg Val Ile Leu Ala Gly Pro
 1905 1910 1915 1920
 Ile Pro Val Thr Pro Ala Ser Ala Ala Gln Arg Arg Gly Arg Ile Gly
 1925 1930 1935
 Arg Asn Pro Ala Gln Glu Asp Asp Gln Tyr Val Phe Ser Gly Asp Pro
 1940 1945 1950
 Leu Lys Asn Asp Glu Asp His Ala His Trp Thr Glu Ala Lys Met Leu
 1955 1960 1965
 Leu Asp Asn Ile Tyr Thr Pro Glu Gly Ile Ile Pro Thr Leu Phe Gly
 1970 1975 1980
 Pro Glu Arg Glu Lys Thr Gln Ala Ile Asp Gly Glu Phe Arg Leu Arg
 1985 1990 1995 2000
 Gly Glu Gln Arg Lys Thr Phe Val Glu Leu Met Arg Arg Gly Asp Leu
 2005 2010 2015
 Pro Val Trp Leu Ser Tyr Lys Val Ala Ser Ala Gly Ile Ser Tyr Lys
 2020 2025 2030
 Asp Arg Glu Trp Cys Phe Thr Gly Glu Arg Asn Asn Gln Ile Leu Glu
 2035 2040 2045
 Glu Asn Met Glu Val Glu Ile Trp Thr Arg Glu Gly Glu Lys Lys Lys
 2050 2055 2060
 Leu Arg Pro Arg Trp Leu Asp Ala Arg Val Tyr Ala Asp Pro Met Ala
 2065 2070 2075 2080
 Leu Lys Asp Phe Lys Glu Phe Ala Ser Gly Arg Lys Ser Ile Thr Leu
 2085 2090 2095
 Asp Ile Leu Thr Glu Ile Ala Ser Leu Pro Thr Tyr Leu Ser Ser Arg
 2100 2105 2110
 Ala Lys Leu Ala Leu Asp Asn Ile Val Met Leu His Thr Thr Glu Arg
 2115 2120 2125
 Gly Gly Arg Ala Tyr Gln His Ala Leu Asn Glu Leu Pro Glu Ser Leu
 2130 2135 2140
 Glu Thr Leu Met Leu Val Ala Leu Leu Gly Ala Met Thr Ala Gly Ile
 2145 2150 2155 2160
 Phe Leu Phe Phe Met Gln Gly Lys Gly Ile Gly Lys Leu Ser Met Gly

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2165										2170					2175					
Leu	Ile	Thr	Ile	Ala	Val	Ala	Ser	Gly	Leu	Leu	Leu	Trp	Val	Ala	Glu	Ile				
			2180					2185						2190						
Gln	Pro	Gln	Trp	Ile	Ala	Ala	Ser	Ile	Ile	Leu	Glu	Phe	Phe	Leu	Met					
		2195					2200					2205								
Val	Leu	Leu	Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Thr	Pro	Gln	Asp	Asn					
	2210					2215					2220									
Gln	Leu	Ile	Tyr	Val	Ile	Leu	Thr	Ile	Leu	Thr	Ile	Ile	Gly	Leu	Ile					
2225					2230					2235					2240					
Ala	Ala	Asn	Glu	Met	Gly	Leu	Ile	Glu	Lys	Thr	Lys	Thr	Asp	Phe	Gly					
			2245					2250						2255						
Phe	Tyr	Gln	Val	Lys	Thr	Glu	Thr	Thr	Ile	Leu	Asp	Val	Asp	Leu	Arg					
		2260						2265					2270							
Pro	Ala	Ser	Ala	Trp	Thr	Leu	Tyr	Ala	Val	Ala	Thr	Thr	Ile	Leu	Thr					
		2275					2280						2285							
Pro	Met	Leu	Arg	His	Thr	Ile	Glu	Asn	Thr	Ser	Ala	Asn	Leu	Ser	Leu					
	2290					2295					2300									
Ala	Ala	Ile	Ala	Asn	Gln	Ala	Ala	Val	Leu	Met	Gly	Leu	Gly	Lys	Gly					
2305					2310						2315				2320					
Trp	Pro	Leu	His	Arg	Met	Asp	Leu	Gly	Val	Pro	Leu	Leu	Ala	Met	Gly					
			2325						2330					2335						
Cys	Tyr	Ser	Gln	Val	Asn	Pro	Thr	Thr	Leu	Thr	Ala	Ser	Leu	Val	Met					
			2340					2345					2350							
Leu	Leu	Val	His	Tyr	Ala	Ile	Ile	Gly	Pro	Gly	Leu	Gln	Ala	Lys	Ala					
	2355					2360						2365								
Thr	Arg	Glu	Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro					
	2370					2375					2380									
Thr	Val	Asp	Gly	Ile	Thr	Val	Ile	Asp	Leu	Glu	Pro	Ile	Ser	Tyr	Asp					
2385					2390						2395				2400					
Pro	Lys	Phe	Glu	Lys	Gln	Leu	Gly	Gln	Val	Met	Leu	Leu	Val	Leu	Cys					
			2405						2410					2415						
Ala	Gly	Gln	Leu	Leu	Leu	Met	Arg	Thr	Thr	Trp	Ala	Phe	Cys	Glu	Val					
		2420						2425					2430							
Leu	Thr	Leu	Ala	Thr	Gly	Pro	Ile	Leu	Thr	Leu	Trp	Glu	Gly	Asn	Pro					
	2435						2440					2445								
Gly	Arg	Phe	Trp	Asn	Thr	Thr	Ile	Ala	Val	Ser	Thr	Ala	Asn	Ile	Phe					
	2450					2455					2460									
Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Gly	Leu	Ala	Phe	Ser	Leu	Ile	Lys					
2465					2470						2475				2480					
Asn	Ala	Gln	Thr	Pro	Arg	Arg	Gly	Thr	Gly	Thr	Thr	Gly	Glu	Thr	Leu					
			2485					2490					2495							
Gly	Glu	Lys	Trp	Lys	Arg	Gln	Leu	Asn	Ser	Leu	Asp	Arg	Lys	Glu	Phe					
		2500						2505					2510							
Glu	Glu	Tyr	Lys	Arg	Ser	Gly	Ile	Leu	Glu	Val	Asp	Arg	Thr	Glu	Ala					
		2515					2520					2525								
Lys	Ser	Ala	Leu	Lys	Asp	Gly	Ser	Lys	Ile	Lys	His	Ala	Val	Ser	Arg					
	2530					2535					2540									
Gly	Ser	Ser	Lys	Ile	Arg	Trp	Ile	Val	Glu	Arg	Gly	Met	Val	Lys	Pro					
2545					2550						2555				2560					
Lys	Gly	Lys	Val	Val	Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr					
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<212> TYPE: DNA

<213> ORGANISM: Dengue 4 virus strain 2A

<400> SEQUENCE: 14

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tcttcttgaa cgacatggga aaggtgagga aagacattcc gcagtgggaa ccatctaagg 9660
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<210> SEQ ID NO 15

<211> LENGTH: 3387

<212> TYPE: PRT

<213> ORGANISM: Recombinant Dengue 4 virus strain rDEN4

<400> SEQUENCE: 15

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Arg Glu Arg Asn Arg Val Ser Thr Pro Gln Gly Leu Val Lys Arg Phe
          20           25           30

Ser Thr Gly Leu Phe Ser Gly Lys Gly Pro Leu Arg Met Val Leu Ala
          35           40           45

Phe Ile Thr Phe Leu Arg Val Leu Ser Ile Pro Pro Thr Ala Gly Ile
          50           55           60

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

Ile Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn Ile Leu Asn Gly
          85           90           95

Arg Lys Arg Ser Thr Ile Thr Leu Leu Cys Leu Ile Pro Thr Val Met
          100          105          110

Ala Phe Ser Leu Ser Thr Arg Asp Gly Glu Pro Leu Met Ile Val Ala
          115          120          125

Lys His Glu Arg Gly Arg Pro Leu Leu Phe Lys Thr Thr Glu Gly Ile
          130          135          140

Asn Lys Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Met Cys Glu Asp
145          150          155          160

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

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580				585				590							
Glu	Thr	Gln	His	Gly	Thr	Thr	Val	Val	Lys	Val	Lys	Tyr	Glu	Gly	Ala
		595					600					605			
Gly	Ala	Pro	Cys	Lys	Val	Pro	Ile	Glu	Ile	Arg	Asp	Val	Asn	Lys	Glu
	610					615					620				
Lys	Val	Val	Gly	Arg	Ile	Ile	Ser	Ser	Thr	Pro	Leu	Ala	Glu	Asn	Thr
	625				630					635					640
Asn	Ser	Val	Thr	Asn	Ile	Glu	Leu	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr
				645					650					655	
Ile	Val	Ile	Gly	Val	Gly	Asn	Ser	Ala	Leu	Thr	Leu	His	Trp	Phe	Arg
			660					665						670	
Lys	Gly	Ser	Ser	Ile	Gly	Lys	Met	Phe	Glu	Ser	Thr	Tyr	Arg	Gly	Ala
		675					680					685			
Lys	Arg	Met	Ala	Ile	Leu	Gly	Glu	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Val
	690					695					700				
Gly	Gly	Leu	Phe	Thr	Ser	Leu	Gly	Lys	Ala	Val	His	Gln	Val	Phe	Gly
	705					710				715					720
Ser	Val	Tyr	Thr	Thr	Met	Phe	Gly	Gly	Val	Ser	Trp	Met	Ile	Arg	Ile
				725					730					735	
Leu	Ile	Gly	Phe	Leu	Val	Leu	Trp	Ile	Gly	Thr	Asn	Ser	Arg	Asn	Thr
			740					745					750		
Ser	Met	Ala	Met	Thr	Cys	Ile	Ala	Val	Gly	Gly	Ile	Thr	Leu	Phe	Leu
		755					760					765			
Gly	Phe	Thr	Val	Gln	Ala	Asp	Met	Gly	Cys	Val	Ala	Ser	Trp	Ser	Gly
	770					775					780				
Lys	Glu	Leu	Lys	Cys	Gly	Ser	Gly	Ile	Phe	Val	Val	Asp	Asn	Val	His
	785				790					795					800
Thr	Trp	Thr	Glu	Gln	Tyr	Lys	Phe	Gln	Pro	Glu	Ser	Pro	Ala	Arg	Leu
				805					810					815	
Ala	Ser	Ala	Ile	Leu	Asn	Ala	His	Lys	Asp	Gly	Val	Cys	Gly	Ile	Arg
			820					825					830		
Ser	Thr	Thr	Arg	Leu	Glu	Asn	Val	Met	Trp	Lys	Gln	Ile	Thr	Asn	Glu
		835					840					845			
Leu	Asn	Tyr	Val	Leu	Trp	Glu	Gly	Gly	His	Asp	Leu	Thr	Val	Val	Ala
	850					855					860				
Gly	Asp	Val	Lys	Gly	Val	Leu	Thr	Lys	Gly	Lys	Arg	Ala	Leu	Thr	Pro
	865				870					875					880
Pro	Val	Ser	Asp	Leu	Lys	Tyr	Ser	Trp	Lys	Thr	Trp	Gly	Lys	Ala	Lys
				885					890					895	
Ile	Phe	Thr	Pro	Glu	Ala	Arg	Asn	Ser	Thr	Phe	Leu	Ile	Asp	Gly	Pro
			900					905					910		
Asp	Thr	Ser	Glu	Cys	Pro	Asn	Glu	Arg	Arg	Ala	Trp	Asn	Ser	Leu	Glu
		915					920					925			
Val	Glu	Asp	Tyr	Gly	Phe	Gly	Met	Phe	Thr	Thr	Asn	Ile	Trp	Met	Lys
	930					935					940				
Phe	Arg	Glu	Gly	Ser	Ser	Glu	Val	Cys	Asp	His	Arg	Leu	Met	Ser	Ala
	945				950					955					960
Ala	Ile	Lys	Asp	Gln	Lys	Ala	Val	His	Ala	Asp	Met	Gly	Tyr	Trp	Ile
				965					970					975	
Glu	Ser	Ser	Lys	Asn	Gln	Thr	Trp	Gln	Ile	Glu	Lys	Ala	Ser	Leu	Ile
			980					985					990		
Glu	Val	Lys	Thr	Cys	Leu	Trp	Pro	Lys	Thr	His	Thr	Leu	Trp	Ser	Asn
		995					1000						1005		

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Gly Val Leu Glu Ser Gln Met Leu Ile Pro Lys Ser Tyr Ala Gly Pro
 1010 1015 1020

Phe Ser Gln His Asn Tyr Arg Gln Gly Tyr Ala Thr Gln Thr Val Gly
 1025 1030 1035 1040

Pro Trp His Leu Gly Lys Leu Glu Ile Asp Phe Gly Glu Cys Pro Gly
 1045 1050 1055

Thr Thr Val Thr Ile Gln Glu Asp Cys Asp His Arg Gly Pro Ser Leu
 1060 1065 1070

Arg Thr Thr Thr Ala Ser Gly Lys Leu Val Thr Gln Trp Cys Cys Arg
 1075 1080 1085

Ser Cys Thr Met Pro Pro Leu Arg Phe Leu Gly Glu Asp Gly Cys Trp
 1090 1095 1100

Tyr Gly Met Glu Ile Arg Pro Leu Ser Glu Lys Glu Glu Asn Met Val
 1105 1110 1115 1120

Lys Ser Gln Val Thr Ala Gly Gln Gly Thr Ser Glu Thr Phe Ser Met
 1125 1130 1135

Gly Leu Leu Cys Leu Thr Leu Phe Val Glu Glu Cys Leu Arg Arg Arg
 1140 1145 1150

Val Thr Arg Lys His Met Ile Leu Val Val Val Ile Thr Leu Cys Ala
 1155 1160 1165

Ile Ile Leu Gly Gly Leu Thr Trp Met Asp Leu Leu Arg Ala Leu Ile
 1170 1175 1180

Met Leu Gly Asp Thr Met Ser Gly Arg Ile Gly Gly Gln Ile His Leu
 1185 1190 1195 1200

Ala Ile Met Ala Val Phe Lys Met Ser Pro Gly Tyr Val Leu Gly Val
 1205 1210 1215

Phe Leu Arg Lys Leu Thr Ser Arg Glu Thr Ala Leu Met Val Ile Gly
 1220 1225 1230

Met Ala Met Thr Thr Val Leu Ser Ile Pro His Asp Leu Met Glu Leu
 1235 1240 1245

Ile Asp Gly Ile Ser Leu Gly Leu Ile Leu Leu Lys Ile Val Thr Gln
 1250 1255 1260

Phe Asp Asn Thr Gln Val Gly Thr Leu Ala Leu Ser Leu Thr Phe Ile
 1265 1270 1275 1280

Arg Ser Thr Met Pro Leu Val Met Ala Trp Arg Thr Ile Met Ala Val
 1285 1290 1295

Leu Phe Val Val Thr Leu Ile Pro Leu Cys Arg Thr Ser Cys Leu Gln
 1300 1305 1310

Lys Gln Ser His Trp Val Glu Ile Thr Ala Leu Ile Leu Gly Ala Gln
 1315 1320 1325

Ala Leu Pro Val Tyr Leu Met Thr Leu Met Lys Gly Ala Ser Arg Arg
 1330 1335 1340

Ser Trp Pro Leu Asn Glu Gly Ile Met Ala Val Gly Leu Val Ser Leu
 1345 1350 1355 1360

Leu Gly Ser Ala Leu Leu Lys Asn Asp Val Pro Leu Ala Gly Pro Met
 1365 1370 1375

Val Ala Gly Gly Leu Leu Leu Ala Ala Tyr Val Met Ser Gly Ser Ser
 1380 1385 1390

Ala Asp Leu Ser Leu Glu Lys Ala Ala Asn Val Gln Trp Asp Glu Met
 1395 1400 1405

Ala Asp Ile Thr Gly Ser Ser Pro Ile Val Glu Val Lys Gln Asp Glu
 1410 1415 1420

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Asp	Gly	Ser	Phe	Ser	Ile	Arg	Asp	Val	Glu	Glu	Thr	Asn	Met	Ile	Thr	1425	1430	1435	1440
Leu	Leu	Val	Lys	Leu	Ala	Leu	Ile	Thr	Val	Ser	Gly	Leu	Tyr	Pro	Leu	1445	1450	1455	
Ala	Ile	Pro	Val	Thr	Met	Thr	Leu	Trp	Tyr	Met	Trp	Gln	Val	Lys	Thr	1460	1465	1470	
Gln	Arg	Ser	Gly	Ala	Leu	Trp	Asp	Val	Pro	Ser	Pro	Ala	Ala	Thr	Lys	1475	1480	1485	
Lys	Ala	Ala	Leu	Ser	Glu	Gly	Val	Tyr	Arg	Ile	Met	Gln	Arg	Gly	Leu	1490	1495	1500	
Phe	Gly	Lys	Thr	Gln	Val	Gly	Val	Gly	Ile	His	Met	Glu	Gly	Val	Phe	1505	1510	1515	1520
His	Thr	Met	Trp	His	Val	Thr	Arg	Gly	Ser	Val	Ile	Cys	His	Glu	Thr	1525	1530	1535	
Gly	Arg	Leu	Glu	Pro	Ser	Trp	Ala	Asp	Val	Arg	Asn	Asp	Met	Ile	Ser	1540	1545	1550	
Tyr	Gly	Gly	Gly	Trp	Arg	Leu	Gly	Asp	Lys	Trp	Asp	Lys	Glu	Glu	Asp	1555	1560	1565	
Val	Gln	Val	Leu	Ala	Ile	Glu	Pro	Gly	Lys	Asn	Pro	Lys	His	Val	Gln	1570	1575	1580	
Thr	Lys	Pro	Gly	Leu	Phe	Lys	Thr	Leu	Thr	Gly	Glu	Ile	Gly	Ala	Val	1585	1590	1595	1600
Thr	Leu	Asp	Phe	Lys	Pro	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Ile	Asn	Arg	1605	1610	1615	
Lys	Gly	Lys	Val	Ile	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val	Thr	Lys	Ser	1620	1625	1630	
Gly	Asp	Tyr	Val	Ser	Ala	Ile	Thr	Gln	Ala	Glu	Arg	Ile	Gly	Glu	Pro	1635	1640	1645	
Asp	Tyr	Glu	Val	Asp	Glu	Asp	Ile	Phe	Arg	Lys	Lys	Arg	Leu	Thr	Ile	1650	1655	1660	
Met	Asp	Leu	His	Pro	Gly	Ala	Gly	Lys	Thr	Lys	Arg	Ile	Leu	Pro	Ser	1665	1670	1675	1680
Ile	Val	Arg	Glu	Ala	Leu	Lys	Arg	Arg	Leu	Arg	Thr	Leu	Ile	Leu	Ala	1685	1690	1695	
Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	1700	1705	1710	
Pro	Ile	Arg	Tyr	Gln	Thr	Pro	Ala	Val	Lys	Ser	Glu	His	Thr	Gly	Arg	1715	1720	1725	
Glu	Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Thr	Arg	Leu	Leu	1730	1735	1740	
Ser	Ser	Thr	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Ile	Val	Met	Asp	Glu	Ala	1745	1750	1755	1760
His	Phe	Thr	Asp	Pro	Ser	Ser	Val	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr	1765	1770	1775	
Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr	Pro	1780	1785	1790	
Pro	Gly	Ala	Thr	Asp	Pro	Phe	Pro	Gln	Ser	Asn	Ser	Pro	Ile	Glu	Asp	1795	1800	1805	
Ile	Glu	Arg	Glu	Ile	Pro	Glu	Arg	Ser	Trp	Asn	Thr	Gly	Phe	Asp	Trp	1810	1815	1820	
Ile	Thr	Asp	Tyr	Gln	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Ile	Lys	1825	1830	1835	1840
Ala	Gly	Asn	Asp	Ile	Ala	Asn	Cys	Leu	Arg	Lys	Ser	Gly	Lys	Lys	Val				

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1845					1850					1855					
Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Asp	Thr	Glu	Tyr	Pro	Lys	Thr	Lys
			1860					1865					1870		
Leu	Thr	Asp	Trp	Asp	Phe	Val	Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly
		1875					1880					1885			
Ala	Asn	Phe	Arg	Ala	Gly	Arg	Val	Ile	Asp	Pro	Arg	Arg	Cys	Leu	Lys
		1890					1895					1900			
Pro	Val	Ile	Leu	Pro	Asp	Gly	Pro	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro
		1905				1910					1915				1920
Ile	Pro	Val	Thr	Pro	Ala	Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly
			1925						1930					1935	
Arg	Asn	Pro	Ala	Gln	Glu	Asp	Asp	Gln	Tyr	Val	Phe	Ser	Gly	Asp	Pro
			1940					1945					1950		
Leu	Lys	Asn	Asp	Glu	Asp	His	Ala	His	Trp	Thr	Glu	Ala	Lys	Met	Leu
		1955					1960						1965		
Leu	Asp	Asn	Ile	Tyr	Thr	Pro	Glu	Gly	Ile	Ile	Pro	Thr	Leu	Phe	Gly
		1970				1975					1980				
Pro	Glu	Arg	Glu	Lys	Thr	Gln	Ala	Ile	Asp	Gly	Glu	Phe	Arg	Leu	Arg
		1985				1990					1995				2000
Gly	Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Arg	Arg	Gly	Asp	Leu
			2005						2010					2015	
Pro	Val	Trp	Leu	Ser	Tyr	Lys	Val	Ala	Ser	Ala	Gly	Ile	Ser	Tyr	Glu
			2020						2025					2030	
Asp	Arg	Glu	Trp	Cys	Phe	Thr	Gly	Glu	Arg	Asn	Asn	Gln	Ile	Leu	Glu
		2035					2040					2045			
Glu	Asn	Met	Glu	Val	Glu	Ile	Trp	Thr	Arg	Glu	Gly	Glu	Lys	Lys	Lys
		2050					2055					2060			
Leu	Arg	Pro	Arg	Trp	Leu	Asp	Ala	Arg	Val	Tyr	Ala	Asp	Pro	Met	Ala
		2065				2070					2075				2080
Leu	Lys	Asp	Phe	Lys	Glu	Phe	Ala	Ser	Gly	Arg	Lys	Ser	Ile	Thr	Leu
			2085						2090					2095	
Asp	Ile	Leu	Thr	Glu	Ile	Ala	Ser	Leu	Pro	Thr	Tyr	Leu	Ser	Ser	Arg
			2100					2105						2110	
Ala	Lys	Leu	Ala	Leu	Asp	Asn	Ile	Val	Met	Leu	His	Thr	Thr	Glu	Arg
		2115					2120							2125	
Gly	Gly	Arg	Ala	Tyr	Gln	His	Ala	Leu	Asn	Glu	Leu	Pro	Glu	Ser	Leu
		2130					2135					2140			
Glu	Thr	Leu	Met	Leu	Val	Ala	Leu	Leu	Gly	Ala	Met	Thr	Ala	Gly	Ile
		2145					2150				2155				2160
Phe	Leu	Phe	Phe	Met	Gln	Gly	Lys	Gly	Ile	Gly	Lys	Leu	Ser	Met	Gly
			2165						2170					2175	
Leu	Ile	Thr	Ile	Ala	Val	Ala	Ser	Gly	Leu	Leu	Trp	Val	Ala	Glu	Ile
			2180					2185						2190	
Gln	Pro	Gln	Trp	Ile	Ala	Ala	Ser	Ile	Ile	Leu	Glu	Phe	Phe	Leu	Met
		2195					2200					2205			
Val	Leu	Leu	Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Thr	Pro	Gln	Asp	Asn
		2210					2215					2220			
Gln	Leu	Ile	Tyr	Val	Ile	Leu	Thr	Ile	Leu	Thr	Ile	Ile	Gly	Leu	Ile
		2225					2230					2235			2240
Ala	Ala	Asn	Glu	Met	Gly	Leu	Ile	Glu	Lys	Thr	Lys	Thr	Asp	Phe	Gly
			2245						2250					2255	
Phe	Tyr	Gln	Val	Lys	Thr	Glu	Thr	Thr	Ile	Leu	Asp	Val	Asp	Leu	Arg
			2260					2265						2270	

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Pro Ala Ser Ala Trp Thr Leu Tyr Ala Val Ala Thr Thr Ile Leu Thr
 2275 2280 2285

Pro Met Leu Arg His Thr Ile Glu Asn Thr Ser Ala Asn Leu Ser Leu
 2290 2295 2300

Ala Ala Ile Ala Asn Gln Ala Ala Val Leu Met Gly Leu Gly Lys Gly
 2305 2310 2315 2320

Trp Pro Leu His Arg Met Asp Leu Gly Val Pro Leu Leu Ala Met Gly
 2325 2330 2335

Cys Tyr Ser Gln Val Asn Pro Thr Thr Leu Thr Ala Ser Leu Val Met
 2340 2345 2350

Leu Leu Val His Tyr Ala Ile Ile Gly Pro Gly Leu Gln Ala Lys Ala
 2355 2360 2365

Thr Arg Glu Ala Gln Lys Arg Thr Ala Ala Gly Ile Met Lys Asn Pro
 2370 2375 2380

Thr Val Asp Gly Ile Thr Val Ile Asp Leu Glu Pro Ile Ser Tyr Asp
 2385 2390 2395 2400

Pro Lys Phe Glu Lys Gln Leu Gly Gln Val Met Leu Leu Val Leu Cys
 2405 2410 2415

Ala Gly Gln Leu Leu Leu Met Arg Thr Thr Trp Ala Phe Cys Glu Val
 2420 2425 2430

Leu Thr Leu Ala Thr Gly Pro Ile Leu Thr Leu Trp Glu Gly Asn Pro
 2435 2440 2445

Gly Arg Phe Trp Asn Thr Thr Ile Ala Val Ser Thr Ala Asn Ile Phe
 2450 2455 2460

Arg Gly Ser Tyr Leu Ala Gly Ala Gly Leu Ala Phe Ser Leu Ile Lys
 2465 2470 2475 2480

Asn Ala Gln Thr Pro Arg Arg Gly Thr Gly Thr Thr Gly Glu Thr Leu
 2485 2490 2495

Gly Glu Lys Trp Lys Arg Gln Leu Asn Ser Leu Asp Arg Lys Glu Phe
 2500 2505 2510

Glu Glu Tyr Lys Arg Ser Gly Ile Leu Glu Val Asp Arg Thr Glu Ala
 2515 2520 2525

Lys Ser Ala Leu Lys Asp Gly Ser Lys Ile Lys His Ala Val Ser Arg
 2530 2535 2540

Gly Ser Ser Lys Ile Arg Trp Ile Val Glu Arg Gly Met Val Lys Pro
 2545 2550 2555 2560

Lys Gly Lys Val Val Asp Leu Gly Cys Gly Arg Gly Gly Trp Ser Tyr
 2565 2570 2575

Tyr Met Ala Thr Leu Lys Asn Val Thr Glu Val Lys Gly Tyr Thr Lys
 2580 2585 2590

Gly Gly Pro Gly His Glu Glu Pro Ile Pro Met Ala Thr Tyr Gly Trp
 2595 2600 2605

Asn Leu Val Lys Leu His Ser Gly Val Asp Val Phe Tyr Lys Pro Thr
 2610 2615 2620

Glu Gln Val Asp Thr Leu Leu Cys Asp Ile Gly Glu Ser Ser Ser Asn
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Leu Asn Asp Met Gly Lys Val Arg Lys Asp Ile Pro Gln Trp Glu Pro	3170	3175	3180
Ser Lys Gly Trp Lys Asn Trp Gln Glu Val Pro Phe Cys Ser His His	3185	3190	3195
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<212> TYPE: DNA

<213> ORGANISM: Recombinant Dengue 4 virus strain rDEN4

<400> SEQUENCE: 16

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tatgctcagc	agttccaacg	gaatggtttc	caacaagcag	aacaacatgg	tcaatccacg	9960
ctcatcacca	gtggatgacc	actgaagata	tgctcaaagt	gtggaacaga	gtgtggatag	10020

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aagacaaccc taatatgact gacaagactc cagtccattc gtgggaagat ataccttacc 10080
tagggaaaag agaggatttg tgggtgtgat cctgattgg actttcttcc agagccacct 10140
gggcgaagaa cattcatagc gccataaccc aggtcaggaa cctgatcgga aaagaggaat 10200
acgtggatta catgccagta atgaaaagat acagtgctcc ttcagagagt gaaggagttc 10260
tgtaattacc aacaacaaac accaaaggct attgaagtca ggccacttgt gccacggttt 10320
gagcaaaccg tgctgctgt agctccgcca ataatgggag gcgtaataat ccccaggag 10380
gccatgcgcc acggaagctg tacgcgtggc atattggact agcggttaga ggagaccct 10440
cccatcactg ataaaacgca gcaaaagggg gccgaagcc aggaggaagc tgtactcctg 10500
gtggaaggac tagaggttag aggagacccc cccaacacaa aaacagcata ttgacgctgg 10560
gaaagaccag agatcctgct gtctctgcaa catcaatcca ggcacagagc gccgcaagat 10620
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<210> SEQ ID NO 17

<211> LENGTH: 3388

<212> TYPE: PRT

<213> ORGANISM: Recombinant Dengue rDEN2/4d30

<400> SEQUENCE: 17

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

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260					265					270					
Thr	Ala	Val	Ala	Pro	Ser	Met	Thr	Met	Arg	Cys	Ile	Gly	Ile	Ser	Asn
	275						280					285			
Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	Gly	Gly	Ser	Trp	Val	Asp	Ile	Val
	290					295					300				
Leu	Glu	His	Gly	Ser	Cys	Val	Thr	Thr	Met	Ala	Lys	Asn	Lys	Pro	Thr
	305					310					315				320
Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	Glu	Ala	Lys	Gln	Pro	Ala	Thr	Leu
				325					330					335	
Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	Leu	Thr	Asn	Thr	Thr	Thr	Glu	Ser
			340					345						350	
Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	Ser	Leu	Asn	Glu	Glu	Gln	Asp	Lys
		355					360					365			
Arg	Phe	Val	Cys	Lys	His	Ser	Met	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly
	370					375					380				
Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	Ile	Val	Thr	Cys	Ala	Met	Phe	Thr
	385					390					395				400
Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	Val	Val	Gln	Pro	Glu	Asn	Leu	Glu
				405					410					415	
Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	Ser	Gly	Glu	Glu	His	Ala	Val	Gly
			420					425					430		
Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	Glu	Ile	Lys	Ile	Thr	Pro	Gln	Ser
		435					440					445			
Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	Gly	Tyr	Gly	Thr	Val	Thr	Met	Glu
	450					455					460				
Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	Phe	Asn	Glu	Met	Val	Leu	Leu	Gln
	465					470					475				480
Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	His	Arg	Gln	Trp	Phe	Leu	Asp	Leu
				485					490					495	
Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	Asp	Thr	Gln	Gly	Ser	Asn	Trp	Ile
			500					505						510	
Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe	Lys	Asn	Pro	His	Ala	Lys	Lys	Gln
		515					520					525			
Asp	Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Met	His	Thr	Ala	Leu
	530					535					540				
Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met	Ser	Ser	Gly	Asn	Leu	Leu	Phe	Thr
	545					550					555				560
Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	Met	Asp	Lys	Leu	Gln	Leu	Lys	Gly
				565					570					575	
Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly	Lys	Phe	Lys	Val	Val	Lys	Glu	Ile
			580					585					590		
Ala	Glu	Thr	Gln	His	Gly	Thr	Ile	Val	Ile	Arg	Val	Gln	Tyr	Glu	Gly
		595					600					605			
Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro	Phe	Glu	Ile	Met	Asp	Leu	Glu	Lys
	610					615					620				
Arg	His	Val	Leu	Gly	Arg	Leu	Ile	Thr	Val	Asn	Pro	Ile	Val	Thr	Glu
	625					630					635				640
Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu	Ala	Glu	Pro	Pro	Phe	Gly	Asp	Ser
				645					650					655	
Tyr	Ile	Ile	Ile	Gly	Val	Glu	Pro	Gly	Gln	Leu	Lys	Leu	Asn	Trp	Phe
			660					665					670		
Lys	Lys	Gly	Ser	Ser	Ile	Gly	Gln	Met	Phe	Glu	Thr	Thr	Met	Arg	Gly
		675					680						685		

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Ala Lys Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser
 690 695 700

Leu Gly Gly Val Phe Thr Ser Ile Gly Lys Ala Leu His Gln Val Phe
 705 710 715 720

Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly Val Ser Trp Thr Met Lys
 725 730 735

Ile Leu Ile Gly Val Ile Ile Thr Trp Ile Gly Met Asn Ser Arg Asn
 740 745 750

Thr Ser Met Ala Met Thr Cys Ile Ala Val Gly Gly Ile Thr Leu Phe
 755 760 765

Leu Gly Phe Thr Val Gln Ala Asp Met Gly Cys Val Ala Ser Trp Ser
 770 775 780

Gly Lys Glu Leu Lys Cys Gly Ser Gly Ile Phe Val Val Asp Asn Val
 785 790 795 800

His Thr Trp Thr Glu Gln Tyr Lys Phe Gln Pro Glu Ser Pro Ala Arg
 805 810 815

Leu Ala Ser Ala Ile Leu Asn Ala His Lys Asp Gly Val Cys Gly Ile
 820 825 830

Arg Ser Thr Thr Arg Leu Glu Asn Val Met Trp Lys Gln Ile Thr Asn
 835 840 845

Glu Leu Asn Tyr Val Leu Trp Glu Gly Gly His Asp Leu Thr Val Val
 850 855 860

Ala Gly Asp Val Lys Gly Val Leu Thr Lys Gly Lys Arg Ala Leu Thr
 865 870 875 880

Pro Pro Val Ser Asp Leu Lys Tyr Ser Trp Lys Thr Trp Gly Lys Ala
 885 890 895

Lys Ile Phe Thr Pro Glu Ala Arg Asn Ser Thr Phe Leu Ile Asp Gly
 900 905 910

Pro Asp Thr Ser Glu Cys Pro Asn Glu Arg Arg Ala Trp Asn Ser Leu
 915 920 925

Glu Val Glu Asp Tyr Gly Phe Gly Met Phe Thr Thr Asn Ile Trp Met
 930 935 940

Lys Phe Arg Glu Gly Ser Ser Glu Val Cys Asp His Arg Leu Met Ser
 945 950 955 960

Ala Ala Ile Lys Asp Gln Lys Ala Val His Ala Asp Met Gly Tyr Trp
 965 970 975

Ile Glu Ser Ser Lys Asn Gln Thr Trp Gln Ile Glu Lys Ala Ser Leu
 980 985 990

Ile Glu Val Lys Thr Cys Leu Trp Pro Lys Thr His Thr Leu Trp Ser
 995 1000 1005

Asn Gly Val Leu Glu Ser Gln Met Leu Ile Pro Lys Ser Tyr Ala Gly
 1010 1015 1020

Pro Phe Ser Gln His Asn Tyr Arg Gln Gly Tyr Ala Thr Gln Thr Val
 1025 1030 1035 1040

Gly Pro Trp His Leu Gly Lys Leu Glu Ile Asp Phe Gly Glu Cys Pro
 1045 1050 1055

Gly Thr Thr Val Thr Ile Gln Glu Asp Cys Asp His Arg Gly Pro Ser
 1060 1065 1070

Leu Arg Thr Thr Thr Ala Ser Gly Lys Leu Val Thr Gln Trp Cys Cys
 1075 1080 1085

Arg Ser Cys Thr Met Pro Pro Leu Arg Phe Leu Gly Glu Asp Gly Cys
 1090 1095 1100

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Trp	Tyr	Gly	Met	Glu	Ile	Arg	Pro	Leu	Ser	Glu	Lys	Glu	Glu	Asn	Met	1105	1110	1115	1120
Val	Lys	Ser	Gln	Val	Thr	Ala	Gly	Gln	Gly	Thr	Ser	Glu	Thr	Phe	Ser	1125	1130	1135	
Met	Gly	Leu	Leu	Cys	Leu	Thr	Leu	Phe	Val	Glu	Glu	Cys	Leu	Arg	Arg	1140	1145	1150	
Arg	Val	Thr	Arg	Lys	His	Met	Ile	Leu	Val	Val	Val	Ile	Thr	Leu	Cys	1155	1160	1165	
Ala	Ile	Ile	Leu	Gly	Gly	Leu	Thr	Trp	Met	Asp	Leu	Leu	Arg	Ala	Leu	1170	1175	1180	
Ile	Met	Leu	Gly	Asp	Thr	Met	Ser	Gly	Arg	Ile	Gly	Gly	Gln	Ile	His	1185	1190	1195	1200
Leu	Ala	Ile	Met	Ala	Val	Phe	Lys	Met	Ser	Pro	Gly	Tyr	Val	Leu	Gly	1205	1210	1215	
Val	Phe	Leu	Arg	Lys	Leu	Thr	Ser	Arg	Glu	Thr	Ala	Leu	Met	Val	Ile	1220	1225	1230	
Gly	Met	Ala	Met	Thr	Thr	Val	Leu	Ser	Ile	Pro	His	Asp	Leu	Met	Glu	1235	1240	1245	
Leu	Ile	Asp	Gly	Ile	Ser	Leu	Gly	Leu	Ile	Leu	Leu	Lys	Ile	Val	Thr	1250	1255	1260	
Gln	Phe	Asp	Asn	Thr	Gln	Val	Gly	Thr	Leu	Ala	Leu	Ser	Leu	Thr	Phe	1265	1270	1275	1280
Ile	Arg	Ser	Thr	Met	Pro	Leu	Val	Met	Ala	Trp	Arg	Thr	Ile	Met	Ala	1285	1290	1295	
Val	Leu	Phe	Val	Val	Thr	Leu	Ile	Pro	Leu	Cys	Arg	Thr	Ser	Cys	Leu	1300	1305	1310	
Gln	Lys	Gln	Ser	His	Trp	Val	Glu	Ile	Thr	Ala	Leu	Ile	Leu	Gly	Ala	1315	1320	1325	
Gln	Ala	Leu	Pro	Val	Tyr	Leu	Met	Thr	Leu	Met	Lys	Gly	Ala	Ser	Arg	1330	1335	1340	
Arg	Ser	Trp	Pro	Leu	Asn	Glu	Gly	Ile	Met	Ala	Val	Gly	Leu	Val	Ser	1345	1350	1355	1360
Leu	Leu	Gly	Ser	Ala	Leu	Leu	Lys	Asn	Asp	Val	Pro	Leu	Ala	Gly	Pro	1365	1370	1375	
Met	Val	Ala	Gly	Gly	Leu	Leu	Leu	Ala	Ala	Tyr	Val	Met	Ser	Gly	Ser	1380	1385	1390	
Ser	Ala	Asp	Leu	Ser	Leu	Glu	Lys	Ala	Ala	Asn	Val	Gln	Trp	Asp	Glu	1395	1400	1405	
Met	Ala	Asp	Ile	Thr	Gly	Ser	Ser	Pro	Ile	Val	Glu	Val	Lys	Gln	Asp	1410	1415	1420	
Glu	Asp	Gly	Ser	Phe	Ser	Ile	Arg	Asp	Val	Glu	Glu	Thr	Asn	Met	Ile	1425	1430	1435	1440
Thr	Leu	Leu	Val	Lys	Leu	Ala	Leu	Ile	Thr	Val	Ser	Gly	Leu	Tyr	Pro	1445	1450	1455	
Leu	Ala	Ile	Pro	Val	Thr	Met	Thr	Leu	Trp	Tyr	Met	Trp	Gln	Val	Lys	1460	1465	1470	
Thr	Gln	Arg	Ser	Gly	Ala	Leu	Trp	Asp	Val	Pro	Ser	Pro	Ala	Ala	Thr	1475	1480	1485	
Lys	Lys	Ala	Ala	Leu	Ser	Glu	Gly	Val	Tyr	Arg	Ile	Met	Gln	Arg	Gly	1490	1495	1500	
Leu	Phe	Gly	Lys	Thr	Gln	Val	Gly	Val	Gly	Ile	His	Met	Glu	Gly	Val	1505	1510	1515	1520
Phe	His	Thr	Met	Trp	His	Val	Thr	Arg	Gly	Ser	Val	Ile	Cys	His	Glu				

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1525					1530					1535					
Thr	Gly	Arg	Leu	Glu	Pro	Ser	Trp	Ala	Asp	Val	Arg	Asn	Asp	Met	Ile
			1540					1545					1550		
Ser	Tyr	Gly	Gly	Gly	Trp	Arg	Leu	Gly	Asp	Lys	Trp	Asp	Lys	Glu	Glu
		1555					1560					1565			
Asp	Val	Gln	Val	Leu	Ala	Ile	Glu	Pro	Gly	Lys	Asn	Pro	Lys	His	Val
	1570					1575					1580				
Gln	Thr	Lys	Pro	Gly	Leu	Phe	Lys	Thr	Leu	Thr	Gly	Glu	Ile	Gly	Ala
1585					1590					1595					1600
Val	Thr	Leu	Asp	Phe	Lys	Pro	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Ile	Asn
			1605					1610						1615	
Arg	Lys	Gly	Lys	Val	Ile	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val	Thr	Lys
		1620						1625					1630		
Ser	Gly	Asp	Tyr	Val	Ser	Ala	Ile	Thr	Gln	Ala	Glu	Arg	Ile	Gly	Glu
		1635					1640					1645			
Pro	Asp	Tyr	Glu	Val	Asp	Glu	Asp	Ile	Phe	Arg	Lys	Lys	Arg	Leu	Thr
	1650					1655					1660				
Ile	Met	Asp	Leu	His	Pro	Gly	Ala	Gly	Lys	Thr	Lys	Arg	Ile	Leu	Pro
1665					1670					1675					1680
Ser	Ile	Val	Arg	Glu	Ala	Leu	Lys	Arg	Arg	Leu	Arg	Thr	Leu	Ile	Leu
			1685					1690						1695	
Ala	Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly
		1700						1705					1710		
Leu	Pro	Ile	Arg	Tyr	Gln	Thr	Pro	Ala	Val	Lys	Ser	Glu	His	Thr	Gly
	1715						1720					1725			
Arg	Glu	Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Thr	Arg	Leu
1730						1735					1740				
Leu	Ser	Ser	Thr	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Ile	Val	Met	Asp	Glu
1745					1750					1755					1760
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Val	Ala	Ala	Arg	Gly	Tyr	Ile	Ser
			1765						1770					1775	
Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr
		1780						1785						1790	
Pro	Pro	Gly	Ala	Thr	Asp	Pro	Phe	Pro	Gln	Ser	Asn	Ser	Pro	Ile	Glu
		1795					1800					1805			
Asp	Ile	Glu	Arg	Glu	Ile	Pro	Glu	Arg	Ser	Trp	Asn	Thr	Gly	Phe	Asp
1810						1815					1820				
Trp	Ile	Thr	Asp	Tyr	Gln	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Ile
1825					1830					1835					1840
Lys	Ala	Gly	Asn	Asp	Ile	Ala	Asn	Cys	Leu	Arg	Lys	Ser	Gly	Lys	Lys
			1845						1850					1855	
Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Asp	Thr	Glu	Tyr	Pro	Lys	Thr
		1860						1865					1870		
Lys	Leu	Thr	Asp	Trp	Asp	Phe	Val	Val	Thr	Thr	Asp	Ile	Ser	Glu	Met
	1875					1880						1885			
Gly	Ala	Asn	Phe	Arg	Ala	Gly	Arg	Val	Ile	Asp	Pro	Arg	Arg	Cys	Leu
	1890					1895				1900					
Lys	Pro	Val	Ile	Leu	Pro	Asp	Gly	Pro	Glu	Arg	Val	Ile	Leu	Ala	Gly
1905					1910					1915					1920
Pro	Ile	Pro	Val	Thr	Pro	Ala	Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile
			1925						1930					1935	
Gly	Arg	Asn	Pro	Ala	Gln	Glu	Asp	Asp	Gln	Tyr	Val	Phe	Ser	Gly	Asp
		1940						1945						1950	

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Pro Leu Lys Asn Asp Glu Asp His Ala His Trp Thr Glu Ala Lys Met
1955 1960 1965

Leu Leu Asp Asn Ile Tyr Thr Pro Glu Gly Ile Ile Pro Thr Leu Phe
1970 1975 1980

Gly Pro Glu Arg Glu Lys Thr Gln Ala Ile Asp Gly Glu Phe Arg Leu
1985 1990 1995 2000

Arg Gly Glu Gln Arg Lys Thr Phe Val Glu Leu Met Arg Arg Gly Asp
2005 2010 2015

Leu Pro Val Trp Leu Ser Tyr Lys Val Ala Ser Ala Gly Ile Ser Tyr
2020 2025 2030

Glu Asp Arg Glu Trp Cys Phe Thr Gly Glu Arg Asn Asn Gln Ile Leu
2035 2040 2045

Glu Glu Asn Met Glu Val Glu Ile Trp Thr Arg Glu Gly Glu Lys Lys
2050 2055 2060

Lys Leu Arg Pro Arg Trp Leu Asp Ala Arg Val Tyr Ala Asp Pro Met
2065 2070 2075 2080

Ala Leu Lys Asp Phe Lys Glu Phe Ala Ser Gly Arg Lys Ser Ile Thr
2085 2090 2095

Leu Asp Ile Leu Thr Glu Ile Ala Ser Leu Pro Thr Tyr Leu Ser Ser
2100 2105 2110

Arg Ala Lys Leu Ala Leu Asp Asn Ile Val Met Leu His Thr Thr Glu
2115 2120 2125

Arg Gly Gly Arg Ala Tyr Gln His Ala Leu Asn Glu Leu Pro Glu Ser
2130 2135 2140

Leu Glu Thr Leu Met Leu Val Ala Leu Leu Gly Ala Met Thr Ala Gly
2145 2150 2155 2160

Ile Phe Leu Phe Phe Met Gln Gly Lys Gly Ile Gly Lys Leu Ser Met
2165 2170 2175

Gly Leu Ile Thr Ile Ala Val Ala Ser Gly Leu Leu Trp Val Ala Glu
2180 2185 2190

Ile Gln Pro Gln Trp Ile Ala Ala Ser Ile Ile Leu Glu Phe Phe Leu
2195 2200 2205

Met Val Leu Leu Ile Pro Glu Pro Glu Lys Gln Arg Thr Pro Gln Asp
2210 2215 2220

Asn Gln Leu Ile Tyr Val Ile Leu Thr Ile Leu Thr Ile Ile Gly Leu
2225 2230 2235 2240

Ile Ala Ala Asn Glu Met Gly Leu Ile Glu Lys Thr Lys Thr Asp Phe
2245 2250 2255

Gly Phe Tyr Gln Val Lys Thr Glu Thr Thr Ile Leu Asp Val Asp Leu
2260 2265 2270

Arg Pro Ala Ser Ala Trp Thr Leu Tyr Ala Val Ala Thr Thr Ile Leu
2275 2280 2285

Thr Pro Met Leu Arg His Thr Ile Glu Asn Thr Ser Ala Asn Leu Ser
2290 2295 2300

Leu Ala Ala Ile Ala Asn Gln Ala Ala Val Leu Met Gly Leu Gly Lys
2305 2310 2315 2320

Gly Trp Pro Leu His Arg Met Asp Leu Gly Val Pro Leu Leu Ala Met
2325 2330 2335

Gly Cys Tyr Ser Gln Val Asn Pro Thr Thr Leu Thr Ala Ser Leu Val
2340 2345 2350

Met Leu Leu Val His Tyr Ala Ile Ile Gly Pro Gly Leu Gln Ala Lys
2355 2360 2365

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Ala Thr Arg Glu Ala Gln Lys Arg Thr Ala Ala Gly Ile Met Lys Asn 2370 2375 2380
Pro Thr Val Asp Gly Ile Thr Val Ile Asp Leu Glu Pro Ile Ser Tyr 2385 2390 2395 2400
Asp Pro Lys Phe Glu Lys Gln Leu Gly Gln Val Met Leu Leu Val Leu 2405 2410 2415
Cys Ala Gly Gln Leu Leu Leu Met Arg Thr Thr Trp Ala Phe Cys Glu 2420 2425 2430
Val Leu Thr Leu Ala Thr Gly Pro Ile Leu Thr Leu Trp Glu Gly Asn 2435 2440 2445
Pro Gly Arg Phe Trp Asn Thr Thr Ile Ala Val Ser Thr Ala Asn Ile 2450 2455 2460
Phe Arg Gly Ser Tyr Leu Ala Gly Ala Gly Leu Ala Phe Ser Leu Ile 2465 2470 2475 2480
Lys Asn Ala Gln Thr Pro Arg Arg Gly Thr Gly Thr Thr Gly Glu Thr 2485 2490 2495
Leu Gly Glu Lys Trp Lys Arg Gln Leu Asn Ser Leu Asp Arg Lys Glu 2500 2505 2510
Phe Glu Glu Tyr Lys Arg Ser Gly Ile Leu Glu Val Asp Arg Thr Glu 2515 2520 2525
Ala Lys Ser Ala Leu Lys Asp Gly Ser Lys Ile Lys His Ala Val Ser 2530 2535 2540
Arg Gly Ser Ser Lys Ile Arg Trp Ile Val Glu Arg Gly Met Val Lys 2545 2550 2555 2560
Pro Lys Gly Lys Val Val Asp Leu Gly Cys Gly Arg Gly Gly Trp Ser 2565 2570 2575
Tyr Tyr Met Ala Thr Leu Lys Asn Val Thr Glu Val Lys Gly Tyr Thr 2580 2585 2590
Lys Gly Gly Pro Gly His Glu Glu Pro Ile Pro Met Ala Thr Tyr Gly 2595 2600 2605
Trp Asn Leu Val Lys Leu His Ser Gly Val Asp Val Phe Tyr Lys Pro 2610 2615 2620
Thr Glu Gln Val Asp Thr Leu Leu Cys Asp Ile Gly Glu Ser Ser Ser 2625 2630 2635 2640
Asn Pro Thr Ile Glu Glu Gly Arg Thr Leu Arg Val Leu Lys Met Val 2645 2650 2655
Glu Pro Trp Leu Ser Ser Lys Pro Glu Phe Cys Ile Lys Val Leu Asn 2660 2665 2670
Pro Tyr Met Pro Thr Val Ile Glu Glu Leu Glu Lys Leu Gln Arg Lys 2675 2680 2685
His Gly Gly Asn Leu Val Arg Cys Pro Leu Ser Arg Asn Ser Thr His 2690 2695 2700
Glu Met Tyr Trp Val Ser Gly Ala Ser Gly Asn Ile Val Ser Ser Val 2705 2710 2715 2720
Asn Thr Thr Ser Lys Met Leu Leu Asn Arg Phe Thr Thr Arg His Arg 2725 2730 2735
Lys Pro Thr Tyr Glu Lys Asp Val Asp Leu Gly Ala Gly Thr Arg Ser 2740 2745 2750
Val Ser Thr Glu Thr Glu Lys Pro Asp Met Thr Ile Ile Gly Arg Arg 2755 2760 2765
Leu Gln Arg Leu Gln Glu Glu His Lys Glu Thr Trp His Tyr Asp Gln 2770 2775 2780
Glu Asn Pro Tyr Arg Thr Trp Ala Tyr His Gly Ser Tyr Glu Ala Pro

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2785	2790	2795	2800
Ser Thr Gly	Ser Ala Ser Ser Met Val	Asn Gly Val Val Lys Leu Leu	
	2805	2810	2815
Thr Lys Pro Trp Asp Val Ile Pro Met Val Thr Gln Leu Ala Met Thr	2820	2825	2830
Asp Thr Thr Pro Phe Gly Gln Gln Arg Val Phe Lys Glu Lys Val Asp	2835	2840	2845
Thr Arg Thr Pro Gln Pro Lys Pro Gly Thr Arg Met Val Met Thr Thr	2850	2855	2860
Thr Ala Asn Trp Leu Trp Ala Leu Leu Gly Lys Lys Lys Asn Pro Arg	2865	2870	2875
Leu Cys Thr Arg Glu Glu Phe Ile Ser Lys Val Arg Ser Asn Ala Ala	2885	2890	2895
Ile Gly Ala Val Phe Gln Glu Glu Gln Gly Trp Thr Ser Ala Ser Glu	2900	2905	2910
Ala Val Asn Asp Ser Arg Phe Trp Glu Leu Val Asp Lys Glu Arg Ala	2915	2920	2925
Leu His Gln Glu Gly Lys Cys Glu Ser Cys Val Tyr Asn Met Met Gly	2930	2935	2940
Lys Arg Glu Lys Lys Leu Gly Glu Phe Gly Arg Ala Lys Gly Ser Arg	2945	2950	2955
Ala Ile Trp Tyr Met Trp Leu Gly Ala Arg Phe Leu Glu Phe Glu Ala	2965	2970	2975
Leu Gly Phe Leu Asn Glu Asp His Trp Phe Gly Arg Glu Asn Ser Trp	2980	2985	2990
Ser Gly Val Glu Gly Glu Gly Leu His Arg Leu Gly Tyr Ile Leu Glu	2995	3000	3005
Glu Ile Asp Lys Lys Asp Gly Asp Leu Met Tyr Ala Asp Asp Thr Ala	3010	3015	3020
Gly Trp Asp Thr Arg Ile Thr Glu Asp Asp Leu Gln Asn Glu Glu Leu	3025	3030	3035
Ile Thr Glu Gln Met Ala Pro His His Lys Ile Leu Ala Lys Ala Ile	3045	3050	3055
Phe Lys Leu Thr Tyr Gln Asn Lys Val Val Lys Val Leu Arg Pro Thr	3060	3065	3070
Pro Arg Gly Ala Val Met Asp Ile Ile Ser Arg Lys Asp Gln Arg Gly	3075	3080	3085
Ser Gly Gln Val Gly Thr Tyr Gly Leu Asn Thr Phe Thr Asn Met Glu	3090	3095	3100
Val Gln Leu Ile Arg Gln Met Glu Ala Glu Gly Val Ile Thr Gln Asp	3105	3110	3115
Asp Met Gln Asn Pro Lys Gly Leu Lys Glu Arg Val Glu Lys Trp Leu	3125	3130	3135
Lys Glu Cys Gly Val Asp Arg Leu Lys Arg Met Ala Ile Ser Gly Asp	3140	3145	3150
Asp Cys Val Val Lys Pro Leu Asp Glu Arg Phe Gly Thr Ser Leu Leu	3155	3160	3165
Phe Leu Asn Asp Met Gly Lys Val Arg Lys Asp Ile Pro Gln Trp Glu	3170	3175	3180
Pro Ser Lys Gly Trp Lys Asn Trp Gln Glu Val Pro Phe Cys Ser His	3185	3190	3195
His Phe His Lys Ile Phe Met Lys Asp Gly Arg Ser Leu Val Val Pro	3205	3210	3215

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<210> SEQ ID NO 18

<211> LENGTH: 10616

<212> TYPE: DNA

<213> ORGANISM: Recombinant dengue virus rDEN2/4d30

<400> SEQUENCE: 18

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<210> SEQ ID NO 19
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 Ala Phe Ser Leu Ser Thr Arg Asp Gly Glu Pro Leu Met Ile Val Ala
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 Lys His Glu Arg Gly Arg Pro Leu Leu Phe Lys Thr Thr Glu Gly Ile
 130 135 140
 Asn Lys Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Met Cys Glu Asp
 145 150 155 160
 Thr Val Thr Tyr Lys Cys Pro Leu Leu Val Asn Thr Glu Pro Glu Asp
 165 170 175
 Ile Asp Cys Trp Cys Asn Leu Thr Ser Thr Trp Val Met Tyr Gly Thr
 180 185 190
 Cys Thr Gln Ser Gly Glu Arg Arg Arg Glu Lys Arg Ser Val Ala Leu
 195 200 205
 Thr Pro His Ser Gly Met Gly Leu Glu Thr Arg Ala Glu Thr Trp Met
 210 215 220
 Ser Ser Glu Gly Ala Trp Lys His Ala Gln Arg Val Glu Ser Trp Ile
 225 230 235 240
 Leu Arg Asn Pro Gly Phe Ala Leu Leu Ala Gly Phe Met Ala Tyr Met
 245 250 255
 Ile Gly Gln Thr Gly Ile Gln Arg Thr Val Phe Phe Val Leu Met Met
 260 265 270
 Leu Val Ala Pro Ser Tyr Gly Met Arg Cys Val Gly Val Gly Asn Arg
 275 280 285
 Asp Phe Val Glu Gly Val Ser Gly Gly Ala Trp Val Asp Leu Val Leu
 290 295 300
 Glu His Gly Gly Cys Val Thr Thr Met Ala Gln Gly Lys Pro Thr Leu
 305 310 315 320
 Asp Phe Glu Leu Thr Lys Thr Thr Ala Lys Glu Val Ala Leu Leu Arg
 325 330 335
 Thr Tyr Cys Ile Glu Ala Ser Ile Ser Asn Ile Thr Thr Ala Thr Arg
 340 345 350
 Cys Pro Thr Gln Gly Glu Pro Tyr Leu Lys Glu Glu Gln Asp Gln Gln
 355 360 365
 Tyr Ile Cys Arg Arg Asp Val Val Asp Arg Gly Trp Gly Asn Gly Cys

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370				375				380							
Gly	Leu	Phe	Gly	Lys	Gly	Gly	Val	Val	Thr	Cys	Ala	Lys	Phe	Ser	Cys
385					390					395					400
Ser	Gly	Lys	Ile	Thr	Gly	Asn	Leu	Val	Gln	Ile	Glu	Asn	Leu	Glu	Tyr
				405					410					415	
Thr	Val	Val	Val	Thr	Val	His	Asn	Gly	Asp	Thr	His	Ala	Val	Gly	Asn
				420					425				430		
Asp	Thr	Ser	Asn	His	Gly	Val	Thr	Ala	Met	Ile	Thr	Pro	Arg	Ser	Pro
		435					440						445		
Ser	Val	Glu	Val	Lys	Leu	Pro	Asp	Tyr	Gly	Glu	Leu	Thr	Leu	Asp	Cys
	450					455					460				
Glu	Pro	Arg	Ser	Gly	Ile	Asp	Phe	Asn	Glu	Met	Ile	Leu	Met	Lys	Met
465					470					475					480
Lys	Lys	Lys	Thr	Trp	Leu	Val	His	Lys	Gln	Trp	Phe	Leu	Asp	Leu	Pro
				485					490					495	
Leu	Pro	Trp	Thr	Ala	Gly	Ala	Asp	Thr	Ser	Glu	Val	His	Trp	Asn	Tyr
			500					505					510		
Lys	Glu	Arg	Met	Val	Thr	Phe	Lys	Val	Pro	His	Ala	Lys	Arg	Gln	Asp
		515					520					525			
Val	Thr	Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Met	His	Ser	Ala	Leu	Ala
	530					535					540				
Gly	Ala	Thr	Glu	Val	Asp	Ser	Gly	Asp	Gly	Asn	His	Met	Phe	Ala	Gly
545					550					555					560
His	Leu	Lys	Cys	Lys	Val	Arg	Met	Glu	Lys	Leu	Arg	Ile	Lys	Gly	Met
				565					570					575	
Ser	Tyr	Thr	Met	Cys	Ser	Gly	Lys	Phe	Ser	Ile	Asp	Lys	Glu	Met	Ala
			580					585					590		
Glu	Thr	Gln	His	Gly	Thr	Thr	Val	Val	Lys	Val	Lys	Tyr	Glu	Gly	Ala
		595					600					605			
Gly	Ala	Pro	Cys	Lys	Val	Pro	Ile	Glu	Ile	Arg	Asp	Val	Asn	Lys	Glu
	610					615					620				
Lys	Val	Val	Gly	Arg	Ile	Ile	Ser	Ser	Thr	Pro	Leu	Ala	Glu	Asn	Thr
625					630					635					640
Asn	Ser	Val	Thr	Asn	Ile	Glu	Leu	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr
				645					650					655	
Ile	Val	Ile	Gly	Val	Gly	Asn	Ser	Ala	Leu	Thr	Leu	His	Trp	Phe	Arg
			660					665					670		
Lys	Gly	Ser	Ser	Ile	Gly	Lys	Met	Phe	Glu	Ser	Thr	Tyr	Arg	Gly	Ala
		675					680					685			
Lys	Arg	Met	Ala	Ile	Leu	Gly	Glu	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Val
	690					695					700				
Gly	Gly	Leu	Phe	Thr	Ser	Leu	Gly	Lys	Ala	Val	His	Gln	Val	Phe	Gly
705					710					715					720
Ser	Val	Tyr	Thr	Thr	Met	Phe	Gly	Gly	Val	Ser	Trp	Met	Ile	Arg	Ile
				725					730					735	
Leu	Ile	Gly	Phe	Leu	Val	Leu	Trp	Ile	Gly	Thr	Asn	Ser	Arg	Asn	Thr
			740					745					750		
Ser	Met	Ala	Met	Thr	Cys	Ile	Ala	Val	Gly	Gly	Ile	Thr	Leu	Phe	Leu
		755					760					765			
Gly	Phe	Thr	Val	Gln	Ala	Asp	Met	Gly	Cys	Val	Ala	Ser	Trp	Ser	Gly
	770					775					780				
Lys	Glu	Leu	Lys	Cys	Gly	Ser	Gly	Ile	Phe	Val	Val	Asp	Asn	Val	His
785					790					795					800

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Thr Trp Thr Glu Gln Tyr Lys Phe Gln Pro Glu Ser Pro Ala Arg Leu
 805 810 815
 Ala Ser Ala Ile Leu Asn Ala His Lys Asp Gly Val Cys Gly Ile Arg
 820 825 830
 Ser Thr Thr Arg Leu Glu Asn Val Met Trp Lys Gln Ile Thr Asn Glu
 835 840 845
 Leu Asn Tyr Val Leu Trp Glu Gly Gly His Asp Leu Thr Val Val Ala
 850 855 860
 Gly Asp Val Lys Gly Val Leu Thr Lys Gly Lys Arg Ala Leu Thr Pro
 865 870 875 880
 Pro Val Ser Asp Leu Lys Tyr Ser Trp Lys Thr Trp Gly Lys Ala Lys
 885 890 895
 Ile Phe Thr Pro Glu Ala Arg Asn Ser Thr Phe Leu Ile Asp Gly Pro
 900 905 910
 Asp Thr Ser Glu Cys Pro Asn Glu Arg Arg Ala Trp Asn Ser Leu Glu
 915 920 925
 Val Glu Asp Tyr Gly Phe Gly Met Phe Thr Thr Asn Ile Trp Met Lys
 930 935 940
 Phe Arg Glu Gly Ser Ser Glu Val Cys Asp His Arg Leu Met Ser Ala
 945 950 955 960
 Ala Ile Lys Asp Gln Lys Ala Val His Ala Asp Met Gly Tyr Trp Ile
 965 970 975
 Glu Ser Ser Lys Asn Gln Thr Trp Gln Ile Glu Lys Ala Ser Leu Ile
 980 985 990
 Glu Val Lys Thr Cys Leu Trp Pro Lys Thr His Thr Leu Trp Ser Asn
 995 1000 1005
 Gly Val Leu Glu Ser Gln Met Leu Ile Pro Lys Ser Tyr Ala Gly Pro
 1010 1015 1020
 Phe Ser Gln His Asn Tyr Arg Gln Gly Tyr Ala Thr Gln Thr Val Gly
 1025 1030 1035 1040
 Pro Trp His Leu Gly Lys Leu Glu Ile Asp Phe Gly Glu Cys Pro Gly
 1045 1050 1055
 Thr Thr Val Thr Ile Gln Glu Asp Cys Asp His Arg Gly Pro Ser Leu
 1060 1065 1070
 Arg Thr Thr Thr Ala Ser Gly Lys Leu Val Thr Gln Trp Cys Cys Arg
 1075 1080 1085
 Ser Cys Thr Met Pro Pro Leu Arg Phe Leu Gly Glu Asp Gly Cys Trp
 1090 1095 1100
 Tyr Gly Met Glu Ile Arg Pro Leu Ser Glu Lys Glu Glu Asn Met Val
 1105 1110 1115 1120
 Lys Ser Gln Val Thr Ala Gly Gln Gly Thr Ser Glu Thr Phe Ser Met
 1125 1130 1135
 Gly Leu Leu Cys Leu Thr Leu Phe Val Glu Glu Cys Leu Arg Arg Arg
 1140 1145 1150
 Val Thr Arg Lys His Met Ile Leu Val Val Val Ile Thr Leu Cys Ala
 1155 1160 1165
 Ile Ile Leu Gly Gly Leu Thr Trp Met Asp Leu Leu Arg Ala Leu Ile
 1170 1175 1180
 Met Leu Gly Asp Thr Met Ser Gly Arg Ile Gly Gly Gln Ile His Leu
 1185 1190 1195 1200
 Ala Ile Met Ala Val Phe Lys Met Ser Pro Gly Tyr Val Leu Gly Val
 1205 1210 1215

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Phe	Leu	Arg	Lys	Leu	Thr	Ser	Arg	Glu	Thr	Ala	Leu	Met	Val	Ile	Gly
			1220					1225					1230		
Met	Ala	Met	Thr	Thr	Val	Leu	Ser	Ile	Pro	His	Asp	Leu	Met	Glu	Leu
		1235					1240					1245			
Ile	Asp	Gly	Ile	Ser	Leu	Gly	Leu	Ile	Leu	Leu	Lys	Ile	Val	Thr	Gln
	1250					1255					1260				
Phe	Asp	Asn	Thr	Gln	Val	Gly	Thr	Leu	Ala	Leu	Ser	Leu	Thr	Phe	Ile
1265				1270					1275						1280
Arg	Ser	Thr	Met	Pro	Leu	Val	Met	Ala	Trp	Arg	Thr	Ile	Met	Ala	Val
				1285					1290					1295	
Leu	Phe	Val	Val	Thr	Leu	Ile	Pro	Leu	Cys	Arg	Thr	Ser	Cys	Leu	Gln
			1300					1305					1310		
Lys	Gln	Ser	His	Trp	Val	Glu	Ile	Thr	Ala	Leu	Ile	Leu	Gly	Ala	Gln
	1315						1320						1325		
Ala	Leu	Pro	Val	Tyr	Leu	Met	Thr	Leu	Met	Lys	Gly	Ala	Ser	Arg	Arg
	1330					1335					1340				
Ser	Trp	Pro	Leu	Asn	Glu	Gly	Ile	Met	Ala	Val	Gly	Leu	Val	Ser	Leu
1345				1350						1355					1360
Leu	Gly	Ser	Ala	Leu	Leu	Lys	Asn	Asp	Val	Pro	Leu	Ala	Gly	Pro	Met
				1365					1370					1375	
Val	Ala	Gly	Gly	Leu	Leu	Leu	Ala	Ala	Tyr	Val	Met	Ser	Gly	Ser	Ser
			1380					1385					1390		
Ala	Asp	Leu	Ser	Leu	Glu	Lys	Ala	Ala	Asn	Val	Gln	Trp	Asp	Glu	Met
		1395					1400					1405			
Ala	Asp	Ile	Thr	Gly	Ser	Ser	Pro	Ile	Ile	Glu	Val	Lys	Gln	Asp	Glu
	1410					1415						1420			
Asp	Gly	Ser	Phe	Ser	Ile	Arg	Asp	Val	Glu	Glu	Thr	Asn	Met	Ile	Thr
1425					1430					1435					1440
Leu	Leu	Val	Lys	Leu	Ala	Leu	Ile	Thr	Val	Ser	Gly	Leu	Tyr	Pro	Leu
				1445					1450					1455	
Ala	Ile	Pro	Val	Thr	Met	Thr	Leu	Trp	Tyr	Met	Trp	Gln	Val	Lys	Thr
			1460					1465					1470		
Gln	Arg	Ser	Gly	Ala	Leu	Trp	Asp	Val	Pro	Ser	Pro	Ala	Ala	Thr	Lys
		1475					1480						1485		
Lys	Ala	Ala	Leu	Ser	Glu	Gly	Val	Tyr	Arg	Ile	Met	Gln	Arg	Gly	Leu
	1490					1495					1500				
Phe	Gly	Lys	Thr	Gln	Val	Gly	Val	Gly	Ile	His	Met	Glu	Gly	Val	Phe
1505					1510					1515					1520
His	Thr	Met	Trp	His	Val	Thr	Arg	Gly	Ser	Val	Ile	Cys	His	Glu	Thr
				1525					1530					1535	
Gly	Arg	Leu	Glu	Pro	Ser	Trp	Ala	Asp	Val	Arg	Asn	Asp	Met	Ile	Ser
			1540					1545					1550		
Tyr	Gly	Gly	Gly	Trp	Arg	Leu	Gly	Asp	Lys	Trp	Asp	Lys	Glu	Glu	Asp
	1555						1560					1565			
Val	Gln	Val	Leu	Ala	Ile	Glu	Pro	Gly	Lys	Asn	Pro	Lys	His	Val	Gln
	1570					1575					1580				
Thr	Lys	Pro	Gly	Leu	Phe	Lys	Thr	Leu	Thr	Gly	Glu	Ile	Gly	Ala	Val
1585					1590					1595					1600
Thr	Leu	Asp	Phe	Lys	Pro	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Ile	Asn	Arg
				1605					1610					1615	
Lys	Gly	Lys	Val	Ile	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val	Thr	Lys	Ser
			1620					1625					1630		
Gly	Asp	Tyr	Val	Ser	Ala	Ile	Thr	Gln	Ala	Glu	Arg	Ile	Gly	Glu	Pro

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1635					1640					1645					
Asp	Tyr	Glu	Val	Asp	Glu	Asp	Ile	Phe	Arg	Lys	Lys	Arg	Leu	Thr	Ile
1650					1655					1660					
Met	Asp	Leu	His	Pro	Gly	Ala	Gly	Lys	Thr	Lys	Arg	Ile	Leu	Pro	Ser
1665					1670					1675					1680
Ile	Val	Arg	Glu	Ala	Leu	Lys	Arg	Arg	Leu	Arg	Thr	Leu	Ile	Leu	Ala
				1685					1690					1695	
Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu
			1700					1705						1710	
Pro	Ile	Arg	Tyr	Gln	Thr	Pro	Ala	Val	Lys	Ser	Glu	His	Thr	Gly	Arg
			1715					1720						1725	
Glu	Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Thr	Arg	Leu	Leu
1730					1735					1740					
Ser	Ser	Thr	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Ile	Val	Met	Asp	Glu	Ala
1745					1750					1755					1760
His	Phe	Thr	Asp	Pro	Ser	Ser	Val	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr
				1765						1770					1775
Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr	Pro
				1780					1785						1790
Pro	Gly	Ala	Thr	Asp	Pro	Phe	Pro	Gln	Ser	Asn	Ser	Pro	Ile	Glu	Asp
				1795				1800						1805	
Ile	Glu	Arg	Glu	Ile	Pro	Glu	Arg	Ser	Trp	Asn	Thr	Gly	Phe	Asp	Trp
1810					1815					1820					
Ile	Thr	Asp	Tyr	Gln	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Ile	Lys
1825					1830					1835					1840
Ala	Gly	Asn	Asp	Ile	Ala	Asn	Cys	Leu	Arg	Lys	Ser	Gly	Lys	Lys	Val
				1845					1850						1855
Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Asp	Thr	Glu	Tyr	Pro	Lys	Thr	Lys
				1860					1865						1870
Leu	Thr	Asp	Trp	Asp	Phe	Val	Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly
				1875					1880						1885
Ala	Asn	Phe	Arg	Ala	Gly	Arg	Val	Ile	Asp	Pro	Arg	Arg	Cys	Leu	Lys
				1890					1895						1900
Pro	Val	Ile	Leu	Pro	Asp	Gly	Pro	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro
1905					1910					1915					1920
Ile	Pro	Val	Thr	Pro	Ala	Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly
				1925					1930						1935
Arg	Asn	Pro	Ala	Gln	Glu	Asp	Asp	Gln	Tyr	Val	Phe	Ser	Gly	Asp	Pro
				1940					1945						1950
Leu	Lys	Asn	Asp	Glu	Asp	His	Ala	His	Trp	Thr	Glu	Ala	Lys	Met	Leu
				1955					1960						1965
Leu	Asp	Asn	Ile	Tyr	Thr	Pro	Glu	Gly	Ile	Ile	Pro	Thr	Leu	Phe	Gly
				1970					1975						1980
Pro	Glu	Arg	Glu	Lys	Thr	Gln	Ala	Ile	Asp	Gly	Glu	Phe	Arg	Leu	Arg
1985					1990					1995					2000
Gly	Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Arg	Arg	Gly	Asp	Leu
				2005					2010						2015
Pro	Val	Trp	Leu	Ser	Tyr	Lys	Val	Ala	Ser	Ala	Gly	Ile	Ser	Tyr	Lys
				2020					2025						2030
Asp	Arg	Glu	Trp	Cys	Phe	Thr	Gly	Glu	Arg	Asn	Asn	Gln	Ile	Leu	Glu
				2035					2040						2045
Glu	Asn	Met	Glu	Val	Glu	Ile	Trp	Thr	Arg	Glu	Gly	Glu	Lys	Lys	Lys
2050					2055					2060					

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Leu Arg Pro Arg Trp Leu Asp Ala Arg Val Tyr Ala Asp Pro Met Ala
 2065 2070 2075 2080
 Leu Lys Asp Phe Lys Glu Phe Ala Ser Gly Arg Lys Ser Ile Thr Leu
 2085 2090 2095
 Asp Ile Leu Thr Glu Ile Ala Ser Leu Pro Thr Tyr Leu Ser Ser Arg
 2100 2105 2110
 Ala Lys Leu Ala Leu Asp Asn Ile Val Met Leu His Thr Thr Glu Arg
 2115 2120 2125
 Gly Gly Arg Ala Tyr Gln His Ala Leu Asn Glu Leu Pro Glu Ser Leu
 2130 2135 2140
 Glu Thr Leu Met Leu Val Ala Leu Leu Gly Ala Met Thr Ala Gly Ile
 2145 2150 2155 2160
 Phe Leu Phe Phe Met Gln Gly Lys Gly Ile Gly Lys Leu Ser Met Gly
 2165 2170 2175
 Leu Ile Thr Ile Ala Val Ala Ser Gly Leu Leu Trp Val Ala Glu Ile
 2180 2185 2190
 Gln Pro Gln Trp Ile Ala Ala Ser Ile Ile Leu Glu Phe Phe Leu Met
 2195 2200 2205
 Val Leu Leu Ile Pro Glu Pro Glu Lys Gln Arg Thr Pro Gln Asp Asn
 2210 2215 2220
 Gln Leu Ile Tyr Val Ile Leu Thr Ile Leu Thr Ile Ile Gly Leu Ile
 2225 2230 2235 2240
 Ala Ala Asn Glu Met Gly Leu Ile Glu Lys Thr Lys Thr Asp Phe Gly
 2245 2250 2255
 Phe Tyr Gln Val Lys Thr Glu Thr Thr Ile Leu Asp Val Asp Leu Arg
 2260 2265 2270
 Pro Ala Ser Ala Trp Thr Leu Tyr Ala Val Ala Thr Thr Ile Leu Thr
 2275 2280 2285
 Pro Met Leu Arg His Thr Ile Glu Asn Thr Ser Ala Asn Leu Ser Leu
 2290 2295 2300
 Ala Ala Ile Ala Asn Gln Ala Ala Val Leu Met Gly Leu Gly Lys Gly
 2305 2310 2315 2320
 Trp Pro Leu His Arg Met Asp Leu Gly Val Pro Leu Leu Ala Met Gly
 2325 2330 2335
 Cys Tyr Ser Gln Val Asn Pro Thr Thr Leu Thr Ala Ser Leu Val Met
 2340 2345 2350
 Leu Leu Val His Tyr Ala Ile Ile Gly Pro Gly Leu Gln Ala Lys Ala
 2355 2360 2365
 Thr Arg Glu Ala Gln Lys Arg Thr Ala Ala Gly Ile Met Lys Asn Pro
 2370 2375 2380
 Thr Val Asp Gly Ile Thr Val Ile Asp Leu Glu Pro Ile Ser Tyr Asp
 2385 2390 2395 2400
 Pro Lys Phe Glu Lys Gln Leu Gly Gln Val Met Leu Leu Val Leu Cys
 2405 2410 2415
 Ala Gly Gln Leu Leu Leu Met Arg Thr Thr Trp Ala Phe Cys Glu Val
 2420 2425 2430
 Leu Thr Leu Ala Thr Gly Pro Ile Leu Thr Leu Trp Glu Gly Asn Pro
 2435 2440 2445
 Gly Arg Phe Trp Asn Thr Thr Ile Ala Val Ser Thr Ala Asn Ile Phe
 2450 2455 2460
 Arg Gly Ser Tyr Leu Ala Gly Ala Gly Leu Ala Phe Ser Leu Ile Lys
 2465 2470 2475 2480

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Asn	Ala	Gln	Thr	Pro	Arg	Arg	Gly	Thr	Gly	Thr	Thr	Gly	Glu	Thr	Leu	2485	2490	2495	
Gly	Glu	Lys	Trp	Lys	Arg	Gln	Leu	Asn	Ser	Leu	Asp	Arg	Lys	Glu	Phe	2500	2505	2510	
Glu	Glu	Tyr	Lys	Arg	Ser	Gly	Ile	Leu	Glu	Val	Asp	Arg	Thr	Glu	Ala	2515	2520	2525	
Lys	Ser	Ala	Leu	Lys	Asp	Gly	Ser	Lys	Ile	Lys	His	Ala	Val	Ser	Arg	2530	2535	2540	
Gly	Ser	Ser	Lys	Ile	Arg	Trp	Ile	Val	Glu	Arg	Gly	Met	Val	Lys	Pro	2545	2550	2555	2560
Lys	Gly	Lys	Val	Val	Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	2565	2570	2575	
Tyr	Met	Ala	Thr	Leu	Lys	Asn	Val	Thr	Glu	Val	Lys	Gly	Tyr	Thr	Lys	2580	2585	2590	
Gly	Gly	Pro	Gly	His	Glu	Glu	Pro	Ile	Pro	Met	Ala	Thr	Tyr	Gly	Trp	2595	2600	2605	
Asn	Leu	Val	Lys	Leu	His	Ser	Gly	Val	Asp	Val	Phe	Tyr	Lys	Pro	Thr	2610	2615	2620	
Glu	Gln	Val	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Asn	2625	2630	2635	2640
Pro	Thr	Ile	Glu	Glu	Gly	Arg	Thr	Leu	Arg	Val	Leu	Lys	Met	Val	Glu	2645	2650	2655	
Pro	Trp	Leu	Ser	Ser	Lys	Pro	Glu	Phe	Cys	Ile	Lys	Val	Leu	Asn	Pro	2660	2665	2670	
Tyr	Met	Pro	Thr	Val	Ile	Glu	Glu	Leu	Glu	Lys	Leu	Gln	Arg	Lys	His	2675	2680	2685	
Gly	Gly	Asn	Leu	Val	Arg	Cys	Pro	Leu	Ser	Arg	Asn	Ser	Thr	His	Glu	2690	2695	2700	
Met	Tyr	Trp	Val	Ser	Gly	Ala	Ser	Gly	Asn	Ile	Val	Ser	Ser	Val	Asn	2705	2710	2715	2720
Thr	Thr	Ser	Lys	Met	Leu	Leu	Asn	Arg	Phe	Thr	Thr	Arg	His	Arg	Lys	2725	2730	2735	
Pro	Thr	Tyr	Glu	Lys	Asp	Val	Asp	Leu	Gly	Ala	Gly	Thr	Arg	Ser	Val	2740	2745	2750	
Ser	Thr	Glu	Thr	Glu	Lys	Pro	Asp	Met	Thr	Ile	Ile	Gly	Arg	Arg	Leu	2755	2760	2765	
Gln	Arg	Leu	Gln	Glu	Glu	His	Lys	Glu	Thr	Trp	His	Tyr	Asp	Gln	Glu	2770	2775	2780	
Asn	Pro	Tyr	Arg	Thr	Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Ser	2785	2790	2795	2800
Thr	Gly	Ser	Ala	Ser	Ser	Met	Val	Asn	Gly	Val	Val	Lys	Leu	Leu	Thr	2805	2810	2815	
Lys	Pro	Trp	Asp	Val	Ile	Pro	Met	Val	Thr	Gln	Leu	Ala	Met	Thr	Asp	2820	2825	2830	
Thr	Thr	Pro	Phe	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	2835	2840	2845	
Arg	Thr	Pro	Gln	Pro	Lys	Pro	Gly	Thr	Arg	Met	Val	Met	Thr	Thr	Thr	2850	2855	2860	
Ala	Asn	Trp	Leu	Trp	Ala	Leu	Leu	Gly	Lys	Lys	Lys	Asn	Pro	Arg	Leu	2865	2870	2875	2880
Cys	Thr	Arg	Glu	Glu	Phe	Ile	Ser	Lys	Val	Arg	Ser	Asn	Ala	Ala	Ile	2885	2890	2895	
Gly	Ala	Val	Phe	Gln	Glu	Glu	Gln	Gly	Trp	Thr	Ser	Ala	Ser	Glu	Ala				

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2900				2905				2910							
Val	Asn	Asp	Ser	Arg	Phe	Trp	Glu	Leu	Val	Asp	Lys	Glu	Arg	Ala	Leu
	2915						2920					2925			
His	Gln	Glu	Gly	Lys	Cys	Glu	Ser	Cys	Val	Tyr	Asn	Met	Met	Gly	Lys
	2930					2935					2940				
Arg	Glu	Lys	Lys	Leu	Gly	Glu	Phe	Gly	Arg	Ala	Lys	Gly	Ser	Arg	Ala
2945				2950						2955					2960
Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg	Phe	Leu	Glu	Phe	Glu	Ala	Leu
			2965						2970					2975	
Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	Phe	Gly	Arg	Glu	Asn	Ser	Trp	Ser
			2980						2985					2990	
Gly	Val	Glu	Gly	Glu	Gly	Leu	His	Arg	Leu	Gly	Tyr	Ile	Leu	Glu	Glu
	2995					3000						3005			
Ile	Asp	Lys	Lys	Asp	Gly	Asp	Leu	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly
	3010					3015					3020				
Trp	Asp	Thr	Arg	Ile	Thr	Glu	Asp	Asp	Leu	Gln	Asn	Glu	Glu	Leu	Ile
3025					3030					3035					3040
Thr	Glu	Gln	Met	Ala	Pro	His	His	Lys	Ile	Leu	Ala	Lys	Ala	Ile	Phe
			3045						3050					3055	
Lys	Leu	Thr	Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Thr	Pro
			3060						3065				3070		
Arg	Gly	Ala	Val	Met	Asp	Ile	Ile	Ser	Arg	Lys	Asp	Gln	Arg	Gly	Ser
		3075					3080					3085			
Gly	Gln	Val	Gly	Thr	Tyr	Gly	Leu	Asn	Thr	Phe	Thr	Asn	Met	Glu	Val
	3090					3095						3100			
Gln	Leu	Ile	Arg	Gln	Met	Glu	Ala	Glu	Gly	Val	Ile	Thr	Gln	Asp	Asp
3105					3110					3115				3120	
Met	Gln	Asn	Pro	Lys	Gly	Leu	Lys	Glu	Arg	Val	Glu	Lys	Trp	Leu	Lys
			3125						3130					3135	
Glu	Cys	Gly	Val	Asp	Arg	Leu	Lys	Arg	Met	Ala	Ile	Ser	Gly	Asp	Asp
			3140						3145				3150		
Cys	Val	Val	Lys	Pro	Leu	Asp	Glu	Arg	Phe	Gly	Thr	Ser	Leu	Leu	Phe
	3155						3160						3165		
Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Ile	Pro	Gln	Trp	Glu	Pro
	3170					3175					3180				
Ser	Lys	Gly	Trp	Lys	Asn	Trp	Gln	Glu	Val	Pro	Phe	Cys	Ser	His	His
3185					3190					3195				3200	
Phe	His	Lys	Ile	Phe	Met	Lys	Asp	Gly	Arg	Ser	Leu	Val	Val	Pro	Cys
			3205						3210					3215	
Arg	Asn	Gln	Asp	Glu	Leu	Ile	Gly	Arg	Ala	Arg	Ile	Ser	Gln	Gly	Ala
			3220						3225				3230		
Gly	Trp	Ser	Leu	Arg	Glu	Thr	Ala	Cys	Leu	Gly	Lys	Ala	Tyr	Ala	Gln
		3235					3240						3245		
Met	Trp	Ser	Leu	Met	Tyr	Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Ala	Ser
	3250					3255					3260				
Met	Ala	Ile	Cys	Ser	Ala	Val	Pro	Thr	Glu	Trp	Phe	Pro	Thr	Ser	Arg
3265					3270					3275				3280	
Thr	Thr	Trp	Ser	Ile	His	Ala	His	His	Gln	Trp	Met	Thr	Thr	Glu	Asp
			3285						3290					3295	
Met	Leu	Lys	Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Asp	Asn	Pro	Asn	Met
			3300						3305				3310		
Thr	Asp	Lys	Thr	Pro	Val	His	Ser	Trp	Glu	Asp	Ile	Pro	Tyr	Leu	Gly
	3315						3320						3325		

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Lys Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly Leu Ser Ser Arg
 3330 3335 3340

Ala Thr Trp Ala Lys Asn Ile His Thr Ala Ile Thr Gln Val Arg Asn
 3345 3350 3355 3360

Leu Ile Gly Lys Glu Glu Tyr Val Asp Tyr Met Pro Val Met Lys Arg
 3365 3370 3375

Tyr Ser Ala Pro Ser Glu Ser Glu Gly Val Leu
 3380 3385

<210> SEQ ID NO 20
 <211> LENGTH: 3392
 <212> TYPE: PRT
 <213> ORGANISM: Dengue 1 virus strain WP

<400> SEQUENCE: 20

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

Lys Arg Ala Arg Asn Arg Val Ser Thr Val Ser Gln Leu Ala Lys Arg
 20 25 30

Phe Ser Lys Gly Leu Leu Ser Gly Gln Gly Pro Met Lys Leu Val Met
 35 40 45

Ala Phe Ile Ala Phe Leu Arg Phe Leu Ala Ile Pro Pro Thr Ala Gly
 50 55 60

Ile Leu Ala Arg Trp Gly Ser Phe Lys Lys Asn Gly Ala Ile Lys Val
 65 70 75 80

Leu Arg Gly Phe Lys Lys Glu Ile Ser Asn Met Leu Asn Ile Met Asn
 85 90 95

Arg Arg Lys Arg Ser Val Thr Met Leu Leu Met Leu Leu Pro Thr Ala
 100 105 110

Leu Ala Phe His Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val
 115 120 125

Ser Lys Gln Glu Arg Gly Lys Ser Leu Leu Phe Lys Thr Ser Ala Gly
 130 135 140

Val Asn Met Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu
 145 150 155 160

Asp Thr Met Thr Tyr Lys Cys Pro Arg Ile Thr Glu Thr Glu Pro Asp
 165 170 175

Asp Val Asp Cys Trp Cys Asn Ala Thr Glu Thr Trp Val Thr Tyr Gly
 180 185 190

Thr Cys Ser Gln Thr Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala
 195 200 205

Leu Ala Pro His Val Gly Leu Gly Leu Glu Thr Arg Thr Glu Thr Trp
 210 215 220

Met Ser Ser Glu Gly Ala Trp Lys Gln Ile Gln Lys Val Glu Thr Trp
 225 230 235 240

Ala Leu Arg His Pro Gly Phe Thr Val Ile Ala Leu Phe Leu Ala His
 245 250 255

Ala Ile Gly Thr Ser Ile Thr Gln Lys Gly Ile Ile Phe Ile Leu Leu
 260 265 270

Met Leu Val Thr Pro Ser Met Ala Met Arg Cys Val Gly Ile Gly Asn
 275 280 285

Arg Asp Phe Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val
 290 295 300

Leu Glu His Gly Ser Cys Val Thr Thr Met Ala Lys Asp Lys Pro Thr

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305	310	315	320
Leu Asp Ile Glu 325	Leu Leu Lys Thr 325	Glu Val Thr Asn Pro Ala 330	Val Leu 335
Arg Lys Leu Cys 340	Ile Glu Ala Lys 340	Ile Ser Asn Thr Thr Thr 345	Asp Ser 350
Arg Cys Pro Thr 355	Gln Gly Glu Ala Thr 360	Leu Val Glu Glu Gln Asp 365	Thr
Asn Phe Val Cys 370	Arg Arg Thr Phe Val 375	Asp Arg Gly Trp Gly Asn 380	Gly
Cys Gly Leu Phe 385	Gly Lys Gly Ser Leu 390	Ile Thr Cys Ala Lys Phe 395	Lys 400
Cys Val Thr Lys 405	Leu Glu Gly Lys Ile 405	Val Gln Tyr Glu Asn 410	Leu Lys 415
Tyr Ser Val Ile 420	Val Thr Val His Thr 420	Gly Asp Gln His Gln Val 425	Gly 430
Asn Glu Thr Thr 435	Glu His Gly Thr Thr 440	Ala Thr Ile Thr Pro Gln 445	Ala
Pro Thr Ser Glu Ile 450	Gln Leu Thr Asp Tyr 455	Gly Ala Leu Thr Leu 460	Asp
Cys Ser Pro Arg Thr 465	Gly Leu Asp Phe Asn 470	Glu Met Val Leu Leu 475	Thr 480
Met Glu Lys Lys Ser 485	Trp Leu Val His Lys 490	Gln Trp Phe Leu Asp 495	Leu
Pro Leu Pro Trp Thr 500	Ser Gly Ala Ser Thr 505	Ser Gln Glu Thr Trp 510	Asn
Arg Gln Asp Leu Leu 515	Val Thr Phe Lys Thr 520	Ala His Ala Lys Lys 525	Gln
Glu Val Val Val Leu 530	Gly Ser Gln Glu Gly 535	Ala Met His Thr Ala 540	Leu
Thr Gly Ala Thr Glu 545	Ile Gln Thr Ser Gly 550	Thr Thr Thr Ile Phe 555	Ala 560
Gly His Leu Lys Cys 565	Arg Leu Lys Met Asp 570	Lys Leu Thr Leu Lys 575	Gly
Met Ser Tyr Val Met 580	Cys Thr Gly Ser Phe 585	Lys Leu Glu Lys Glu 590	Val
Ala Glu Thr Gln His 595	Gly Thr Val Leu Val 600	Gln Val Lys Tyr Glu 605	Gly
Thr Asp Ala Pro Cys 610	Lys Ile Pro Phe Ser 615	Ser Ser Gln Asp Glu 620	Lys Gly
Val Thr Gln Asn Gly 625	Arg Leu Ile Thr Ala 630	Asn Pro Ile Val Thr 635	Asp 640
Lys Glu Lys Pro Val 645	Asn Ile Glu Ala Glu 650	Pro Pro Phe Gly Glu 655	Ser
Tyr Ile Val Val Gly 660	Ala Gly Glu Lys Ala 665	Leu Lys Leu Ser Trp 670	Phe
Lys Lys Gly Ser Ser 675	Ile Gly Lys Met Phe 680	Glu Ala Thr Ala Arg 685	Gly
Ala Arg Arg Met Ala 690	Ile Leu Gly Asp Thr 695	Ala Trp Asp Phe Gly 700	Ser
Ile Gly Gly Val Phe 705	Thr Ser Val Gly Lys 710	Leu Ile His Gln Ile 715	Phe 720
Gly Thr Ala Tyr Gly 725	Val Leu Phe Ser Gly 730	Val Ser Trp Thr Met 735	Lys

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Ile Gly Ile Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser
 740 745 750

Thr Ser Leu Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr
 755 760 765

Leu Gly Val Met Val Gln Ala Asp Ser Gly Cys Val Ile Asn Trp Lys
 770 775 780

Gly Arg Glu Leu Lys Cys Gly Ser Gly Ile Phe Val Thr Asn Glu Val
 785 790 795 800

His Thr Trp Thr Glu Gln Tyr Lys Phe Gln Ala Asp Ser Pro Lys Arg
 805 810 815

Leu Ser Ala Ala Ile Gly Lys Ala Trp Glu Glu Gly Val Cys Gly Ile
 820 825 830

Arg Ser Ala Thr Arg Leu Glu Asn Ile Met Trp Lys Gln Ile Ser Asn
 835 840 845

Glu Leu Asn His Ile Leu Leu Glu Asn Asp Met Lys Phe Thr Val Val
 850 855 860

Val Gly Asp Val Ser Gly Ile Leu Ala Gln Gly Lys Lys Met Ile Arg
 865 870 875 880

Pro Gln Pro Met Glu His Lys Tyr Ser Trp Lys Ser Trp Gly Lys Ala
 885 890 895

Lys Ile Ile Gly Ala Asp Val Gln Asn Thr Thr Phe Ile Ile Asp Gly
 900 905 910

Pro Asn Thr Pro Glu Cys Pro Asp Asn Gln Arg Ala Trp Asn Ile Trp
 915 920 925

Glu Val Glu Asp Tyr Gly Phe Gly Ile Phe Thr Thr Asn Ile Trp Leu
 930 935 940

Lys Leu Arg Asp Ser Tyr Thr Gln Val Cys Asp His Arg Leu Met Ser
 945 950 955 960

Ala Ala Ile Lys Asp Ser Lys Ala Val His Ala Asp Met Gly Tyr Trp
 965 970 975

Ile Glu Ser Glu Lys Asn Glu Thr Trp Lys Leu Ala Arg Ala Ser Phe
 980 985 990

Ile Glu Val Lys Thr Cys Ile Trp Pro Lys Ser His Thr Leu Trp Ser
 995 1000 1005

Asn Gly Val Leu Glu Ser Glu Met Ile Ile Pro Lys Ile Tyr Gly Gly
 1010 1015 1020

Pro Ile Ser Gln His Asn Tyr Arg Pro Gly Tyr Phe Thr Gln Thr Ala
 1025 1030 1035 1040

Gly Pro Trp His Leu Gly Lys Leu Glu Leu Asp Phe Asp Leu Cys Glu
 1045 1050 1055

Gly Thr Thr Val Val Val Asp Glu His Cys Gly Asn Arg Gly Pro Ser
 1060 1065 1070

Leu Arg Thr Thr Thr Val Thr Gly Lys Thr Ile His Glu Trp Cys Cys
 1075 1080 1085

Arg Ser Cys Thr Leu Pro Pro Leu Arg Phe Lys Gly Glu Asp Gly Cys
 1090 1095 1100

Trp Tyr Gly Met Glu Ile Arg Pro Val Lys Glu Lys Glu Glu Asn Leu
 1105 1110 1115 1120

Val Lys Ser Met Val Ser Ala Gly Ser Gly Glu Val Asp Ser Phe Ser
 1125 1130 1135

Leu Gly Leu Leu Cys Ile Ser Ile Met Ile Glu Glu Val Met Arg Ser
 1140 1145 1150

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Arg	Trp	Ser	Arg	Lys	Met	Leu	Met	Thr	Gly	Thr	Leu	Ala	Val	Phe	Leu
		1155					1160					1165			
Leu	Leu	Thr	Met	Gly	Gln	Leu	Thr	Trp	Asn	Asp	Leu	Ile	Arg	Leu	Cys
	1170					1175					1180				
Ile	Met	Val	Gly	Ala	Asn	Ala	Ser	Asp	Lys	Met	Gly	Met	Gly	Thr	Thr
1185					1190					1195					1200
Tyr	Leu	Ala	Leu	Met	Ala	Thr	Phe	Arg	Met	Arg	Pro	Met	Phe	Ala	Val
				1205					1210						1215
Gly	Leu	Leu	Phe	Arg	Arg	Leu	Thr	Ser	Arg	Glu	Val	Leu	Leu	Leu	Thr
			1220					1225					1230		
Val	Gly	Leu	Ser	Leu	Val	Ala	Ser	Val	Glu	Leu	Pro	Asn	Ser	Leu	Glu
		1235					1240					1245			
Glu	Leu	Gly	Asp	Gly	Leu	Ala	Met	Gly	Ile	Met	Met	Leu	Lys	Leu	Leu
	1250					1255					1260				
Thr	Asp	Phe	Gln	Ser	His	Gln	Leu	Trp	Ala	Thr	Leu	Leu	Ser	Leu	Thr
1265					1270					1275					1280
Phe	Val	Lys	Thr	Thr	Phe	Ser	Leu	His	Tyr	Ala	Trp	Lys	Thr	Met	Ala
				1285						1290					1295
Met	Ile	Leu	Ser	Ile	Val	Ser	Leu	Phe	Pro	Leu	Cys	Leu	Ser	Thr	Thr
			1300					1305					1310		
Ser	Gln	Lys	Thr	Thr	Trp	Leu	Pro	Val	Leu	Leu	Gly	Ser	Leu	Gly	Cys
		1315					1320					1325			
Lys	Pro	Leu	Thr	Met	Phe	Leu	Ile	Thr	Glu	Asn	Lys	Ile	Trp	Gly	Arg
	1330					1335						1340			
Lys	Ser	Trp	Pro	Leu	Asn	Glu	Gly	Ile	Met	Ala	Val	Gly	Ile	Val	Ser
1345					1350					1355					1360
Ile	Leu	Leu	Ser	Ser	Leu	Leu	Lys	Asn	Asp	Val	Pro	Leu	Ala	Gly	Pro
				1365					1370					1375	
Leu	Ile	Ala	Gly	Gly	Met	Leu	Ile	Ala	Cys	Tyr	Val	Ile	Ser	Gly	Ser
			1380					1385					1390		
Ser	Ala	Asp	Leu	Ser	Leu	Glu	Lys	Ala	Ala	Glu	Val	Ser	Trp	Glu	Glu
		1395					1400						1405		
Glu	Ala	Glu	His	Ser	Gly	Ala	Ser	His	Asn	Ile	Leu	Val	Glu	Val	Gln
	1410					1415						1420			
Asp	Asp	Gly	Thr	Met	Lys	Ile	Lys	Asp	Glu	Glu	Arg	Asp	Asp	Thr	Leu
1425					1430					1435					1440
Thr	Ile	Leu	Leu	Lys	Ala	Thr	Leu	Leu	Ala	Ile	Ser	Gly	Val	Tyr	Pro
				1445					1450						1455
Met	Ser	Ile	Pro	Ala	Thr	Leu	Phe	Val	Trp	Tyr	Phe	Trp	Gln	Lys	Lys
			1460					1465					1470		
Lys	Gln	Arg	Ser	Gly	Val	Leu	Trp	Asp	Thr	Pro	Ser	Pro	Pro	Glu	Val
		1475					1480					1485			
Glu	Arg	Ala	Val	Leu	Asp	Asp	Gly	Ile	Tyr	Arg	Ile	Leu	Gln	Arg	Gly
	1490					1495					1500				
Leu	Leu	Gly	Arg	Ser	Gln	Val	Gly	Val	Gly	Val	Phe	Gln	Glu	Gly	Val
1505					1510					1515					1520
Phe	His	Thr	Met	Trp	His	Val	Thr	Arg	Gly	Ala	Val	Leu	Met	Tyr	Gln
				1525					1530					1535	
Gly	Lys	Arg	Leu	Glu	Pro	Ser	Trp	Ala	Ser	Val	Lys	Lys	Asp	Leu	Ile
			1540					1545					1550		
Ser	Tyr	Gly	Gly	Gly	Trp	Arg	Phe	Gln	Gly	Ser	Trp	Asn	Ala	Gly	Glu
		1555					1560					1565			
Glu	Val	Gln	Val	Ile	Ala	Val	Glu	Pro	Gly	Lys	Asn	Pro	Lys	Asn	Val

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1570	1575	1580
Gln Thr Ala Pro Gly Thr Phe Lys Thr Pro Glu Gly Glu Val Gly Ala 1585	1590	1595
Ile Ala Leu Asp Phe Lys Pro Gly Thr Ser Gly Ser Pro Ile Val Asn 1605	1610	1615
Arg Glu Gly Lys Ile Val Gly Leu Tyr Gly Asn Gly Val Val Thr Thr 1620	1625	1630
Ser Gly Thr Tyr Val Ser Ala Ile Ala Gln Ala Lys Ala Ser Gln Glu 1635	1640	1645
Gly Pro Leu Pro Glu Ile Glu Asp Glu Val Phe Arg Lys Arg Asn Leu 1650	1655	1660
Thr Ile Met Asp Leu His Pro Gly Ser Gly Lys Thr Arg Arg Tyr Leu 1665	1670	1675
Pro Ala Ile Val Arg Glu Ala Ile Arg Arg Asn Val Arg Thr Leu Val 1685	1690	1695
Leu Ala Pro Thr Arg Val Val Ala Ser Glu Met Ala Glu Ala Leu Lys 1700	1705	1710
Gly Met Pro Ile Arg Tyr Gln Thr Thr Ala Val Lys Ser Glu His Thr 1715	1720	1725
Gly Lys Glu Ile Val Asp Leu Met Cys His Ala Thr Phe Thr Met Arg 1730	1735	1740
Leu Leu Ser Pro Val Arg Val Pro Asn Tyr Asn Met Ile Ile Met Asp 1745	1750	1755
Glu Ala His Phe Thr Asp Pro Ala Ser Ile Ala Ala Arg Gly Tyr Ile 1765	1770	1775
Ser Thr Arg Val Gly Met Gly Glu Ala Ala Ala Ile Phe Met Thr Ala 1780	1785	1790
Thr Pro Pro Gly Ser Val Glu Ala Phe Pro Gln Ser Asn Ala Val Ile 1795	1800	1805
Gln Asp Glu Glu Arg Asp Ile Pro Glu Arg Ser Trp Asn Ser Gly Tyr 1810	1815	1820
Asp Trp Ile Thr Asp Phe Pro Gly Lys Thr Val Trp Phe Val Pro Ser 1825	1830	1835
Ile Lys Ser Gly Asn Asp Ile Ala Asn Cys Leu Arg Lys Asn Gly Lys 1845	1850	1855
Arg Val Val Gln Leu Ser Arg Lys Thr Phe Asp Thr Glu Tyr Gln Lys 1860	1865	1870
Thr Lys Asn Asn Asp Trp Asp Tyr Val Val Thr Thr Asp Ile Ser Glu 1875	1880	1885
Met Gly Ala Asn Phe Arg Ala Asp Arg Val Ile Asp Pro Arg Arg Cys 1890	1895	1900
Leu Lys Pro Val Ile Leu Lys Asp Gly Pro Glu Arg Val Ile Leu Ala 1905	1910	1915
Gly Pro Met Pro Val Thr Val Ala Ser Ala Ala Gln Arg Arg Gly Arg 1925	1930	1935
Ile Gly Arg Asn Gln Asn Lys Glu Gly Asp Gln Tyr Ile Tyr Met Gly 1940	1945	1950
Gln Pro Leu Asn Asn Asp Glu Asp His Ala His Trp Thr Glu Ala Lys 1955	1960	1965
Met Leu Leu Asp Asn Ile Asn Thr Pro Glu Gly Ile Ile Pro Ala Leu 1970	1975	1980
Phe Glu Pro Glu Arg Glu Lys Ser Ala Ala Ile Asp Gly Glu Tyr Arg 1985	1990	1995
		2000

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Leu Arg Gly Glu Ala Arg Lys Thr Phe Val Glu Leu Met Arg Arg Gly
2005 2010 2015

Asp Leu Pro Val Trp Leu Ser Tyr Lys Val Ala Ser Glu Gly Phe Gln
2020 2025 2030

Tyr Ser Asp Arg Arg Trp Cys Phe Asp Gly Glu Arg Asn Asn Gln Val
2035 2040 2045

Leu Glu Glu Asn Met Asp Val Glu Ile Trp Thr Lys Glu Gly Glu Arg
2050 2055 2060

Lys Lys Leu Arg Pro Arg Trp Leu Asp Ala Arg Thr Tyr Ser Asp Pro
2065 2070 2075 2080

Leu Ala Leu Arg Glu Phe Lys Glu Phe Ala Ala Gly Arg Arg Ser Val
2085 2090 2095

Ser Gly Asp Leu Ile Leu Glu Ile Gly Lys Leu Pro Gln His Leu Thr
2100 2105 2110

Gln Arg Ala Gln Asn Ala Leu Asp Asn Leu Val Met Leu His Asn Ser
2115 2120 2125

Glu Gln Gly Gly Lys Ala Tyr Arg His Ala Met Glu Glu Leu Pro Asp
2130 2135 2140

Thr Ile Glu Thr Leu Met Leu Leu Ala Leu Ile Ala Val Leu Thr Gly
2145 2150 2155 2160

Gly Val Thr Leu Phe Phe Leu Ser Gly Arg Gly Leu Gly Lys Thr Ser
2165 2170 2175

Ile Gly Leu Leu Cys Val Ile Ala Ser Ser Ala Leu Leu Trp Met Ala
2180 2185 2190

Ser Val Glu Pro His Trp Ile Ala Ala Ser Ile Ile Leu Glu Phe Phe
2195 2200 2205

Leu Met Val Leu Leu Ile Pro Glu Pro Asp Arg Gln Arg Thr Pro Gln
2210 2215 2220

Asp Asn Gln Leu Ala Tyr Val Val Ile Gly Leu Leu Phe Met Ile Leu
2225 2230 2235 2240

Thr Ala Ala Ala Asn Glu Met Gly Leu Leu Glu Thr Thr Lys Lys Asp
2245 2250 2255

Leu Gly Ile Gly His Ala Ala Ala Glu Asn His His His Ala Ala Met
2260 2265 2270

Leu Asp Val Asp Leu His Pro Ala Ser Ala Trp Thr Leu Tyr Ala Val
2275 2280 2285

Ala Thr Thr Ile Ile Thr Pro Met Met Arg His Thr Ile Glu Asn Thr
2290 2295 2300

Thr Ala Asn Ile Ser Leu Thr Ala Ile Ala Asn Gln Ala Ala Ile Leu
2305 2310 2315 2320

Met Gly Leu Asp Lys Gly Trp Pro Ile Ser Lys Met Asp Ile Gly Val
2325 2330 2335

Pro Leu Leu Ala Leu Gly Cys Tyr Ser Gln Val Asn Pro Leu Thr Leu
2340 2345 2350

Thr Ala Ala Val Phe Met Leu Val Ala His Tyr Ala Ile Ile Gly Pro
2355 2360 2365

Gly Leu Gln Ala Lys Ala Thr Arg Glu Ala Gln Lys Arg Thr Ala Ala
2370 2375 2380

Gly Ile Met Lys Asn Pro Thr Val Asp Gly Ile Val Ala Ile Asp Leu
2385 2390 2395 2400

Asp Pro Val Val Tyr Asp Ala Lys Phe Glu Lys Gln Leu Gly Gln Ile
2405 2410 2415

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Met Leu Leu Ile Leu Cys Thr Ser Gln Ile Leu Leu Met Arg Thr Thr
2420 2425 2430

Trp Ala Leu Cys Glu Ser Ile Thr Leu Ala Thr Gly Pro Leu Thr Thr
2435 2440 2445

Leu Trp Glu Gly Ser Pro Gly Lys Phe Trp Asn Thr Thr Ile Ala Val
2450 2455 2460

Ser Met Ala Asn Ile Phe Arg Gly Ser Tyr Leu Ala Gly Ala Gly Leu
2465 2470 2475 2480

Ala Phe Ser Leu Met Lys Ser Leu Gly Gly Gly Arg Arg Gly Thr Gly
2485 2490 2495

Ala Gln Gly Glu Thr Leu Gly Glu Lys Trp Lys Arg Gln Leu Asn Gln
2500 2505 2510

Leu Ser Lys Ser Glu Phe Asn Thr Tyr Lys Arg Ser Gly Ile Ile Glu
2515 2520 2525

Val Asp Arg Ser Glu Ala Lys Glu Gly Leu Lys Arg Gly Glu Pro Thr
2530 2535 2540

Lys His Ala Val Ser Arg Gly Thr Ala Lys Leu Arg Trp Phe Val Glu
2545 2550 2555 2560

Arg Asn Leu Val Lys Pro Glu Gly Lys Val Ile Asp Leu Gly Cys Gly
2565 2570 2575

Arg Gly Gly Trp Ser Tyr Tyr Cys Ala Gly Leu Lys Lys Val Thr Glu
2580 2585 2590

Val Lys Gly Tyr Thr Lys Gly Gly Pro Gly His Glu Glu Pro Ile Pro
2595 2600 2605

Met Ala Thr Tyr Gly Trp Asn Leu Val Lys Leu Tyr Ser Gly Lys Asp
2610 2615 2620

Val Phe Phe Thr Pro Pro Glu Lys Cys Asp Thr Leu Leu Cys Asp Ile
2625 2630 2635 2640

Gly Glu Ser Ser Pro Asn Pro Thr Ile Glu Glu Gly Arg Thr Leu Arg
2645 2650 2655

Val Leu Lys Met Val Glu Pro Trp Leu Arg Gly Asn Gln Phe Cys Ile
2660 2665 2670

Lys Ile Leu Asn Pro Tyr Met Pro Ser Val Val Glu Thr Leu Glu Gln
2675 2680 2685

Met Gln Arg Lys His Gly Gly Met Leu Val Arg Asn Pro Leu Ser Arg
2690 2695 2700

Asn Ser Thr His Glu Met Tyr Trp Val Ser Cys Gly Thr Gly Asn Ile
2705 2710 2715 2720

Val Ser Ala Val Asn Met Thr Ser Arg Met Leu Leu Asn Arg Phe Thr
2725 2730 2735

Met Ala His Arg Lys Pro Thr Tyr Glu Arg Asp Val Asp Leu Gly Ala
2740 2745 2750

Gly Thr Arg His Val Ala Val Glu Pro Glu Val Ala Asn Leu Asp Ile
2755 2760 2765

Ile Gly Gln Arg Ile Glu Asn Ile Lys Asn Gly His Lys Ser Thr Trp
2770 2775 2780

His Tyr Asp Glu Asp Asn Pro Tyr Lys Thr Trp Ala Tyr His Gly Ser
2785 2790 2795 2800

Tyr Glu Val Lys Pro Ser Gly Ser Ala Ser Ser Met Val Asn Gly Val
2805 2810 2815

Val Arg Leu Leu Thr Lys Pro Trp Asp Val Ile Pro Met Val Thr Gln
2820 2825 2830

Ile Ala Met Thr Asp Thr Thr Pro Phe Gly Gln Gln Arg Val Phe Lys

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2835	2840	2845
Glu Lys Val Asp Thr Arg Thr Pro Lys Ala Lys Arg Gly Thr Ala Gln 2850 2855 2860		
Ile Met Glu Val Thr Ala Arg Trp Leu Trp Gly Phe Leu Ser Arg Asn 2865 2870 2875 2880		
Lys Lys Pro Arg Ile Cys Thr Arg Glu Glu Phe Thr Arg Lys Val Arg 2885 2890 2895		
Ser Asn Ala Ala Ile Gly Ala Val Phe Val Asp Glu Asn Gln Trp Asn 2900 2905 2910		
Ser Ala Lys Glu Ala Val Glu Asp Glu Arg Phe Trp Asp Leu Val His 2915 2920 2925		
Arg Glu Arg Glu Leu His Lys Gln Gly Lys Cys Ala Thr Cys Val Tyr 2930 2935 2940		
Asn Met Met Gly Lys Arg Glu Lys Lys Leu Gly Glu Phe Gly Lys Ala 2945 2950 2955 2960		
Lys Gly Ser Arg Ala Ile Trp Tyr Met Trp Leu Gly Ala Arg Phe Leu 2965 2970 2975		
Glu Phe Glu Ala Leu Gly Phe Met Asn Glu Asp His Trp Phe Ser Arg 2980 2985 2990		
Glu Asn Ser Leu Ser Gly Val Glu Gly Glu Gly Leu His Lys Leu Gly 2995 3000 3005		
Tyr Ile Leu Arg Asp Ile Ser Lys Ile Pro Gly Gly Asn Met Tyr Ala 3010 3015 3020		
Asp Asp Thr Ala Gly Trp Asp Thr Arg Ile Thr Glu Asp Asp Leu Gln 3025 3030 3035 3040		
Asn Glu Ala Lys Ile Thr Asp Ile Met Glu Pro Glu His Ala Leu Leu 3045 3050 3055		
Ala Thr Ser Ile Phe Lys Leu Thr Tyr Gln Asn Lys Val Val Arg Val 3060 3065 3070		
Gln Arg Pro Ala Lys Asn Gly Thr Val Met Asp Val Ile Ser Arg Arg 3075 3080 3085		
Asp Gln Arg Gly Ser Gly Gln Val Gly Thr Tyr Gly Leu Asn Thr Phe 3090 3095 3100		
Thr Asn Met Glu Ala Gln Leu Ile Arg Gln Met Glu Ser Glu Gly Ile 3105 3110 3115 3120		
Phe Ser Pro Ser Glu Leu Glu Thr Pro Asn Leu Ala Glu Arg Val Leu 3125 3130 3135		
Asp Trp Leu Lys Lys His Gly Thr Glu Arg Leu Lys Arg Met Ala Ile 3140 3145 3150		
Ser Gly Asp Asp Cys Val Val Lys Pro Ile Asp Asp Arg Phe Ala Thr 3155 3160 3165		
Ala Leu Thr Ala Leu Asn Asp Met Gly Lys Val Arg Lys Asp Ile Pro 3170 3175 3180		
Gln Trp Glu Pro Ser Lys Gly Trp Asn Asp Trp Gln Gln Val Pro Phe 3185 3190 3195 3200		
Cys Ser His His Phe His Gln Leu Ile Met Lys Asp Gly Arg Glu Ile 3205 3210 3215		
Val Val Pro Cys Arg Asn Gln Asp Glu Leu Val Gly Arg Ala Arg Val 3220 3225 3230		
Ser Gln Gly Ala Gly Trp Ser Leu Arg Glu Thr Ala Cys Leu Gly Lys 3235 3240 3245		
Ser Tyr Ala Gln Met Trp Gln Leu Met Tyr Phe His Arg Arg Asp Leu 3250 3255 3260		

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245			250			255									
Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	Arg	Ala	Leu	Ile	Phe	Ile	Leu	Leu
			260					265				270			
Thr	Ala	Val	Ala	Pro	Ser	Met	Thr	Met	Arg	Cys	Ile	Gly	Ile	Ser	Asn
			275				280					285			
Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	Gly	Gly	Ser	Trp	Val	Asp	Ile	Val
			290			295					300				
Leu	Glu	His	Gly	Ser	Cys	Val	Thr	Thr	Met	Ala	Lys	Asn	Lys	Pro	Thr
305					310					315				320	
Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	Glu	Ala	Lys	Gln	Pro	Ala	Thr	Leu
			325						330					335	
Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	Leu	Thr	Asn	Thr	Thr	Thr	Asp	Ser
			340					345						350	
Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	Ser	Leu	Asn	Glu	Glu	Gln	Asp	Lys
			355				360					365			
Arg	Phe	Val	Cys	Lys	His	Ser	Met	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly
			370			375					380				
Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	Ile	Val	Thr	Cys	Ala	Met	Phe	Thr
385					390					395					400
Cys	Lys	Lys	Asn	Met	Lys	Gly	Lys	Val	Val	Gln	Pro	Glu	Asn	Leu	Glu
			405						410					415	
Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	Ser	Gly	Glu	Glu	His	Ala	Val	Gly
			420					425					430		
Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	Glu	Ile	Lys	Ile	Thr	Pro	Gln	Ser
			435				440					445			
Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	Gly	Tyr	Gly	Thr	Val	Thr	Met	Glu
			450			455					460				
Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	Phe	Asn	Glu	Met	Val	Leu	Leu	Gln
465					470					475					480
Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	His	Arg	Gln	Trp	Phe	Leu	Asp	Leu
			485						490					495	
Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	Asp	Thr	Gln	Gly	Ser	Asn	Trp	Ile
			500					505					510		
Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe	Lys	Asn	Pro	His	Ala	Lys	Lys	Gln
			515					520					525		
Asp	Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Met	His	Thr	Ala	Leu
			530			535					540				
Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met	Ser	Ser	Gly	Asn	Leu	Leu	Phe	Thr
545					550					555					560
Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	Met	Asp	Lys	Leu	Gln	Leu	Lys	Gly
			565						570					575	
Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly	Lys	Phe	Lys	Val	Val	Lys	Glu	Ile
			580					585					590		
Ala	Glu	Thr	Gln	His	Gly	Thr	Ile	Val	Ile	Arg	Val	Gln	Tyr	Glu	Gly
			595				600						605		
Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro	Phe	Glu	Ile	Met	Asp	Leu	Glu	Lys
			610			615					620				
Arg	His	Val	Leu	Gly	Arg	Leu	Ile	Thr	Val	Asn	Pro	Ile	Val	Thr	Glu
625					630					635					640
Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu	Ala	Glu	Pro	Pro	Phe	Gly	Asp	Ser
			645						650					655	
Tyr	Ile	Ile	Ile	Gly	Val	Glu	Pro	Gly	Gln	Leu	Lys	Leu	Asn	Trp	Phe
			660					665					670		

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Lys Lys Gly Ser Ser Ile Gly Gln Met Ile Glu Thr Thr Met Arg Gly
 675 680 685
 Ala Lys Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser
 690 695 700
 Leu Gly Gly Val Phe Thr Ser Ile Gly Lys Ala Leu His Gln Val Phe
 705 710 715 720
 Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly Val Ser Trp Thr Met Lys
 725 730 735
 Ile Leu Ile Gly Val Ile Ile Thr Trp Ile Gly Met Asn Ser Arg Ser
 740 745 750
 Thr Ser Leu Ser Val Ser Leu Val Leu Val Gly Val Val Thr Leu Tyr
 755 760 765
 Leu Gly Val Met Val Gln Ala Asp Ser Gly Cys Val Val Ser Trp Lys
 770 775 780
 Asn Lys Glu Leu Lys Cys Gly Ser Gly Ile Phe Ile Thr Asp Asn Val
 785 790 795 800
 His Thr Trp Thr Glu Gln Tyr Lys Phe Gln Pro Glu Ser Pro Ser Lys
 805 810 815
 Leu Ala Ser Ala Ile Gln Lys Ala His Glu Glu Gly Ile Cys Gly Ile
 820 825 830
 Arg Ser Val Thr Arg Leu Glu Asn Leu Met Trp Lys Gln Ile Thr Pro
 835 840 845
 Glu Leu Asn His Ile Leu Ser Glu Asn Glu Val Lys Leu Thr Ile Met
 850 855 860
 Thr Gly Asp Ile Lys Gly Ile Met Gln Ala Gly Lys Arg Ser Leu Gln
 865 870 875 880
 Pro Gln Pro Thr Glu Leu Lys Tyr Ser Trp Lys Thr Trp Gly Lys Ala
 885 890 895
 Lys Met Leu Ser Thr Glu Ser His Asn Gln Thr Phe Leu Ile Asp Gly
 900 905 910
 Pro Glu Thr Ala Glu Cys Pro Asn Thr Asn Arg Ala Trp Asn Ser Leu
 915 920 925
 Glu Val Glu Asp Tyr Gly Phe Gly Val Phe Thr Thr Asn Ile Trp Leu
 930 935 940
 Lys Leu Arg Glu Lys Gln Asp Val Phe Cys Asp Ser Lys Leu Met Ser
 945 950 955 960
 Ala Ala Ile Lys Asp Asn Arg Ala Val His Ala Asp Met Gly Tyr Trp
 965 970 975
 Ile Glu Ser Ala Leu Asn Asp Thr Trp Lys Ile Glu Lys Ala Ser Phe
 980 985 990
 Ile Glu Val Lys Ser Cys His Trp Pro Lys Ser His Thr Leu Trp Ser
 995 1000 1005
 Asn Gly Val Leu Glu Ser Glu Met Ile Ile Pro Lys Asn Phe Ala Gly
 1010 1015 1020
 Pro Val Ser Gln His Asn Tyr Arg Pro Gly Tyr His Thr Gln Thr Ala
 1025 1030 1035 1040
 Gly Pro Trp His Leu Gly Lys Leu Glu Met Asp Phe Asp Phe Cys Glu
 1045 1050 1055
 Gly Thr Thr Val Val Val Thr Glu Asp Cys Gly Asn Arg Gly Pro Ser
 1060 1065 1070
 Leu Arg Thr Thr Thr Ala Ser Gly Lys Leu Ile Thr Glu Trp Cys Cys
 1075 1080 1085

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1505	1510	1515	1520
Phe His Thr Met Trp His Val Thr Arg Gly Ala Val Leu Met His Lys 1525		1530	1535
Gly Lys Arg Ile Glu Pro Ser Trp Ala Asp Val Lys Lys Asp Leu Ile 1540		1545	1550
Ser Tyr Gly Gly Gly Trp Lys Leu Glu Gly Glu Trp Lys Glu Gly Glu 1555		1560	1565
Glu Val Gln Val Leu Ala Leu Glu Pro Gly Lys Asn Pro Arg Ala Val 1570		1575	1580
Gln Thr Lys Pro Gly Leu Phe Lys Thr Asn Ala Gly Thr Ile Gly Ala 1585		1590	1595
Val Ser Leu Asp Phe Ser Pro Gly Thr Ser Gly Ser Pro Ile Ile Asp 1605		1610	1615
Lys Lys Gly Lys Val Val Gly Leu Tyr Gly Asn Gly Val Val Thr Arg 1620		1625	1630
Ser Gly Ala Tyr Val Ser Ala Ile Ala Gln Thr Glu Lys Ser Ile Glu 1635		1640	1645
Asp Asn Pro Glu Ile Glu Asp Asp Ile Phe Arg Lys Arg Lys Leu Thr 1650		1655	1660
Ile Met Asp Leu His Pro Gly Ala Gly Lys Thr Lys Arg Tyr Leu Pro 1665		1670	1675
Ala Ile Val Arg Glu Ala Ile Lys Arg Gly Leu Arg Thr Leu Ile Leu 1685		1690	1695
Ala Pro Thr Arg Val Val Ala Ala Glu Met Glu Glu Ala Leu Arg Gly 1700		1705	1710
Leu Pro Ile Arg Tyr Gln Thr Pro Ala Ile Arg Ala Glu His Thr Gly 1715		1720	1725
Arg Glu Ile Val Asp Leu Met Cys His Ala Thr Phe Thr Met Arg Leu 1730		1735	1740
Leu Ser Pro Val Arg Val Pro Asn Tyr Asn Leu Ile Ile Met Asp Glu 1745		1750	1755
Ala His Phe Thr Asp Pro Ala Ser Ile Ala Ala Arg Gly Tyr Ile Ser 1765		1770	1775
Thr Arg Val Glu Met Gly Glu Ala Ala Gly Ile Phe Met Thr Ala Thr 1780		1785	1790
Pro Pro Gly Ser Arg Asp Pro Phe Pro Gln Ser Asn Ala Pro Ile Met 1795		1800	1805
Asp Glu Glu Arg Glu Ile Pro Glu Arg Ser Trp Ser Ser Gly His Glu 1810		1815	1820
Trp Val Thr Asp Phe Lys Gly Lys Thr Val Trp Phe Val Pro Ser Ile 1825		1830	1835
Lys Ala Gly Asn Asp Ile Ala Ala Cys Leu Arg Lys Asn Gly Lys Lys 1845		1850	1855
Val Ile Gln Leu Ser Arg Lys Thr Phe Asp Ser Glu Tyr Val Lys Thr 1860		1865	1870
Arg Thr Asn Asp Trp Asp Phe Val Val Thr Thr Asp Ile Ser Glu Met 1875		1880	1885
Gly Ala Asn Phe Lys Ala Glu Arg Val Ile Asp Pro Arg Arg Cys Met 1890		1895	1900
Lys Pro Val Ile Leu Thr Asp Gly Glu Glu Arg Val Ile Leu Ala Gly 1905		1910	1915
Pro Met Pro Val Thr His Ser Ser Ala Ala Gln Arg Arg Gly Arg Ile 1925		1930	1935

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Gly Arg Asn Pro Lys Asn Glu Asn Asp Gln Tyr Ile Tyr Met Gly Glu
 1940 1945 1950

Pro Leu Glu Asn Asp Glu Asp Cys Ala His Trp Lys Glu Ala Lys Met
 1955 1960 1965

Leu Leu Asp Asn Ile Asn Thr Pro Glu Gly Ile Ile Pro Ser Met Phe
 1970 1975 1980

Glu Pro Glu Arg Glu Lys Val Asp Ala Ile Asp Gly Glu Tyr Arg Leu
 1985 1990 1995 2000

Arg Gly Glu Ala Arg Lys Thr Phe Val Asp Leu Met Arg Arg Gly Asp
 2005 2010 2015

Leu Pro Val Trp Leu Ala Tyr Arg Val Ala Ala Glu Gly Ile Asn Tyr
 2020 2025 2030

Ala Asp Arg Arg Trp Cys Phe Asp Gly Ile Lys Asn Asn Gln Ile Leu
 2035 2040 2045

Glu Glu Asn Val Glu Val Glu Ile Trp Thr Lys Glu Gly Glu Arg Lys
 2050 2055 2060

Lys Leu Lys Pro Arg Trp Leu Asp Ala Arg Ile Tyr Ser Asp Pro Leu
 2065 2070 2075 2080

Thr Leu Lys Glu Phe Lys Glu Phe Ala Ala Gly Arg Lys Ser Leu Thr
 2085 2090 2095

Leu Asn Leu Ile Thr Glu Met Gly Arg Leu Pro Thr Phe Met Thr Gln
 2100 2105 2110

Lys Ala Arg Asp Ala Leu Asp Asn Leu Ala Val Leu His Thr Ala Glu
 2115 2120 2125

Ala Gly Gly Arg Ala Tyr Asn His Ala Leu Ser Glu Leu Pro Glu Thr
 2130 2135 2140

Leu Glu Thr Leu Leu Leu Leu Thr Leu Leu Ala Thr Val Thr Gly Gly
 2145 2150 2155 2160

Ile Phe Leu Phe Leu Met Ser Gly Arg Gly Ile Gly Lys Met Thr Leu
 2165 2170 2175

Gly Met Cys Cys Ile Ile Thr Ala Ser Ile Leu Leu Trp Tyr Ala Gln
 2180 2185 2190

Ile Gln Pro His Trp Ile Ala Ala Ser Ile Ile Leu Glu Phe Phe Leu
 2195 2200 2205

Ile Val Leu Leu Ile Pro Glu Pro Glu Lys Gln Arg Thr Pro Gln Asp
 2210 2215 2220

Asn Gln Leu Thr Tyr Val Val Ile Ala Ile Leu Thr Val Val Ala Ala
 2225 2230 2235 2240

Thr Met Ala Asn Glu Met Gly Phe Leu Glu Lys Thr Lys Lys Asp Leu
 2245 2250 2255

Gly Leu Gly Ser Ile Thr Thr Gln Gln Pro Glu Ser Asn Ile Leu Asp
 2260 2265 2270

Ile Asp Leu Arg Pro Ala Ser Ala Trp Thr Leu Tyr Ala Val Ala Thr
 2275 2280 2285

Thr Phe Val Thr Pro Met Leu Arg His Ser Ile Glu Asn Ser Ser Val
 2290 2295 2300

Asn Val Ser Leu Thr Ala Ile Ala Asn Gln Ala Thr Val Leu Met Gly
 2305 2310 2315 2320

Leu Gly Lys Gly Trp Pro Leu Ser Lys Met Asp Ile Gly Val Pro Leu
 2325 2330 2335

Leu Ala Ile Gly Cys Tyr Ser Gln Val Asn Pro Ile Thr Leu Thr Ala
 2340 2345 2350

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Ala Leu Phe Leu Leu Val Ala His Tyr Ala Ile Ile Gly Pro Gly Leu
2355 2360 2365

Gln Ala Lys Ala Thr Arg Glu Ala Gln Lys Arg Ala Ala Ala Gly Ile
2370 2375 2380

Met Lys Asn Pro Thr Val Asp Gly Ile Thr Val Ile Asp Leu Asp Pro
2385 2390 2395 2400

Ile Pro Tyr Asp Pro Lys Phe Glu Lys Gln Leu Gly Gln Val Met Leu
2405 2410 2415

Leu Val Leu Cys Val Thr Gln Val Leu Met Met Arg Thr Thr Trp Ala
2420 2425 2430

Leu Cys Glu Ala Leu Thr Leu Ala Thr Gly Pro Ile Ser Thr Leu Trp
2435 2440 2445

Glu Gly Asn Pro Gly Arg Phe Trp Asn Thr Thr Ile Ala Val Ser Met
2450 2455 2460

Ala Asn Ile Phe Arg Gly Ser Tyr Leu Ala Gly Ala Gly Leu Leu Phe
2465 2470 2475 2480

Ser Ile Met Lys Asn Thr Thr Asn Thr Arg Arg Gly Thr Gly Asn Ile
2485 2490 2495

Gly Glu Thr Leu Gly Glu Lys Trp Lys Ser Arg Leu Asn Ala Leu Gly
2500 2505 2510

Lys Ser Glu Phe Gln Ile Tyr Lys Lys Ser Gly Ile Gln Glu Val Asp
2515 2520 2525

Arg Thr Leu Ala Lys Glu Gly Ile Lys Arg Gly Glu Thr Asp His His
2530 2535 2540

Ala Val Ser Arg Gly Ser Ala Lys Leu Arg Trp Phe Val Glu Arg Asn
2545 2550 2555 2560

Met Val Thr Pro Glu Gly Lys Val Val Asp Leu Gly Cys Gly Arg Gly
2565 2570 2575

Gly Trp Ser Tyr Tyr Cys Gly Gly Leu Lys Asn Val Arg Glu Val Lys
2580 2585 2590

Gly Leu Thr Lys Gly Gly Pro Gly His Glu Glu Pro Ile Pro Met Ser
2595 2600 2605

Thr Tyr Gly Trp Asn Leu Val Arg Leu Gln Ser Gly Val Asp Val Phe
2610 2615 2620

Phe Thr Pro Pro Glu Lys Cys Asp Thr Leu Leu Cys Asp Ile Gly Glu
2625 2630 2635 2640

Ser Ser Pro Asn Pro Thr Val Glu Ala Gly Arg Thr Leu Arg Val Leu
2645 2650 2655

Asn Leu Val Glu Asn Trp Leu Asn Asn Asn Thr Gln Phe Cys Ile Lys
2660 2665 2670

Val Leu Asn Pro Tyr Met Pro Ser Val Ile Glu Lys Met Glu Ala Leu
2675 2680 2685

Gln Arg Lys Tyr Gly Gly Ala Leu Val Arg Asn Pro Leu Ser Arg Asn
2690 2695 2700

Ser Thr His Glu Met Tyr Trp Val Ser Asn Ala Ser Gly Asn Ile Val
2705 2710 2715 2720

Ser Ser Val Asn Met Ile Ser Arg Met Leu Ile Asn Arg Phe Thr Met
2725 2730 2735

Arg His Lys Lys Ala Thr Tyr Glu Pro Asp Val Asp Leu Gly Ser Gly
2740 2745 2750

Thr Arg Asn Ile Gly Ile Glu Ser Glu Ile Pro Asn Leu Asp Ile Ile
2755 2760 2765

Gly Lys Arg Ile Glu Lys Ile Lys Gln Glu His Glu Thr Ser Trp His

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2770	2775	2780
Tyr Asp Gln Asp His Pro Tyr Lys Thr Trp Ala Tyr His Gly Ser Tyr 2785	2790	2795
Glu Thr Lys Gln Thr Gly Ser Ala Ser Ser Met Val Asn Gly Val Val 2805	2810	2815
Arg Leu Leu Thr Lys Pro Trp Asp Val Val Pro Met Val Thr Gln Met 2820	2825	2830
Ala Met Thr Asp Thr Thr Pro Phe Gly Gln Gln Arg Val Phe Lys Glu 2835	2840	2845
Lys Val Asp Thr Arg Thr Gln Glu Pro Lys Glu Gly Thr Lys Lys Leu 2850	2855	2860
Met Lys Ile Thr Ala Glu Trp Leu Trp Lys Glu Leu Gly Lys Lys Lys 2865	2870	2875
Thr Pro Arg Met Cys Thr Arg Glu Glu Phe Thr Arg Lys Val Arg Ser 2885	2890	2895
Asn Ala Ala Leu Gly Ala Ile Phe Thr Asp Glu Asn Lys Trp Lys Ser 2900	2905	2910
Ala Arg Glu Ala Val Glu Asp Ser Arg Phe Trp Glu Leu Val Asp Lys 2915	2920	2925
Glu Arg Asn Leu His Leu Glu Gly Lys Cys Glu Thr Cys Val Tyr Asn 2930	2935	2940
Met Met Gly Lys Arg Glu Lys Lys Leu Gly Glu Phe Gly Lys Ala Lys 2945	2950	2955
Gly Ser Arg Ala Ile Trp Tyr Met Trp Leu Gly Ala Arg Phe Leu Glu 2965	2970	2975
Phe Glu Ala Leu Gly Phe Leu Asn Glu Asp His Trp Phe Ser Arg Glu 2980	2985	2990
Asn Ser Leu Ser Gly Val Glu Gly Glu Gly Leu His Lys Leu Gly Tyr 2995	3000	3005
Ile Leu Arg Asp Val Ser Lys Lys Glu Gly Gly Ala Met Tyr Ala Asp 3010	3015	3020
Asp Thr Ala Gly Trp Asp Thr Arg Ile Thr Leu Glu Asp Leu Lys Asn 3025	3030	3035
Glu Glu Met Val Thr Asn His Met Glu Gly Glu His Lys Lys Leu Ala 3045	3050	3055
Glu Ala Ile Phe Lys Leu Thr Tyr Gln Asn Lys Val Val Arg Val Gln 3060	3065	3070
Arg Pro Thr Pro Arg Gly Thr Val Met Asp Ile Ile Ser Arg Arg Asp 3075	3080	3085
Gln Arg Gly Ser Gly Gln Val Gly Thr Tyr Gly Leu Asn Thr Phe Thr 3090	3095	3100
Asn Met Glu Ala Gln Leu Ile Arg Gln Met Glu Gly Glu Gly Val Phe 3105	3110	3115
Lys Ser Ile Gln His Leu Thr Val Thr Glu Glu Ile Ala Val Gln Asn 3125	3130	3135
Trp Leu Ala Arg Val Gly Arg Glu Arg Leu Ser Arg Met Ala Ile Ser 3140	3145	3150
Gly Asp Asp Cys Val Val Lys Pro Leu Asp Asp Arg Phe Ala Ser Ala 3155	3160	3165
Leu Thr Ala Leu Asn Asp Met Gly Lys Val Arg Lys Asp Ile Gln Gln 3170	3175	3180
Trp Glu Pro Ser Arg Gly Trp Asn Asp Trp Thr Gln Val Pro Phe Cys 3185	3190	3195
		3200

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Ser His His Phe His Glu Leu Ile Met Lys Asp Gly Arg Val Leu Val
 3205 3210 3215

Val Pro Cys Arg Asn Gln Asp Glu Leu Ile Gly Arg Ala Arg Ile Ser
 3220 3225 3230

Gln Gly Ala Gly Trp Ser Leu Arg Glu Thr Ala Cys Leu Gly Lys Ser
 3235 3240 3245

Tyr Ala Gln Met Trp Ser Leu Met Tyr Phe His Arg Arg Asp Leu Arg
 3250 3255 3260

Leu Ala Ala Asn Ala Ile Cys Ser Ala Val Pro Ser His Trp Val Pro
 3265 3270 3275 3280

Thr Ser Arg Thr Thr Trp Ser Ile His Ala Lys His Glu Trp Met Thr
 3285 3290 3295

Thr Glu Asp Met Leu Thr Val Trp Asn Arg Val Trp Ile Gln Glu Asn
 3300 3305 3310

Pro Trp Met Glu Asp Lys Thr Pro Val Glu Ser Trp Glu Glu Ile Pro
 3315 3320 3325

Tyr Leu Gly Lys Arg Glu Asp Gln Trp Cys Gly Ser Leu Ile Gly Leu
 3330 3335 3340

Thr Ser Arg Ala Thr Trp Ala Lys Asn Ile Gln Thr Ala Ile Asn Gln
 3345 3350 3355 3360

Val Arg Ser Leu Ile Gly Asn Glu Glu Tyr Thr Asp Tyr Met Pro Ser
 3365 3370 3375

Met Lys Arg Phe Arg Arg Glu Glu Glu Glu Ala Gly Val Leu Trp
 3380 3385 3390

<210> SEQ ID NO 22
 <211> LENGTH: 3390
 <212> TYPE: PRT
 <213> ORGANISM: Dengue 3 virus strain H87

<400> SEQUENCE: 22

Met Asn Asn Gln Arg Lys Lys Thr Gly Lys Pro Ser Ile Asn Met Leu
 1 5 10 15

Lys Arg Val Arg Asn Arg Val Ser Thr Gly Ser Gln Leu Ala Lys Arg
 20 25 30

Phe Ser Arg Gly Leu Leu Asn Gly Gln Gly Pro Met Lys Leu Val Met
 35 40 45

Ala Phe Ile Ala Phe Leu Arg Phe Leu Ala Ile Pro Pro Thr Ala Gly
 50 55 60

Val Leu Ala Arg Trp Gly Thr Phe Lys Lys Ser Gly Ala Ile Lys Val
 65 70 75 80

Leu Lys Gly Phe Lys Lys Glu Ile Ser Asn Met Leu Ser Ile Ile Asn
 85 90 95

Lys Arg Lys Lys Thr Ser Leu Cys Leu Met Met Met Leu Pro Ala Thr
 100 105 110

Leu Ala Phe His Leu Thr Ser Arg Asp Gly Glu Pro Arg Met Ile Val
 115 120 125

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

Ile Asn Met Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Met Cys Asp
 145 150 155 160

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

Asp Ile Asp Cys Trp Cys Asn Leu Thr Ser Thr Trp Val Thr Tyr Gly

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180				185				190							
Thr	Cys	Asn	Gln	Ala	Gly	Glu	His	Arg	Arg	Asp	Lys	Arg	Ser	Val	Ala
		195					200					205			
Leu	Ala	Pro	His	Val	Gly	Met	Gly	Leu	Asp	Thr	Arg	Thr	Gln	Thr	Trp
	210					215					220				
Met	Ser	Ala	Glu	Gly	Ala	Trp	Arg	Gln	Val	Glu	Lys	Val	Glu	Thr	Trp
	225				230						235				240
Ala	Leu	Arg	His	Pro	Gly	Phe	Thr	Ile	Leu	Ala	Leu	Phe	Leu	Ala	His
			245						250					255	
Tyr	Ile	Gly	Thr	Ser	Leu	Thr	Gln	Lys	Val	Val	Ile	Phe	Ile	Leu	Leu
			260						265					270	
Met	Leu	Val	Thr	Pro	Ser	Met	Thr	Met	Arg	Cys	Val	Gly	Val	Gly	Asn
		275					280					285			
Arg	Asp	Phe	Val	Glu	Gly	Leu	Ser	Gly	Ala	Thr	Trp	Val	Asp	Val	Val
		290				295					300				
Leu	Glu	His	Gly	Gly	Cys	Val	Thr	Thr	Met	Ala	Lys	Asn	Lys	Pro	Thr
	305				310					315					320
Leu	Asp	Ile	Glu	Leu	Gln	Lys	Thr	Glu	Ala	Thr	Gln	Leu	Ala	Thr	Leu
			325						330					335	
Arg	Lys	Leu	Cys	Ile	Glu	Gly	Lys	Ile	Thr	Asn	Ile	Thr	Thr	Asp	Ser
			340						345					350	
Arg	Cys	Pro	Thr	Gln	Gly	Glu	Ala	Ile	Leu	Pro	Glu	Glu	Gln	Asp	Gln
		355					360							365	
Asn	Tyr	Val	Cys	Lys	His	Thr	Tyr	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly
		370				375					380				
Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Gln
	385				390					395					400
Cys	Leu	Glu	Ser	Ile	Glu	Gly	Lys	Val	Val	Gln	His	Glu	Asn	Leu	Lys
			405						410					415	
Tyr	Thr	Val	Ile	Ile	Thr	Val	His	Thr	Gly	Asp	Gln	His	Gln	Val	Gly
			420						425				430		
Asn	Glu	Thr	Gln	Gly	Val	Thr	Ala	Glu	Ile	Thr	Ser	Gln	Ala	Ser	Thr
		435					440						445		
Ala	Glu	Ala	Ile	Leu	Pro	Glu	Tyr	Gly	Thr	Leu	Gly	Leu	Glu	Cys	Ser
	450					455					460				
Pro	Arg	Thr	Gly	Leu	Asp	Phe	Asn	Glu	Met	Ile	Leu	Leu	Thr	Met	Lys
			465		470					475					480
Asn	Lys	Ala	Trp	Met	Val	His	Arg	Gln	Trp	Phe	Phe	Asp	Leu	Pro	Leu
			485						490					495	
Pro	Trp	Thr	Ser	Gly	Ala	Thr	Thr	Lys	Thr	Pro	Thr	Trp	Asn	Arg	Lys
			500						505				510		
Glu	Leu	Leu	Val	Thr	Phe	Lys	Asn	Ala	His	Ala	Lys	Lys	Gln	Glu	Val
		515					520						525		
Val	Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Met	His	Thr	Ala	Leu	Thr	Gly
		530				535					540				
Ala	Thr	Glu	Ile	Gln	Thr	Ser	Gly	Gly	Thr	Ser	Ile	Phe	Ala	Gly	His
			545		550					555					560
Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Lys	Leu	Lys	Gly	Met	Ser
			565						570					575	
Tyr	Ala	Met	Cys	Leu	Asn	Thr	Phe	Val	Leu	Lys	Lys	Glu	Val	Ser	Glu
			580						585				590		
Thr	Gln	His	Gly	Thr	Ile	Leu	Ile	Lys	Val	Glu	Tyr	Lys	Gly	Glu	Asp
		595					600						605		

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Ala Pro Cys Lys Ile Pro Phe Ser Thr Glu Asp Gly Gln Gly Lys Ala
610 615 620

His Asn Gly Arg Leu Ile Thr Ala Asn Pro Val Val Thr Lys Lys Glu
625 630 635 640

Glu Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Asn Ile
645 650 655

Val Ile Gly Ile Gly Asp Lys Ala Leu Lys Ile Asn Trp Tyr Arg Lys
660 665 670

Gly Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg
675 680 685

Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
690 695 700

Gly Val Leu Asn Ser Leu Gly Lys Met Val His Gln Ile Phe Gly Ser
705 710 715 720

Ala Tyr Thr Ala Leu Phe Ser Gly Val Ser Trp Ile Met Lys Ile Gly
725 730 735

Ile Gly Val Leu Leu Thr Trp Ile Gly Leu Asn Ser Lys Asn Thr Ser
740 745 750

Met Ser Phe Ser Cys Ile Ala Ile Gly Ile Ile Thr Leu Tyr Leu Gly
755 760 765

Val Val Val Gln Ala Asp Met Gly Cys Val Ile Asn Trp Lys Gly Lys
770 775 780

Glu Leu Lys Cys Gly Ser Gly Ile Phe Val Thr Asn Glu Val His Thr
785 790 795 800

Trp Thr Glu Gln Tyr Lys Phe Gln Ala Asp Ser Pro Lys Arg Val Ala
805 810 815

Thr Ala Ile Ala Gly Ala Trp Glu Asn Gly Val Cys Gly Ile Arg Ser
820 825 830

Thr Thr Arg Met Glu Asn Leu Leu Trp Lys Gln Ile Ala Asn Glu Leu
835 840 845

Asn Tyr Ile Leu Trp Glu Asn Asp Ile Lys Leu Thr Val Val Val Gly
850 855 860

Asp Ile Thr Gly Val Leu Glu Gln Gly Lys Arg Thr Leu Thr Pro Gln
865 870 875 880

Pro Met Glu Leu Lys Tyr Ser Trp Lys Thr Trp Gly Leu Ala Lys Ile
885 890 895

Val Thr Ala Glu Thr Gln Asn Ser Ser Phe Ile Ile Asp Gly Pro Ser
900 905 910

Thr Pro Glu Cys Pro Ser Ala Ser Arg Ala Trp Asn Val Trp Glu Val
915 920 925

Glu Asp Tyr Gly Phe Gly Val Phe Thr Thr Asn Ile Trp Leu Lys Leu
930 935 940

Arg Glu Val Tyr Thr Gln Leu Cys Asp His Arg Leu Met Ser Ala Ala
945 950 955 960

Val Lys Asp Glu Arg Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu
965 970 975

Ser Gln Lys Asn Gly Ser Trp Lys Leu Glu Lys Ala Ser Leu Ile Glu
980 985 990

Val Lys Thr Cys Thr Trp Pro Lys Ser His Thr Leu Trp Ser Asn Gly
995 1000 1005

Val Leu Glu Ser Asp Met Ile Ile Pro Lys Ser Leu Ala Gly Pro Ile
1010 1015 1020

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Ser Gln His Asn His Arg Pro Gly Tyr His Thr Gln Thr Ala Gly Pro
 1025 1030 1035 1040
 Trp His Leu Gly Lys Leu Glu Leu Asp Phe Asn Tyr Cys Glu Gly Thr
 1045 1050 1055
 Thr Val Val Ile Ser Glu Asn Cys Gly Thr Arg Gly Pro Ser Leu Arg
 1060 1065 1070
 Thr Thr Thr Val Ser Gly Lys Leu Ile His Glu Trp Cys Cys Arg Ser
 1075 1080 1085
 Cys Thr Leu Pro Pro Leu Arg Tyr Met Gly Glu Asp Gly Cys Trp Tyr
 1090 1095 1100
 Gly Met Glu Ile Arg Pro Ile Asn Glu Lys Glu Glu Asn Met Val Lys
 1105 1110 1115 1120
 Ser Leu Ala Ser Ala Gly Ser Gly Lys Val Asp Asn Phe Thr Met Gly
 1125 1130 1135
 Val Leu Cys Leu Ala Ile Leu Phe Glu Glu Val Met Arg Gly Lys Phe
 1140 1145 1150
 Gly Lys Lys His Met Ile Ala Gly Val Leu Phe Thr Phe Val Leu Leu
 1155 1160 1165
 Leu Ser Gly Gln Ile Thr Trp Arg Gly Met Ala His Thr Leu Ile Met
 1170 1175 1180
 Ile Gly Ser Asn Ala Ser Asp Arg Met Gly Met Gly Val Thr Tyr Leu
 1185 1190 1195 1200
 Ala Leu Ile Ala Thr Phe Lys Ile Gln Pro Phe Leu Ala Leu Gly Phe
 1205 1210 1215
 Phe Leu Arg Lys Leu Thr Ser Arg Glu Asn Leu Leu Leu Gly Val Gly
 1220 1225 1230
 Leu Ala Met Ala Ala Thr Leu Arg Leu Pro Glu Asp Ile Glu Gln Met
 1235 1240 1245
 Ala Asn Gly Ile Ala Leu Gly Leu Met Ala Leu Lys Leu Ile Thr Gln
 1250 1255 1260
 Phe Glu Thr Tyr Gln Leu Trp Thr Ala Leu Val Ser Leu Thr Cys Ser
 1265 1270 1275 1280
 Asn Thr Ile Phe Thr Leu Thr Val Ala Trp Arg Thr Ala Thr Leu Ile
 1285 1290 1295
 Leu Ala Gly Ile Ser Leu Leu Pro Val Cys Gln Ser Ser Ser Met Arg
 1300 1305 1310
 Lys Thr Asp Trp Leu Pro Met Thr Val Ala Ala Met Gly Val Pro Pro
 1315 1320 1325
 Leu Pro Leu Phe Ile Phe Ser Leu Lys Asp Thr Leu Lys Arg Arg Ser
 1330 1335 1340
 Trp Pro Leu Asn Glu Gly Val Met Ala Val Gly Leu Val Ser Ile Leu
 1345 1350 1355 1360
 Ala Ser Ser Leu Leu Arg Asn Asp Val Pro Met Ala Gly Pro Leu Val
 1365 1370 1375
 Ala Gly Gly Leu Leu Ile Ala Cys Tyr Val Ile Thr Gly Thr Ser Ala
 1380 1385 1390
 Asp Leu Thr Val Glu Lys Ala Ala Asp Val Thr Trp Glu Glu Glu Ala
 1395 1400 1405
 Glu Gln Thr Gly Val Ser His Asn Leu Met Ile Thr Val Asp Asp Asp
 1410 1415 1420
 Gly Thr Met Arg Ile Lys Asp Asp Glu Thr Glu Asn Ile Leu Thr Val
 1425 1430 1435 1440
 Leu Leu Lys Thr Ala Leu Leu Ile Val Ser Gly Ile Phe Pro Tyr Ser

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1445										1450					1455																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
Ile	Pro	Ala	Thr	Met	Leu	Val	Trp	His	Thr	Trp	Gln	Lys	Gln	Thr	Gln									1460					1465					1470						Arg	Ser	Gly	Val	Leu	Trp	Asp	Val	Pro	Ser	Pro	Pro	Glu	Thr	Gln	Lys							1475					1480						1485							Ala	Glu	Leu	Glu	Glu	Gly	Val	Tyr	Arg	Ile	Lys	Gln	Gln	Gly	Ile	Phe							1490				1495						1500								Gly	Lys	Thr	Gln	Val	Gly	Val	Gly	Val	Gln	Lys	Glu	Gly	Val	Phe	His					1505					1510					1515					1520					Thr	Met	Trp	His	Val	Thr	Arg	Gly	Ala	Val	Leu	Thr	His	Asn	Gly	Lys									1525					1530						1535					Arg	Leu	Glu	Pro	Asn	Trp	Ala	Ser	Val	Lys	Lys	Asp	Leu	Ile	Ser	Tyr								1540					1545						1550						Gly	Gly	Gly	Trp	Arg	Leu	Ser	Ala	Gln	Trp	Gln	Lys	Gly	Glu	Glu	Val							1555					1560						1565							Gln	Val	Ile	Ala	Val	Glu	Pro	Gly	Lys	Asn	Pro	Lys	Asn	Phe	Gln	Thr						1570					1575						1580								Met	Pro	Gly	Ile	Phe	Gln	Thr	Thr	Thr	Gly	Glu	Ile	Gly	Ala	Ile	Ala					1585					1590					1595					1600					Leu	Asp	Phe	Lys	Pro	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Ile	Asn	Arg	Glu									1605					1610						1615					Gly	Lys	Val	Val	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val	Thr	Lys	Asn	Gly							1620						1625						1630						Gly	Tyr	Val	Ser	Gly	Ile	Ala	Gln	Thr	Asn	Ala	Glu	Pro	Asp	Gly	Pro							1635					1640						1645							Thr	Pro	Glu	Leu	Glu	Glu	Glu	Met	Phe	Lys	Lys	Arg	Asn	Leu	Thr	Ile							1650				1655						1660								Met	Asp	Leu	His	Pro	Gly	Ser	Gly	Lys	Thr	Arg	Lys	Tyr	Leu	Pro	Ala					1665					1670					1675					1680					Ile	Val	Arg	Glu	Ala	Ile	Lys	Arg	Arg	Leu	Arg	Thr	Leu	Ile	Leu	Ala									1685					1690						1695					Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Met	Lys	Gly	Leu								1700					1705						1710						Pro	Ile	Arg	Tyr	Gln	Thr	Thr	Ala	Thr	Lys	Ser	Glu	His	Thr	Gly	Arg							1715					1720						1725							Glu	Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Met	Arg	Leu	Leu							1730				1735						1740								Ser	Pro	Val	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Ile	Ile	Met	Asp	Glu	Ala					1745					1750					1755					1760					His	Phe	Thr	Asp	Pro	Ala	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr									1765					1770					1775						Arg	Val	Gly	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr	Pro								1780					1785						1790						Pro	Gly	Thr	Ala	Asp	Ala	Phe	Pro	Gln	Ser	Asn	Ala	Pro	Ile	Gln	Asp							1795					1800						1805							Glu	Glu	Arg	Asp	Ile	Pro	Glu	Arg	Ser	Trp	Asn	Ser	Gly	Asn	Glu	Trp							1810				1815						1820								Ile	Thr	Asp	Phe	Val	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Ile	Lys					1825					1830					1835					1840					Ala	Gly	Asn	Val	Ile	Ala	Asn	Cys	Leu	Arg	Lys	Asn	Gly	Lys	Lys	Val								1845						1850					1855						Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Asp	Thr	Glu	Tyr	Gln	Lys	Thr	Lys							1860						1865						1870					
				1460					1465					1470						Arg	Ser	Gly	Val	Leu	Trp	Asp	Val	Pro	Ser	Pro	Pro	Glu	Thr	Gln	Lys							1475					1480						1485							Ala	Glu	Leu	Glu	Glu	Gly	Val	Tyr	Arg	Ile	Lys	Gln	Gln	Gly	Ile	Phe							1490				1495						1500								Gly	Lys	Thr	Gln	Val	Gly	Val	Gly	Val	Gln	Lys	Glu	Gly	Val	Phe	His					1505					1510					1515					1520					Thr	Met	Trp	His	Val	Thr	Arg	Gly	Ala	Val	Leu	Thr	His	Asn	Gly	Lys									1525					1530						1535					Arg	Leu	Glu	Pro	Asn	Trp	Ala	Ser	Val	Lys	Lys	Asp	Leu	Ile	Ser	Tyr								1540					1545						1550						Gly	Gly	Gly	Trp	Arg	Leu	Ser	Ala	Gln	Trp	Gln	Lys	Gly	Glu	Glu	Val							1555					1560						1565							Gln	Val	Ile	Ala	Val	Glu	Pro	Gly	Lys	Asn	Pro	Lys	Asn	Phe	Gln	Thr						1570					1575						1580								Met	Pro	Gly	Ile	Phe	Gln	Thr	Thr	Thr	Gly	Glu	Ile	Gly	Ala	Ile	Ala					1585					1590					1595					1600					Leu	Asp	Phe	Lys	Pro	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Ile	Asn	Arg	Glu									1605					1610						1615					Gly	Lys	Val	Val	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val	Thr	Lys	Asn	Gly							1620						1625						1630						Gly	Tyr	Val	Ser	Gly	Ile	Ala	Gln	Thr	Asn	Ala	Glu	Pro	Asp	Gly	Pro							1635					1640						1645							Thr	Pro	Glu	Leu	Glu	Glu	Glu	Met	Phe	Lys	Lys	Arg	Asn	Leu	Thr	Ile							1650				1655						1660								Met	Asp	Leu	His	Pro	Gly	Ser	Gly	Lys	Thr	Arg	Lys	Tyr	Leu	Pro	Ala					1665					1670					1675					1680					Ile	Val	Arg	Glu	Ala	Ile	Lys	Arg	Arg	Leu	Arg	Thr	Leu	Ile	Leu	Ala									1685					1690						1695					Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Met	Lys	Gly	Leu								1700					1705						1710						Pro	Ile	Arg	Tyr	Gln	Thr	Thr	Ala	Thr	Lys	Ser	Glu	His	Thr	Gly	Arg							1715					1720						1725							Glu	Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Met	Arg	Leu	Leu							1730				1735						1740								Ser	Pro	Val	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Ile	Ile	Met	Asp	Glu	Ala					1745					1750					1755					1760					His	Phe	Thr	Asp	Pro	Ala	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr									1765					1770					1775						Arg	Val	Gly	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr	Pro								1780					1785						1790						Pro	Gly	Thr	Ala	Asp	Ala	Phe	Pro	Gln	Ser	Asn	Ala	Pro	Ile	Gln	Asp							1795					1800						1805							Glu	Glu	Arg	Asp	Ile	Pro	Glu	Arg	Ser	Trp	Asn	Ser	Gly	Asn	Glu	Trp							1810				1815						1820								Ile	Thr	Asp	Phe	Val	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Ile	Lys					1825					1830					1835					1840					Ala	Gly	Asn	Val	Ile	Ala	Asn	Cys	Leu	Arg	Lys	Asn	Gly	Lys	Lys	Val								1845						1850					1855						Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Asp	Thr	Glu	Tyr	Gln	Lys	Thr	Lys							1860						1865						1870																									
Arg	Ser	Gly	Val	Leu	Trp	Asp	Val	Pro	Ser	Pro	Pro	Glu	Thr	Gln	Lys							1475					1480						1485							Ala	Glu	Leu	Glu	Glu	Gly	Val	Tyr	Arg	Ile	Lys	Gln	Gln	Gly	Ile	Phe							1490				1495						1500								Gly	Lys	Thr	Gln	Val	Gly	Val	Gly	Val	Gln	Lys	Glu	Gly	Val	Phe	His					1505					1510					1515					1520					Thr	Met	Trp	His	Val	Thr	Arg	Gly	Ala	Val	Leu	Thr	His	Asn	Gly	Lys									1525					1530						1535					Arg	Leu	Glu	Pro	Asn	Trp	Ala	Ser	Val	Lys	Lys	Asp	Leu	Ile	Ser	Tyr								1540					1545						1550						Gly	Gly	Gly	Trp	Arg	Leu	Ser	Ala	Gln	Trp	Gln	Lys	Gly	Glu	Glu	Val							1555					1560						1565							Gln	Val	Ile	Ala	Val	Glu	Pro	Gly	Lys	Asn	Pro	Lys	Asn	Phe	Gln	Thr						1570					1575						1580								Met	Pro	Gly	Ile	Phe	Gln	Thr	Thr	Thr	Gly	Glu	Ile	Gly	Ala	Ile	Ala					1585					1590					1595					1600					Leu	Asp	Phe	Lys	Pro	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Ile	Asn	Arg	Glu									1605					1610						1615					Gly	Lys	Val	Val	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val	Thr	Lys	Asn	Gly							1620						1625						1630						Gly	Tyr	Val	Ser	Gly	Ile	Ala	Gln	Thr	Asn	Ala	Glu	Pro	Asp	Gly	Pro							1635					1640						1645							Thr	Pro	Glu	Leu	Glu	Glu	Glu	Met	Phe	Lys	Lys	Arg	Asn	Leu	Thr	Ile							1650				1655						1660								Met	Asp	Leu	His	Pro	Gly	Ser	Gly	Lys	Thr	Arg	Lys	Tyr	Leu	Pro	Ala					1665					1670					1675					1680					Ile	Val	Arg	Glu	Ala	Ile	Lys	Arg	Arg	Leu	Arg	Thr	Leu	Ile	Leu	Ala									1685					1690						1695					Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Met	Lys	Gly	Leu								1700					1705						1710						Pro	Ile	Arg	Tyr	Gln	Thr	Thr	Ala	Thr	Lys	Ser	Glu	His	Thr	Gly	Arg							1715					1720						1725							Glu	Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Met	Arg	Leu	Leu							1730				1735						1740								Ser	Pro	Val	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Ile	Ile	Met	Asp	Glu	Ala					1745					1750					1755					1760					His	Phe	Thr	Asp	Pro	Ala	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr									1765					1770					1775						Arg	Val	Gly	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr	Pro								1780					1785						1790						Pro	Gly	Thr	Ala	Asp	Ala	Phe	Pro	Gln	Ser	Asn	Ala	Pro	Ile	Gln	Asp							1795					1800						1805							Glu	Glu	Arg	Asp	Ile	Pro	Glu	Arg	Ser	Trp	Asn	Ser	Gly	Asn	Glu	Trp							1810				1815						1820								Ile	Thr	Asp	Phe	Val	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Ile	Lys					1825					1830					1835					1840					Ala	Gly	Asn	Val	Ile	Ala	Asn	Cys	Leu	Arg	Lys	Asn	Gly	Lys	Lys	Val								1845						1850					1855						Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Asp	Thr	Glu	Tyr	Gln	Lys	Thr	Lys							1860						1865						1870																																													
		1475					1480						1485							Ala	Glu	Leu	Glu	Glu	Gly	Val	Tyr	Arg	Ile	Lys	Gln	Gln	Gly	Ile	Phe							1490				1495						1500								Gly	Lys	Thr	Gln	Val	Gly	Val	Gly	Val	Gln	Lys	Glu	Gly	Val	Phe	His					1505					1510					1515					1520					Thr	Met	Trp	His	Val	Thr	Arg	Gly	Ala	Val	Leu	Thr	His	Asn	Gly	Lys									1525					1530						1535					Arg	Leu	Glu	Pro	Asn	Trp	Ala	Ser	Val	Lys	Lys	Asp	Leu	Ile	Ser	Tyr								1540					1545						1550						Gly	Gly	Gly	Trp	Arg	Leu	Ser	Ala	Gln	Trp	Gln	Lys	Gly	Glu	Glu	Val							1555					1560						1565							Gln	Val	Ile	Ala	Val	Glu	Pro	Gly	Lys	Asn	Pro	Lys	Asn	Phe	Gln	Thr						1570					1575						1580								Met	Pro	Gly	Ile	Phe	Gln	Thr	Thr	Thr	Gly	Glu	Ile	Gly	Ala	Ile	Ala					1585					1590					1595					1600					Leu	Asp	Phe	Lys	Pro	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Ile	Asn	Arg	Glu									1605					1610						1615					Gly	Lys	Val	Val	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val	Thr	Lys	Asn	Gly							1620						1625						1630						Gly	Tyr	Val	Ser	Gly	Ile	Ala	Gln	Thr	Asn	Ala	Glu	Pro	Asp	Gly	Pro							1635					1640						1645							Thr	Pro	Glu	Leu	Glu	Glu	Glu	Met	Phe	Lys	Lys	Arg	Asn	Leu	Thr	Ile							1650				1655						1660								Met	Asp	Leu	His	Pro	Gly	Ser	Gly	Lys	Thr	Arg	Lys	Tyr	Leu	Pro	Ala					1665					1670					1675					1680					Ile	Val	Arg	Glu	Ala	Ile	Lys	Arg	Arg	Leu	Arg	Thr	Leu	Ile	Leu	Ala									1685					1690						1695					Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Met	Lys	Gly	Leu								1700					1705						1710						Pro	Ile	Arg	Tyr	Gln	Thr	Thr	Ala	Thr	Lys	Ser	Glu	His	Thr	Gly	Arg							1715					1720						1725							Glu	Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Met	Arg	Leu	Leu							1730				1735						1740								Ser	Pro	Val	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Ile	Ile	Met	Asp	Glu	Ala					1745					1750					1755					1760					His	Phe	Thr	Asp	Pro	Ala	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr									1765					1770					1775						Arg	Val	Gly	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr	Pro								1780					1785						1790						Pro	Gly	Thr	Ala	Asp	Ala	Phe	Pro	Gln	Ser	Asn	Ala	Pro	Ile	Gln	Asp							1795					1800						1805							Glu	Glu	Arg	Asp	Ile	Pro	Glu	Arg	Ser	Trp	Asn	Ser	Gly	Asn	Glu	Trp							1810				1815						1820								Ile	Thr	Asp	Phe	Val	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Ile	Lys					1825					1830					1835					1840					Ala	Gly	Asn	Val	Ile	Ala	Asn	Cys	Leu	Arg	Lys	Asn	Gly	Lys	Lys	Val								1845						1850					1855						Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Asp	Thr	Glu	Tyr	Gln	Lys	Thr	Lys							1860						1865						1870																																																																	
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Leu Asn Asp Trp Asp Phe Val Val Thr Thr Asp Ile Ser Glu Met Gly
 1875 1880 1885

Ala Asn Phe Ile Ala Asp Arg Val Ile Asp Pro Arg Arg Cys Leu Lys
 1890 1895 1900

Pro Val Ile Leu Thr Asp Gly Pro Glu Arg Val Ile Leu Ala Gly Pro
 1905 1910 1915 1920

Met Pro Val Thr Val Ala Ser Ala Ala Gln Arg Arg Gly Arg Val Gly
 1925 1930 1935

Arg Asn Pro Gln Lys Glu Asn Asp Gln Tyr Ile Phe Met Gly Gln Pro
 1940 1945 1950

Leu Asn Lys Asp Glu Asp His Ala His Trp Thr Glu Ala Lys Met Leu
 1955 1960 1965

Leu Asp Asn Ile Asn Thr Pro Glu Gly Ile Ile Pro Ala Leu Phe Glu
 1970 1975 1980

Pro Glu Arg Glu Lys Ser Ala Ala Ile Asp Gly Glu Tyr Arg Leu Lys
 1985 1990 1995 2000

Gly Glu Ser Arg Lys Thr Phe Val Glu Leu Met Arg Arg Gly Asp Leu
 2005 2010 2015

Pro Val Trp Leu Ala His Lys Val Ala Ser Glu Gly Ile Lys Tyr Thr
 2020 2025 2030

Asp Arg Lys Trp Cys Phe Asp Gly Glu Arg Asn Asn Gln Ile Leu Glu
 2035 2040 2045

Glu Asn Met Asp Val Glu Ile Trp Thr Lys Glu Gly Glu Lys Lys Lys
 2050 2055 2060

Leu Arg Pro Arg Trp Leu Asp Ala Arg Thr Tyr Ser Asp Pro Leu Ala
 2065 2070 2075 2080

Leu Lys Glu Phe Lys Asp Phe Ala Ala Gly Arg Lys Ser Ile Ala Leu
 2085 2090 2095

Asp Leu Val Thr Glu Ile Gly Arg Val Pro Ser His Leu Ala His Arg
 2100 2105 2110

Thr Arg Asn Ala Leu Asp Asn Leu Val Met Leu His Thr Ser Glu His
 2115 2120 2125

Gly Gly Arg Ala Tyr Arg His Ala Val Glu Glu Leu Pro Glu Thr Met
 2130 2135 2140

Glu Thr Leu Leu Leu Leu Gly Leu Met Ile Leu Leu Thr Gly Gly Ala
 2145 2150 2155 2160

Met Leu Phe Leu Ile Ser Gly Lys Gly Ile Gly Lys Thr Ser Ile Gly
 2165 2170 2175

Leu Ile Cys Val Ile Ala Ser Ser Gly Met Leu Trp Met Ala Asp Val
 2180 2185 2190

Pro Leu Gln Trp Ile Ala Ser Ala Ile Val Leu Glu Phe Phe Met Met
 2195 2200 2205

Val Leu Leu Ile Pro Glu Pro Glu Lys Gln Arg Thr Pro Gln Asp Asn
 2210 2215 2220

Gln Leu Ala Tyr Val Val Ile Gly Ile Leu Thr Leu Ala Ala Ile Val
 2225 2230 2235 2240

Ala Ala Asn Glu Met Gly Leu Leu Glu Thr Thr Lys Arg Asp Leu Gly
 2245 2250 2255

Met Ser Lys Glu Pro Gly Val Val Ser Pro Thr Ser Tyr Leu Asp Val
 2260 2265 2270

Asp Leu His Pro Ala Ser Ala Trp Thr Leu Tyr Ala Val Ala Thr Thr
 2275 2280 2285

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Val	Ile	Thr	Pro	Met	Leu	Arg	His	Thr	Ile	Glu	Asn	Ser	Thr	Ala	Asn	2290	2295	2300	
Val	Ser	Leu	Ala	Ala	Ile	Ala	Asn	Gln	Ala	Val	Val	Leu	Met	Gly	Leu	2305	2310	2315	2320
Asp	Lys	Gly	Trp	Pro	Ile	Ser	Lys	Met	Asp	Leu	Gly	Val	Pro	Leu	Leu	2325	2330	2335	
Ala	Leu	Gly	Cys	Tyr	Ser	Gln	Val	Asn	Pro	Leu	Thr	Leu	Ile	Ala	Ala	2340	2345	2350	
Val	Leu	Leu	Leu	Val	Thr	His	Tyr	Ala	Ile	Ile	Gly	Pro	Gly	Leu	Gln	2355	2360	2365	
Ala	Lys	Ala	Thr	Arg	Glu	Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	2370	2375	2380	
Lys	Asn	Pro	Thr	Val	Asp	Gly	Ile	Met	Thr	Ile	Asp	Leu	Asp	Pro	Val	2385	2390	2395	2400
Ile	Tyr	Asp	Ser	Lys	Phe	Glu	Lys	Gln	Leu	Gly	Gln	Val	Met	Leu	Leu	2405	2410	2415	
Val	Leu	Cys	Ala	Val	Gln	Leu	Leu	Leu	Met	Arg	Thr	Ser	Trp	Ala	Leu	2420	2425	2430	
Cys	Glu	Val	Leu	Thr	Leu	Ala	Thr	Gly	Pro	Ile	Thr	Thr	Leu	Trp	Glu	2435	2440	2445	
Gly	Ser	Pro	Gly	Lys	Phe	Trp	Asn	Thr	Thr	Ile	Ala	Val	Ser	Met	Ala	2450	2455	2460	
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Gly	Leu	Ala	Leu	Ser	2465	2470	2475	2480
Ile	Met	Lys	Ser	Val	Gly	Thr	Gly	Lys	Arg	Gly	Thr	Gly	Ser	Gln	Gly	2485	2490	2495	
Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Lys	Lys	Leu	Asn	Gln	Leu	Ser	Arg	2500	2505	2510	
Lys	Glu	Phe	Asp	Leu	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	Glu	Val	Asp	Arg	2515	2520	2525	
Thr	Glu	Ala	Lys	Glu	Gly	Leu	Lys	Arg	Gly	Glu	Ile	Thr	His	His	Ala	2530	2535	2540	
Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Gln	Trp	Phe	Val	Glu	Arg	Asn	Met	2545	2550	2555	2560
Val	Ile	Pro	Glu	Gly	Arg	Val	Ile	Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	2565	2570	2575	
Trp	Ser	Tyr	Tyr	Cys	Ala	Gly	Leu	Lys	Lys	Val	Thr	Glu	Val	Arg	Gly	2580	2585	2590	
Tyr	Thr	Lys	Gly	Gly	Pro	Gly	His	Glu	Glu	Pro	Val	Pro	Met	Ser	Thr	2595	2600	2605	
Tyr	Gly	Trp	Asn	Ile	Val	Lys	Leu	Met	Ser	Gly	Lys	Asp	Val	Phe	Tyr	2610	2615	2620	
Leu	Pro	Pro	Glu	Lys	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	2625	2630	2635	2640
Ser	Pro	Ser	Pro	Thr	Val	Glu	Glu	Ser	Arg	Thr	Ile	Arg	Val	Leu	Lys	2645	2650	2655	
Met	Val	Glu	Pro	Trp	Leu	Lys	Asn	Asn	Gln	Phe	Cys	Ile	Lys	Val	Leu	2660	2665	2670	
Asn	Pro	Tyr	Met	Pro	Thr	Val	Ile	Glu	His	Leu	Glu	Arg	Leu	Gln	Arg	2675	2680	2685	
Lys	His	Gly	Gly	Met	Leu	Val	Arg	Asn	Pro	Leu	Ser	Arg	Asn	Ser	Thr	2690	2695	2700	
His	Glu	Met	Tyr	Trp	Ile	Ser	Asn	Gly	Thr	Gly	Asn	Ile	Val	Ser	Ser				

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2705	2710	2715	2720
Val Asn Met	Val Ser Arg Leu Leu Leu	Asn Arg Phe Thr Met	Thr His
	2725	2730	2735
Arg Arg Pro	Thr Ile Glu Lys Asp	Val Asp Leu Gly Ala Gly	Thr Arg
	2740	2745	2750
His Val Asn Ala	Glu Pro Glu Thr Pro	Asn Met Asp	Val Ile Gly Glu
	2755	2760	2765
Arg Ile Lys Arg	Ile Lys Glu Glu His	Ser Ser Thr Trp	His Tyr Asp
	2770	2775	2780
Asp Glu Asn Pro	Tyr Lys Thr Trp Ala Tyr	His Gly Ser Tyr	Glu Val
	2785	2790	2795
Lys Ala Thr Gly	Ser Ala Ser Ser Met	Ile Asn Gly Val	Val Lys Leu
	2805	2810	2815
Leu Thr Lys Pro	Trp Asp Val Val Pro	Met Val Thr Gln	Met Ala Met
	2820	2825	2830
Thr Asp Thr Thr	Pro Phe Gly Gln Gln	Arg Val Phe Lys	Glu Lys Val
	2835	2840	2845
Asp Thr Arg Thr	Pro Arg Pro Met Pro	Gly Thr Arg Lys	Val Met Glu
	2850	2855	2860
Ile Thr Ala Glu	Trp Leu Trp Arg Thr	Leu Gly Arg Asn	Lys Arg Pro
	2865	2870	2875
Arg Leu Cys Thr	Arg Glu Glu Phe Thr	Lys Lys Val Arg	Thr Asn Ala
	2885	2890	2895
Ala Met Gly Ala	Val Phe Thr Glu Glu	Asn Gln Trp Asp	Ser Ala Arg
	2900	2905	2910
Ala Ala Val Glu	Asp Glu Glu Phe Trp	Lys Leu Val Asp	Arg Glu Arg
	2915	2920	2925
Glu Leu His Lys	Leu Gly Lys Cys Gly	Ser Cys Val Tyr	Asn Met Met
	2930	2935	2940
Gly Lys Arg Glu	Lys Lys Leu Gly Glu	Phe Gly Lys Ala	Lys Gly Ser
	2945	2950	2955
Arg Ala Ile Trp	Tyr Met Trp Leu Gly	Ala Arg Tyr Leu	Glu Phe Glu
	2965	2970	2975
Ala Leu Gly Phe	Leu Asn Glu Asp His	Trp Phe Ser Arg	Glu Asn Ser
	2980	2985	2990
Tyr Ser Gly Val	Glu Gly Glu Gly Leu	His Lys Leu Gly	Tyr Ile Leu
	2995	3000	3005
Arg Asp Ile Ser	Lys Ile Pro Gly Gly	Ala Met Tyr Ala	Asp Asp Thr
	3010	3015	3020
Ala Gly Trp Asp	Thr Arg Ile Thr Glu	Asp Asp Leu His	Asn Glu Glu
	3025	3030	3035
Lys Ile Thr Gln	Gln Met Asp Pro Glu	His Arg Gln Leu	Ala Asn Ala
	3045	3050	3055
Ile Phe Lys Leu	Thr Tyr Gln Asn Lys	Val Val Lys Val	Gln Arg Pro
	3060	3065	3070
Thr Pro Lys Gly	Thr Val Met Asp Ile	Ile Ser Arg Lys	Asp Gln Arg
	3075	3080	3085
Gly Ser Gly Gln	Val Gly Thr Tyr Gly	Leu Asn Thr Phe	Thr Asn Met
	3090	3095	3100
Glu Ala Gln Leu	Ile Arg Gln Met Glu	Gly Glu Gly Val	Leu Ser Lys
	3105	3110	3115
Ala Asp Leu Glu	Asn Pro His Pro Leu	Glu Lys Lys Ile	Thr Gln Trp
	3125	3130	3135

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Leu Glu Thr Lys Gly Val Glu Arg Leu Lys Arg Met Ala Ile Ser Gly
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 Asp Asp Cys Val Val Lys Pro Ile Asp Asp Arg Phe Ala Asn Ala Leu
 3155 3160 3165
 Leu Ala Leu Asn Asp Met Gly Lys Val Arg Lys Asp Ile Pro Gln Trp
 3170 3175 3180
 Gln Pro Ser Lys Gly Trp His Asp Trp Gln Gln Val Pro Phe Cys Ser
 3185 3190 3195 3200
 His His Phe His Glu Leu Ile Met Lys Asp Gly Arg Lys Leu Val Val
 3205 3210 3215
 Pro Cys Arg Pro Gln Asp Glu Leu Ile Gly Arg Ala Arg Ile Ser Gln
 3220 3225 3230
 Gly Ala Gly Trp Ser Leu Arg Glu Thr Ala Cys Leu Gly Lys Ala Tyr
 3235 3240 3245
 Ala Gln Met Trp Thr Leu Met Tyr Phe His Arg Arg Asp Leu Arg Leu
 3250 3255 3260
 Ala Ser Asn Ala Ile Cys Ser Ala Val Pro Val His Trp Val Pro Thr
 3265 3270 3275 3280
 Ser Arg Thr Thr Trp Ser Ile His Ala His His Gln Trp Met Thr Thr
 3285 3290 3295
 Glu Asp Met Leu Thr Val Trp Asn Arg Val Trp Ile Glu Asp Asn Pro
 3300 3305 3310
 Trp Met Glu Asp Lys Thr Pro Val Thr Thr Trp Glu Asp Val Pro Tyr
 3315 3320 3325
 Leu Gly Lys Arg Glu Asp Gln Trp Cys Gly Ser Leu Ile Gly Leu Thr
 3330 3335 3340
 Ser Arg Ala Thr Trp Ala Gln Asn Ile Leu Thr Ala Ile Gln Gln Val
 3345 3350 3355 3360
 Arg Ser Leu Ile Gly Asn Glu Glu Phe Leu Asp Tyr Met Pro Ser Met
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 3380 3385 3390

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<210> SEQ ID NO 24
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 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 24

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 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

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<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 25

gattgtgacc atggcggccc atctttg 27

<210> SEQ ID NO 26
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 26

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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 27

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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 28

ctaggaaaca cataatatta gttgtgg 27

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cagatccacc taaccataat ggcagtg 27

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ggaaactcac ctcgaggag acagc 25

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 31

ttgggtagag gtcaccgcac tcatcc 26

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<210> SEQ ID NO 32
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 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 32

 gtagaaatag ccgctctcat cctag 25

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 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 33

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<210> SEQ ID NO 34
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 <400> SEQUENCE: 34

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 <220> FEATURE:
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<210> SEQ ID NO 37
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 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 37

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<210> SEQ ID NO 38
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 <212> TYPE: DNA
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 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

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<400> SEQUENCE: 38
gaaattggat cggtaacctt agatttc 27

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<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 39
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<210> SEQ ID NO 40
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 40
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<210> SEQ ID NO 41
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<400> SEQUENCE: 41
gattaactat catgaactta caccc 25

<210> SEQ ID NO 42
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 42
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<210> SEQ ID NO 43
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 43
tccagtgata ccggctagcg ctgctc 26

<210> SEQ ID NO 44
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 44
gcctcagagg tggccaaagg aag 23

<210> SEQ ID NO 45
<211> LENGTH: 26

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<212> TYPE: DNA
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 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 45

 acatggaggc agagatctgg actaga 26

 <210> SEQ ID NO 46
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 <212> TYPE: DNA
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 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 46

 aaagcatggc caaggatgct gtc 23

 <210> SEQ ID NO 47
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 <212> TYPE: DNA
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 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 47

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 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 48

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 <210> SEQ ID NO 49
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 49

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 <210> SEQ ID NO 50
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 50

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 <212> TYPE: DNA
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 <400> SEQUENCE: 51

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ctcataaaga acgttcaaac cct 23

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<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 52

cattagacag acgcgagttt gaag 24

<210> SEQ ID NO 53
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<223> OTHER INFORMATION: Oligonucleotide

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tggcgacgct caagatagtg actgaag 27

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<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 54

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<400> SEQUENCE: 55

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<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 56

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<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 57

ggaaagaaga aacacccgag actgtgc 27

<210> SEQ ID NO 58
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<212> TYPE: DNA
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<220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 58

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 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 59

 ccagtggatt actacagaag atatgctc 28

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 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 60

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 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 61

 ctgtaattac caacatcaaa caccaaag 28

 <210> SEQ ID NO 62
 <211> LENGTH: 26
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 62

 ccaacaacaa ccaccaagg ctattg 26

 <210> SEQ ID NO 63
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide

 <400> SEQUENCE: 63

 ggattggtgt tgtcgatcca acagg 25

 <210> SEQ ID NO 64
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Primer

 <400> SEQUENCE: 64

 ctggtggaag cccaacacaa aaac 24

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<210> SEQ ID NO 65
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 65

ctggtggaag gaagagagaa attggcaact cccaacaca aaaac 45

<210> SEQ ID NO 66
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 66

agaccccccc aagcatattg ac 22

<210> SEQ ID NO 67
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 67

agaccccccc aatatttcct cctcctatag catattgac 39

<210> SEQ ID NO 68
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 68

cccaacacaa agcatattga c 21

<210> SEQ ID NO 69
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<212> TYPE: DNA
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<222> LOCATION: (1)...(6)
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 69

gcagcn 6

<210> SEQ ID NO 70
<211> LENGTH: 5
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide

<400> SEQUENCE: 70

gcagc 5

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What is claimed is:

1. An immunogenic composition comprising an attenuated dengue virus or attenuated chimeric dengue virus comprising (a) a nucleic acid encoding a structural protein from dengue serotype 1, dengue serotype 2, dengue serotype 3, or dengue serotype 4; and (b) a nucleic acid comprising remaining coding and non-coding regions of a dengue serotype 4 virus (DEN4 backbone), wherein the DEN4 backbone comprises a 30 nucleotide deletion in the 3' untranslated region corresponding to nucleotides 172-143 (DEN4Δ30 backbone), wherein the numbering is based upon a prototypic DEN4
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2. The composition of claim 1, wherein the nucleic acid encoding the structural protein is from the dengue serotype 4 virus (DEN4Δ30).

3. The composition of claim 2, further comprising a first attenuated chimeric virus having a nucleic acid encoding a structural protein from dengue serotype 1 virus and a DEN4Δ30 backbone (DEN1/4Δ30).

4. The composition of claim 3, further comprising a second attenuated chimeric virus comprising a nucleic acid encoding a structural protein from dengue serotype 2 virus and a DEN4Δ30 backbone (DEN2/4Δ30).

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5. The composition of claim 4, further comprising a third attenuated chimeric virus comprising a nucleic acid encoding a structural protein from dengue serotype 3 virus and a DEN4Δ30 backbone (DEN3/4Δ30).

6. The composition of claim 5, wherein a nucleic acid encoding the NS3 protein of at least one of DEN4Δ30, the first attenuated chimeric virus, the second attenuated chimeric virus, and the third attenuated chimeric virus comprises a mutation at nucleotide position 4995 from T to C.

7. The composition of claim 1, wherein the nucleic acid encoding the structural protein is from the dengue serotype 1 virus.

8. The composition of claim 1, wherein the nucleic acid encoding the structural protein is from the dengue serotype 2 virus.

9. The composition of claim 1, wherein the nucleic acid encoding the structural protein is from the dengue serotype 3 virus.

10. The composition of claim 1, wherein the mutation in the DEN4 backbone is a mutation at nucleotide position 4995 from T to C.

* * * * *