SEQUENCE LISTING

<110> VLP THERAPEUTICS, LLP

<120> FLAVIVIRUS VIRUS LIKE PARTICLE

<130> 6725231

<150> 62/048,897
<151> 2014-09-11

<160> 24

<170> PatentIn version 3.5

<210> 1
<211> 5498
<212> DNA
<213> Dengue virus

<220>
<221> misc_feature
<223> DENV1 prM E (Env F108A)

<220>
<221> CDS
<222> (1046)..(3073)

<400> 1
tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60

cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120

ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180

accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240

attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat 300

tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360

tttcccagtc acgacgttgt aaaacgacgg ccagtgaatt gacgcgtttg acattgatta 420

ttgactagtt attaatagta atcaattacg gggtcattag ttcatagccc atatatggag 480

ttccgcgtta cataacttac ggtaaatggc ccgcctggct gaccgcccaa cgacccccgc 540

ccattgacgt caataatgac gtatgttccc atagtaacgc caatagggac tttccattga 600

cgtcaatggg tggagtattt acggtaaact gcccacttgg cagtacatca agtgtatcat 660

atgccaagta cgcccccctat tgacgtcaat gacggtaaat ggcccgcctg gcattatgcc 720

cagtacatga ccttatggga ctttcctact tggcagtaca tctacgtatt agtcatcgct 780

attaccatgg tgatgcggtt ttggcagtac atcaatgggc gtggatagcg gtttgactca 840

cggggatttc caagtctcca ccccattgac gtcaatggga gtttgttttg gcaccaaaat 900

caacgggact ttccaaaatg tcgtaacaac tccgccccat tgacgcaaat gggcggtagg 960

cgtgtacggt gggaggtcta tataagcaga gctcgtttag tgaaccgtca gataactgca 1020

ggtcgacgat atcgcggccg ccacc atg tcg gtg acc atg ctc ctc atg ctg 1072
Met Ser Val Thr Met Leu Leu Met Leu
1 5

```
ctg ccc aca gcc ctg gcg ttc cat ctg acc acc cga ggg gga gag ccg        1120
Leu Pro Thr Ala Leu Ala Phe His Leu Thr Thr Arg Gly Gly Glu Pro
10                  15                  20                  25

cac atg ata gtt agc aag cag gaa aga gga aaa tca ctt ttg ttt aag        1168
His Met Ile Val Ser Lys Gln Glu Arg Gly Lys Ser Leu Leu Phe Lys
                30                  35                  40

acc tct gca ggt gtc aac atg tgc acc ctt att gca atg gat ttg gga        1216
Thr Ser Ala Gly Val Asn Met Cys Thr Leu Ile Ala Met Asp Leu Gly
            45                  50                  55

gag tta tgt gag gac aca atg acc tac aaa tgc ccc cgg atc act gag        1264
Glu Leu Cys Glu Asp Thr Met Thr Tyr Lys Cys Pro Arg Ile Thr Glu
        60                  65                  70

acg gaa cca gat gac gtt gac tgt tgg tgc aat gcc acg gag aca tgg        1312
Thr Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Ala Thr Glu Thr Trp
    75                  80                  85

gtg acc tat gga aca tgt tct caa act ggt gaa cac cga cga gac aaa        1360
Val Thr Tyr Gly Thr Cys Ser Gln Thr Gly Glu His Arg Arg Asp Lys
90                  95                  100                 105

cgt tcc gtc gca ctg gca cca cac gta ggg ctt ggt cta gaa aca aga        1408
Arg Ser Val Ala Leu Ala Pro His Val Gly Leu Gly Leu Glu Thr Arg
                110                 115                 120

acc gaa acg tgg atg tcc tct gaa ggc gct tgg aaa caa ata caa aaa        1456
Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys Gln Ile Gln Lys
            125                 130                 135

gtg gag acc tgg gct ctg aga cac cca gga ttc acg gtg ata gcc ctt        1504
Val Glu Thr Trp Ala Leu Arg His Pro Gly Phe Thr Val Ile Ala Leu
        140                 145                 150

ttt cta gca cat gcc ata gga aca tcc atc acc cag aaa ggg atc att        1552
Phe Leu Ala His Ala Ile Gly Thr Ser Ile Thr Gln Lys Gly Ile Ile
    155                 160                 165

ttt att ttg ctg atg ctg gta act cca tcc atg gcc atg cgg tgc gtg        1600
Phe Ile Leu Leu Met Leu Val Thr Pro Ser Met Ala Met Arg Cys Val
170                 175                 180                 185

gga ata ggc aac aga gac ttc gtg gaa gga ctg tca gga gct acg tgg        1648
Gly Ile Gly Asn Arg Asp Phe Val Glu Gly Leu Ser Gly Ala Thr Trp
                190                 195                 200

gtg gat gtg gta ctg gag cat gga agt tgc gtc act acc atg gca aaa        1696
Val Asp Val Val Leu Glu His Gly Ser Cys Val Thr Thr Met Ala Lys
            205                 210                 215

gac aaa cca aca ctg gac att gaa ctc ttg aag acg gag gtc aca aac        1744
Asp Lys Pro Thr Leu Asp Ile Glu Leu Leu Lys Thr Glu Val Thr Asn
        220                 225                 230

cct gcc gtc ctg cgc aaa ctg tgc att gaa gct aaa ata tca aac acc        1792
Pro Ala Val Leu Arg Lys Leu Cys Ile Glu Ala Lys Ile Ser Asn Thr
    235                 240                 245

acc acc gat tcg aga tgt cca aca caa gga gaa gcc acg ctg gtg gaa        1840
Thr Thr Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Thr Leu Val Glu
250                 255                 260                 265

gaa cag gac acg aac ttt gtg tgt cga cga acg ttc gtg gac aga ggc        1888
Glu Gln Asp Thr Asn Phe Val Cys Arg Arg Thr Phe Val Asp Arg Gly
                270                 275                 280
```

```
tgg ggc aat ggt tgt ggg cta gcc gga aaa ggt agc tta ata acg tgt        1936
Trp Gly Asn Gly Cys Gly Leu Ala Gly Lys Gly Ser Leu Ile Thr Cys
            285                 290                 295

gct aag ttt aag tgt gtg aca aaa ctg gaa gga aag ata gtc caa tat        1984
Ala Lys Phe Lys Cys Val Thr Lys Leu Glu Gly Lys Ile Val Gln Tyr
        300                 305                 310

gaa aac tta aaa tat tca gtg ata gtc acc gta cac act gga gac cag        2032
Glu Asn Leu Lys Tyr Ser Val Ile Val Thr Val His Thr Gly Asp Gln
    315                 320                 325

cac caa gtt gga aat gag acc aca gaa cat gga aca act gca acc ata        2080
His Gln Val Gly Asn Glu Thr Thr Glu His Gly Thr Thr Ala Thr Ile
330                 335                 340                 345

aca cct caa gct ccc acg tcg gaa ata cag ctg aca gac tac gga gct        2128
Thr Pro Gln Ala Pro Thr Ser Glu Ile Gln Leu Thr Asp Tyr Gly Ala
                350                 355                 360

cta aca ttg gat tgt tca cct aga aca ggg cta gac ttt aat gag atg        2176
Leu Thr Leu Asp Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn Glu Met
            365                 370                 375

gtg ttg ttg aca atg gaa aaa aaa tca tgg ctc gtc cac aaa caa tgg        2224
Val Leu Leu Thr Met Glu Lys Lys Ser Trp Leu Val His Lys Gln Trp
        380                 385                 390

ttt cta gac tta cca ctg cct tgg acc tcg ggg gct tca aca tcc caa        2272
Phe Leu Asp Leu Pro Leu Pro Trp Thr Ser Gly Ala Ser Thr Ser Gln
    395                 400                 405

gag act tgg aat aga caa gac ttg ctg gtc aca ttt aag aca gct cat        2320
Glu Thr Trp Asn Arg Gln Asp Leu Leu Val Thr Phe Lys Thr Ala His
410                 415                 420                 425

gca aaa aag cag gaa gta gtc gta cta gga tca caa gaa gga gca atg        2368
Ala Lys Lys Gln Glu Val Val Val Leu Gly Ser Gln Glu Gly Ala Met
                430                 435                 440

cac act gcg ttg act gga gcg aca gaa atc caa acg tct gga acg aca        2416
His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Thr Ser Gly Thr Thr
            445                 450                 455

aca att ttt gca gga cac ctg aaa tgc aga cta aaa atg gat aaa ctg        2464
Thr Ile Phe Ala Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu
        460                 465                 470

act tta aaa ggg atg tca tat gta atg tgc aca ggg tca ttc aag tta        2512
Thr Leu Lys Gly Met Ser Tyr Val Met Cys Thr Gly Ser Phe Lys Leu
    475                 480                 485

gag aag gaa gtg gct gag acc cag cat gga act gtt cta gtg cag gtt        2560
Glu Lys Glu Val Ala Glu Thr Gln His Gly Thr Val Leu Val Gln Val
490                 495                 500                 505

aaa tac gaa gga aca gat gca cca tgc aag atc ccc ttc tcg tcc caa        2608
Lys Tyr Glu Gly Thr Asp Ala Pro Cys Lys Ile Pro Phe Ser Ser Gln
                510                 515                 520

gat gag aag gga gta acc cag aat ggg aga ttg ata aca gcc aac ccc        2656
Asp Glu Lys Gly Val Thr Gln Asn Gly Arg Leu Ile Thr Ala Asn Pro
            525                 530                 535

ata gtc act gac aaa gaa aaa cca gtc aac att gaa gcg gag cca cct        2704
Ile Val Thr Asp Lys Glu Lys Pro Val Asn Ile Glu Ala Glu Pro Pro
        540                 545                 550
```

```
ttt ggt gag agc tac att gtg gta gga gca ggt gaa aaa gct ttg aaa       2752
Phe Gly Glu Ser Tyr Ile Val Val Gly Ala Gly Glu Lys Ala Leu Lys
    555                 560                 565

cta agc tgg ttc aag aag gga agc agt ata ggg aaa atg ttt gaa gca       2800
Leu Ser Trp Phe Lys Lys Gly Ser Ser Ile Gly Lys Met Phe Glu Ala
570                 575                 580                 585

act gcc cgt gga gca cga agg atg gcc atc ctg gga gac act gca tgg       2848
Thr Ala Arg Gly Ala Arg Arg Met Ala Ile Leu Gly Asp Thr Ala Trp
                590                 595                 600

gac ttc ggt tct ata gga ggg gtg ttc acg tct gtg gga aaa ctg ata       2896
Asp Phe Gly Ser Ile Gly Gly Val Phe Thr Ser Val Gly Lys Leu Ile
            605                 610                 615

cac cag att ttt ggg act gcg tat gga gtt ttg ttc agc ggt gtt tct       2944
His Gln Ile Phe Gly Thr Ala Tyr Gly Val Leu Phe Ser Gly Val Ser
        620                 625                 630

tgg acc atg aag ata gga ata ggg att ctg ctg aca tgg cta gga tta       2992
Trp Thr Met Lys Ile Gly Ile Gly Ile Leu Leu Thr Trp Leu Gly Leu
    635                 640                 645

aac tca agg agc acg tcc ctt tca atg acg tgt atc gca gtt ggc atg       3040
Asn Ser Arg Ser Thr Ser Leu Ser Met Thr Cys Ile Ala Val Gly Met
650                 655                 660                 665

gtc acg ctg tac cta gga gtc atg gtt cag gcg taataaagat ctgctgtgcc     3093
Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
                670                 675

ttctagttgc cagccatctg ttgtttgccc ctcccccgtg ccttccttga ccctggaagg     3153

tgccactccc actgtccttt cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag     3213

gtgtcattct attctggggg gtggggtggg gcaggacagc aaggggggagg attgggaaga     3273

caatagcagg catgctgggg atgcggtggg ctctatggct cgagcatggt catagctgtt     3333

tcctgtgtga aattgttatc cgctcacaat tccacacaac atacgagccg gaagcataaa     3393

gtgtaaagcc tggggtgcct aatgagtgag ctaactcaca ttaattgcgt tgcgctcact     3453

gcccgctttc cagtcgggaa acctgtcgtg ccagctgcat taatgaatcg gccaacgcgc     3513

ggggagaggc ggtttgcgta ttgggcgctc ttccgcttcc tcgctcactg actcgctgcg     3573

ctcggtcgtt cggctgcggc gagcggtatc agctcactca aaggcggtaa tacggttatc     3633

cacagaatca ggggataacg caggaaagaa catgtgagca aaaggccagc aaaaggccag     3693

gaaccgtaaa aaggccgcgt tgctggcgtt tttccatagg ctccgccccc ctgacgagca     3753

tcacaaaaat cgacgctcaa gtcagaggtg gcgaaacccg acaggactat aaagatacca     3813

ggcgtttccc cctggaagct ccctcgtgcg ctctcctgtt ccgaccctgc cgcttaccgg     3873

atacctgtcc gcctttctcc cttcgggaag cgtggcgctt tctcatagct cacgctgtag     3933

gtatctcagt tcggtgtagg tcgttcgctc caagctgggc tgtgtgcacg aacccccgt      3993

tcagcccgac cgctgcgcct tatccggtaa ctatcgtctt gagtccaacc cggtaagaca     4053

cgacttatcg ccactggcag cagccactgg taacaggatt agcagagcga ggtatgtagg     4113

cggtgctaca gagttcttga agtggtggcc taactacggc tacactagaa gaacagtatt     4173
```

tggtatctgc gctctgctga agccagttac cttcggaaaa agagttggta gctcttgatc 4233

cggcaaacaa accaccgctg gtagcggtgg ttttttttgtt tgcaagcagc agattacgcg 4293

cagaaaaaaa ggatctcaag aagatccttt gatcttttct acggggtctg acgctcagtg 4353

gaacgaaaac tcacgttaag ggattttggt catgagatta tcaaaaagga tcttcaccta 4413

gatcctttta aattaaaaat gaagttttaa atcaatctaa agtatatatg agtaaacttg 4473

gtctgacagt tagaaaaact catcgagcat caaatgaaac tgcaatttat tcatatcagg 4533

attatcaata ccatattttt gaaaaagccg tttctgtaat gaaggagaaa actcaccgag 4593

gcagttccat aggatggcaa gatcctggta tcggtctgcg attccgactc gtccaacatc 4653

aatacaacct attaatttcc cctcgtcaaa aataaggtta tcaagtgaga aatcaccatg 4713

agtgacgact gaatccggtg agaatggcaa aagtttatgc atttctttcc agacttgttc 4773

aacaggccag ccattacgct cgtcatcaaa atcactcgca tcaaccaaac cgttattcat 4833

tcgtgattgc gcctgagcga gacgaaatac gcgatcgctg ttaaaaggac aattacaaac 4893

aggaatcgaa tgcaaccggc gcaggaacac tgccagcgca tcaacaatat tttcacctga 4953

atcaggatat tcttctaata cctggaatgc tgttttccca gggatcgcag tggtgagtaa 5013

ccatgcatca tcaggagtac ggataaaatg cttgatggtc ggaagaggca taaattccgt 5073

cagccagttt agtctgacca tctcatctgt aacatcattg gcaacgctac ctttgccatg 5133

tttcagaaac aactctggcg catcgggctt cccatacaat cgatagattg tcgcacctga 5193

ttgcccgaca ttatcgcgag cccatttata cccatataaa tcagcatcca tgttggaatt 5253

taatcgcggc ctagagcaag acgtttcccg ttgaatatgg ctcatactct tccttttca 5313

atattattga agcatttatc agggttattg tctcatgagc ggatacatat ttgaatgtat 5373

ttagaaaaat aaacaaatag gggttccgcg cacatttccc cgaaaagtgc cacctgacgt 5433

ctaagaaacc attattatca tgacattaac ctataaaaat aggcgtatca cgaggccctt 5493

tcgtc 5498

<210> 2
<211> 676
<212> PRT
<213> Dengue virus

<400> 2

Met Ser Val Thr Met Leu Leu Met Leu Leu Pro Thr Ala Leu Ala Phe
1 5 10 15

His Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val Ser Lys Gln
20 25 30

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

Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Met
50 55 60

```
Thr Tyr Lys Cys Pro Arg Ile Thr Glu Thr Glu Pro Asp Asp Val Asp
65                  70                  75                  80

Cys Trp Cys Asn Ala Thr Glu Thr Trp Val Thr Tyr Gly Thr Cys Ser
                85                  90                  95

Gln Thr Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala Pro
            100                 105                 110

His Val Gly Leu Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser
        115                 120                 125

Glu Gly Ala Trp Lys Gln Ile Gln Lys Val Glu Thr Trp Ala Leu Arg
    130                 135                 140

His Pro Gly Phe Thr Val Ile Ala Leu Phe Leu Ala His Ala Ile Gly
145                 150                 155                 160

Thr Ser Ile Thr Gln Lys Gly Ile Ile Phe Ile Leu Leu Met Leu Val
                165                 170                 175

Thr Pro Ser Met Ala Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe
            180                 185                 190

Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu His
        195                 200                 205

Gly Ser Cys Val Thr Thr Met Ala Lys Asp Lys Pro Thr Leu Asp Ile
    210                 215                 220

Glu Leu Leu Lys Thr Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu
225                 230                 235                 240

Cys Ile Glu Ala Lys Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro
                245                 250                 255

Thr Gln Gly Glu Ala Thr Leu Val Glu Glu Gln Asp Thr Asn Phe Val
            260                 265                 270

Cys Arg Arg Thr Phe Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
        275                 280                 285

Ala Gly Lys Gly Ser Leu Ile Thr Cys Ala Lys Phe Lys Cys Val Thr
    290                 295                 300

Lys Leu Glu Gly Lys Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser Val
305                 310                 315                 320

Ile Val Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr
                325                 330                 335
```

```
Thr Glu His Gly Thr Thr Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser
            340                 345                 350

Glu Ile Gln Leu Thr Asp Tyr Gly Ala Leu Thr Leu Asp Cys Ser Pro
        355                 360                 365

Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Thr Met Glu Lys
    370                 375                 380

Lys Ser Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro
385                 390                 395                 400

Trp Thr Ser Gly Ala Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln Asp
                405                 410                 415

Leu Leu Val Thr Phe Lys Thr Ala His Ala Lys Lys Gln Glu Val Val
            420                 425                 430

Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala
        435                 440                 445

Thr Glu Ile Gln Thr Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu
    450                 455                 460

Lys Cys Arg Leu Lys Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr
465                 470                 475                 480

Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr
                485                 490                 495

Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala
            500                 505                 510

Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln
        515                 520                 525

Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys
    530                 535                 540

Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val
545                 550                 555                 560

Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly
                565                 570                 575

Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg
            580                 585                 590

Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
        595                 600                 605
```

Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala
610 615 620

Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile
625 630 635 640

Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu
645 650 655

Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val
660 665 670

Met Val Gln Ala
675

<210> 3
<211> 5498
<212> DNA
<213> Dengue virus

<220>
<221> misc_feature
<223> DENV1 prM E (Env K203N)

<220>
<221> CDS
<222> (1046)..(3073)

<400> 3
tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60

cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120

ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180

accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240

attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat 300

tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360

tttcccagtc acgacgttgt aaaacgacgg ccagtgaatt gacgcgtttg acattgatta 420

ttgactagtt attaatagta atcaattacg gggtcattag ttcatagccc atatatggag 480

ttccgcgtta cataacttac ggtaaatggc ccgcctggct gaccgcccaa cgacccccgc 540

ccattgacgt caataatgac gtatgttccc atagtaacgc caatagggac tttccattga 600

cgtcaatggg tggagtattt acggtaaact gcccacttgg cagtacatca agtgtatcat 660

atgccaagta cgcccccctat tgacgtcaat gacggtaaat ggcccgcctg gcattatgcc 720

cagtacatga ccttatggga ctttcctact tggcagtaca tctacgtatt agtcatcgct 780

attaccatgg tgatgcggtt ttggcagtac atcaatgggc gtggatagcg gtttgactca 840

cggggatttc caagtctcca ccccattgac gtcaatggga gtttgttttg gcaccaaaat 900

caacgggact ttccaaaatg tcgtaacaac tccgccccat tgacgcaaat gggcggtagg 960

```
cgtgtacggt gggaggtcta tataagcaga gctcgtttag tgaaccgtca gataactgca      1020

ggtcgacgat atcgcggccg ccacc atg tcg gtg acc atg ctc ctc atg ctg        1072
                            Met Ser Val Thr Met Leu Leu Met Leu
                            1               5

ctg ccc aca gcc ctg gcg ttc cat ctg acc acc cga ggg gga gag ccg        1120
Leu Pro Thr Ala Leu Ala Phe His Leu Thr Thr Arg Gly Gly Glu Pro
10                  15                  20                  25

cac atg ata gtt agc aag cag gaa aga gga aaa tca ctt ttg ttt aag        1168
His Met Ile Val Ser Lys Gln Glu Arg Gly Lys Ser Leu Leu Phe Lys
                30                  35                  40

acc tct gca ggt gtc aac atg tgc acc ctt att gca atg gat ttg gga        1216
Thr Ser Ala Gly Val Asn Met Cys Thr Leu Ile Ala Met Asp Leu Gly
            45                  50                  55

gag tta tgt gag gac aca atg acc tac aaa tgc ccc cgg atc act gag        1264
Glu Leu Cys Glu Asp Thr Met Thr Tyr Lys Cys Pro Arg Ile Thr Glu
        60                  65                  70

acg gaa cca gat gac gtt gac tgt tgg tgc aat gcc acg gag aca tgg        1312
Thr Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Ala Thr Glu Thr Trp
    75                  80                  85

gtg acc tat gga aca tgt tct caa act ggt gaa cac cga cga gac aaa        1360
Val Thr Tyr Gly Thr Cys Ser Gln Thr Gly Glu His Arg Arg Asp Lys
90                  95                  100                 105

cgt tcc gtc gca ctg gca cca cac gta ggg ctt ggt cta gaa aca aga        1408
Arg Ser Val Ala Leu Ala Pro His Val Gly Leu Gly Leu Glu Thr Arg
                110                 115                 120

acc gaa acg tgg atg tcc tct gaa ggc gct tgg aaa caa ata caa aaa        1456
Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys Gln Ile Gln Lys
            125                 130                 135

gtg gag acc tgg gct ctg aga cac cca gga ttc acg gtg ata gcc ctt        1504
Val Glu Thr Trp Ala Leu Arg His Pro Gly Phe Thr Val Ile Ala Leu
        140                 145                 150

ttt cta gca cat gcc ata gga aca tcc atc acc cag aaa ggg atc att        1552
Phe Leu Ala His Ala Ile Gly Thr Ser Ile Thr Gln Lys Gly Ile Ile
    155                 160                 165

ttt att ttg ctg atg ctg gta act cca tcc atg gcc atg cgg tgc gtg        1600
Phe Ile Leu Leu Met Leu Val Thr Pro Ser Met Ala Met Arg Cys Val
170                 175                 180                 185

gga ata ggc aac aga gac ttc gtg gaa gga ctg tca gga gct acg tgg        1648
Gly Ile Gly Asn Arg Asp Phe Val Glu Gly Leu Ser Gly Ala Thr Trp
                190                 195                 200

gtg gat gtg gta ctg gag cat gga agt tgc gtc act acc atg gca aaa        1696
Val Asp Val Val Leu Glu His Gly Ser Cys Val Thr Thr Met Ala Lys
            205                 210                 215

gac aaa cca aca ctg gac att gaa ctc ttg aag acg gag gtc aca aac        1744
Asp Lys Pro Thr Leu Asp Ile Glu Leu Leu Lys Thr Glu Val Thr Asn
        220                 225                 230

cct gcc gtc ctg cgc aaa ctg tgc att gaa gct aaa ata tca aac acc        1792
Pro Ala Val Leu Arg Lys Leu Cys Ile Glu Ala Lys Ile Ser Asn Thr
    235                 240                 245

acc acc gat tcg aga tgt cca aca caa gga gaa gcc acg ctg gtg gaa        1840
```

```
Thr Thr Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Thr Leu Val Glu
250                 255                 260                 265

gaa cag gac acg aac ttt gtg tgt cga cga acg ttc gtg gac aga ggc      1888
Glu Gln Asp Thr Asn Phe Val Cys Arg Arg Thr Phe Val Asp Arg Gly
                270                 275                 280

tgg ggc aat ggt tgt ggg cta ttc gga aaa ggt agc tta ata acg tgt      1936
Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Ile Thr Cys
            285                 290                 295

gct aag ttt aag tgt gtg aca aaa ctg gaa gga aag ata gtc caa tat      1984
Ala Lys Phe Lys Cys Val Thr Lys Leu Glu Gly Lys Ile Val Gln Tyr
        300                 305                 310

gaa aac tta aaa tat tca gtg ata gtc acc gta cac act gga gac cag      2032
Glu Asn Leu Lys Tyr Ser Val Ile Val Thr Val His Thr Gly Asp Gln
    315                 320                 325

cac caa gtt gga aat gag acc aca gaa cat gga aca act gca acc ata      2080
His Gln Val Gly Asn Glu Thr Thr Glu His Gly Thr Thr Ala Thr Ile
330                 335                 340                 345

aca cct caa gct ccc acg tcg gaa ata cag ctg aca gac tac gga gct      2128
Thr Pro Gln Ala Pro Thr Ser Glu Ile Gln Leu Thr Asp Tyr Gly Ala
                350                 355                 360

cta aca ttg gat tgt tca cct aga aca ggg cta gac ttt aat gag atg      2176
Leu Thr Leu Asp Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn Glu Met
            365                 370                 375

gtg ttg ttg aca atg gaa aat aaa tca tgg ctc gtc cac aaa caa tgg      2224
Val Leu Leu Thr Met Glu Asn Lys Ser Trp Leu Val His Lys Gln Trp
        380                 385                 390

ttt cta gac tta cca ctg cct tgg acc tcg ggg gct tca aca tcc caa      2272
Phe Leu Asp Leu Pro Leu Pro Trp Thr Ser Gly Ala Ser Thr Ser Gln
    395                 400                 405

gag act tgg aat aga caa gac ttg ctg gtc aca ttt aag aca gct cat      2320
Glu Thr Trp Asn Arg Gln Asp Leu Leu Val Thr Phe Lys Thr Ala His
410                 415                 420                 425

gca aaa aag cag gaa gta gtc gta cta gga tca caa gaa gga gca atg      2368
Ala Lys Lys Gln Glu Val Val Val Leu Gly Ser Gln Glu Gly Ala Met
                430                 435                 440

cac act gcg ttg act gga gcg aca gaa atc caa acg tct gga acg aca      2416
His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Thr Ser Gly Thr Thr
            445                 450                 455

aca att ttt gca gga cac ctg aaa tgc aga cta aaa atg gat aaa ctg      2464
Thr Ile Phe Ala Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu
        460                 465                 470

act tta aaa ggg atg tca tat gta atg tgc aca ggg tca ttc aag tta      2512
Thr Leu Lys Gly Met Ser Tyr Val Met Cys Thr Gly Ser Phe Lys Leu
    475                 480                 485

gag aag gaa gtg gct gag acc cag cat gga act gtt cta gtg cag gtt      2560
Glu Lys Glu Val Ala Glu Thr Gln His Gly Thr Val Leu Val Gln Val
490                 495                 500                 505

aaa tac gaa gga aca gat gca cca tgc aag atc ccc ttc tcg tcc caa      2608
Lys Tyr Glu Gly Thr Asp Ala Pro Cys Lys Ile Pro Phe Ser Ser Gln
                510                 515                 520

gat gag aag gga gta acc cag aat ggg aga ttg ata aca gcc aac ccc      2656
```

```
Asp Glu Lys Gly Val Thr Gln Asn Gly Arg Leu Ile Thr Ala Asn Pro
            525                 530                 535

ata gtc act gac aaa gaa aaa cca gtc aac att gaa gcg gag cca cct      2704
Ile Val Thr Asp Lys Glu Lys Pro Val Asn Ile Glu Ala Glu Pro Pro
        540                 545                 550

ttt ggt gag agc tac att gtg gta gga gca ggt gaa aaa gct ttg aaa      2752
Phe Gly Glu Ser Tyr Ile Val Val Gly Ala Gly Glu Lys Ala Leu Lys
    555                 560                 565

cta agc tgg ttc aag aag gga agc agt ata ggg aaa atg ttt gaa gca      2800
Leu Ser Trp Phe Lys Lys Gly Ser Ser Ile Gly Lys Met Phe Glu Ala
570                 575                 580                 585

act gcc cgt gga gca cga agg atg gcc atc ctg gga gac act gca tgg      2848
Thr Ala Arg Gly Ala Arg Arg Met Ala Ile Leu Gly Asp Thr Ala Trp
                590                 595                 600

gac ttc ggt tct ata gga ggg gtg ttc acg tct gtg gga aaa ctg ata      2896
Asp Phe Gly Ser Ile Gly Gly Val Phe Thr Ser Val Gly Lys Leu Ile
            605                 610                 615

cac cag att ttt ggg act gcg tat gga gtt ttg ttc agc ggt gtt tct      2944
His Gln Ile Phe Gly Thr Ala Tyr Gly Val Leu Phe Ser Gly Val Ser
        620                 625                 630

tgg acc atg aag ata gga ata ggg att ctg ctg aca tgg cta gga tta      2992
Trp Thr Met Lys Ile Gly Ile Gly Ile Leu Leu Thr Trp Leu Gly Leu
    635                 640                 645

aac tca agg agc acg tcc ctt tca atg acg tgt atc gca gtt ggc atg      3040
Asn Ser Arg Ser Thr Ser Leu Ser Met Thr Cys Ile Ala Val Gly Met
650                 655                 660                 665

gtc acg ctg tac cta gga gtc atg gtt cag gcg taataaagat ctgctgtgcc    3093
Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
                670                 675

ttctagttgc cagccatctg ttgtttgccc ctcccccgtg ccttccttga ccctggaagg    3153

tgccactccc actgtccttt cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag    3213

gtgtcattct attctggggg gtggggtggg gcaggacagc aaggggggagg attgggaaga   3273

caatagcagg catgctgggg atgcggtggg ctctatggct cgagcatggt catagctgtt    3333

tcctgtgtga aattgttatc cgctcacaat tccacacaac atacgagccg gaagcataaa    3393

gtgtaaagcc tggggtgcct aatgagtgag ctaactcaca ttaattgcgt tgcgctcact    3453

gcccgctttc cagtcgggaa acctgtcgtg ccagctgcat taatgaatcg gccaacgcgc    3513

ggggagaggc ggtttgcgta ttgggcgctc ttccgcttcc tcgctcactg actcgctgcg    3573

ctcggtcgtt cggctgcggc gagcggtatc agctcactca aaggcggtaa tacggttatc    3633

cacagaatca ggggataacg caggaaagaa catgtgagca aaaggccagc aaaaggccag    3693

gaaccgtaaa aaggccgcgt tgctggcgtt tttccatagg ctccgccccc ctgacgagca    3753

tcacaaaaat cgacgctcaa gtcagaggtg gcgaaacccg acaggactat aaagatacca    3813

ggcgtttccc cctggaagct ccctcgtgcg ctctcctgtt ccgaccctgc cgcttaccgg    3873

atacctgtcc gcctttctcc cttcgggaag cgtggcgctt tctcatagct cacgctgtag    3933

gtatctcagt tcggtgtagg tcgttcgctc caagctgggc tgtgtgcacg aacccccccgt   3993
```

tcagcccgac cgctgcgcct tatccggtaa ctatcgtctt gagtccaacc cggtaagaca 4053

cgacttatcg ccactggcag cagccactgg taacaggatt agcagagcga ggtatgtagg 4113

cggtgctaca gagttcttga agtggtggcc taactacggc tacactagaa gaacagtatt 4173

tggtatctgc gctctgctga agccagttac cttcggaaaa agagttggta gctcttgatc 4233

cggcaaacaa accaccgctg gtagcggtgg ttttttttgtt tgcaagcagc agattacgcg 4293

cagaaaaaaa ggatctcaag aagatccttt gatcttttct acggggtctg acgctcagtg 4353

gaacgaaaac tcacgttaag ggattttggt catgagatta tcaaaaagga tcttcaccta 4413

gatcctttta aattaaaaat gaagttttaa atcaatctaa agtatatatg agtaaacttg 4473

gtctgacagt tagaaaaact catcgagcat caaatgaaac tgcaatttat tcatatcagg 4533

attatcaata ccatattttt gaaaaagccg tttctgtaat gaaggagaaa actcaccgag 4593

gcagttccat aggatggcaa gatcctggta tcggtctgcg attccgactc gtccaacatc 4653

aatacaacct attaatttcc cctcgtcaaa aataaggtta tcaagtgaga aatcaccatg 4713

agtgacgact gaatccggtg agaatggcaa aagtttatgc atttctttcc agacttgttc 4773

aacaggccag ccattacgct cgtcatcaaa atcactcgca tcaaccaaac cgttattcat 4833

tcgtgattgc gcctgagcga gacgaaatac gcgatcgctg ttaaaaggac aattacaaac 4893

aggaatcgaa tgcaaccggc gcaggaacac tgccagcgca tcaacaatat tttcacctga 4953

atcaggatat tcttctaata cctggaatgc tgttttccca gggatcgcag tggtgagtaa 5013

ccatgcatca tcaggagtac ggataaaatg cttgatggtc ggaagaggca taaattccgt 5073

cagccagttt agtctgacca tctcatctgt aacatcattg gcaacgctac ctttgccatg 5133

tttcagaaac aactctggcg catcgggctt cccatacaat cgatagattg tcgcacctga 5193

ttgcccgaca ttatcgcgag cccatttata cccatataaa tcagcatcca tgttggaatt 5253

taatcgcggc ctagagcaag acgtttcccg ttgaatatgg ctcatactct tccttttca 5313

atattattga agcatttatc agggttattg tctcatgagc ggatacatat ttgaatgtat 5373

ttagaaaaat aaacaaatag gggttccgcg cacatttccc cgaaaagtgc cacctgacgt 5433

ctaagaaacc attattatca tgacattaac ctataaaaat aggcgtatca cgaggccctt 5493

tcgtc 5498

<210> 4
<211> 676
<212> PRT
<213> Dengue virus

<400> 4

Met Ser Val Thr Met Leu Leu Met Leu Leu Pro Thr Ala Leu Ala Phe
1 5 10 15

His Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val Ser Lys Gln
20 25 30

```
Glu Arg Gly Lys Ser Leu Leu Phe Lys Thr Ser Ala Gly Val Asn Met
        35                  40                  45

Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Met
    50                  55                  60

Thr Tyr Lys Cys Pro Arg Ile Thr Glu Thr Glu Pro Asp Asp Val Asp
65                  70                  75                  80

Cys Trp Cys Asn Ala Thr Glu Thr Trp Val Thr Tyr Gly Thr Cys Ser
                85                  90                  95

Gln Thr Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala Pro
            100                 105                 110

His Val Gly Leu Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser
        115                 120                 125

Glu Gly Ala Trp Lys Gln Ile Gln Lys Val Glu Thr Trp Ala Leu Arg
    130                 135                 140

His Pro Gly Phe Thr Val Ile Ala Leu Phe Leu Ala His Ala Ile Gly
145                 150                 155                 160

Thr Ser Ile Thr Gln Lys Gly Ile Ile Phe Ile Leu Leu Met Leu Val
                165                 170                 175

Thr Pro Ser Met Ala Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe
            180                 185                 190

Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu His
        195                 200                 205

Gly Ser Cys Val Thr Thr Met Ala Lys Asp Lys Pro Thr Leu Asp Ile
    210                 215                 220

Glu Leu Leu Lys Thr Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu
225                 230                 235                 240

Cys Ile Glu Ala Lys Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro
                245                 250                 255

Thr Gln Gly Glu Ala Thr Leu Val Glu Glu Gln Asp Thr Asn Phe Val
            260                 265                 270

Cys Arg Arg Thr Phe Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
        275                 280                 285

Phe Gly Lys Gly Ser Leu Ile Thr Cys Ala Lys Phe Lys Cys Val Thr
    290                 295                 300
```

```
Lys Leu Glu Gly Lys Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser Val
305                 310                 315                 320

Ile Val Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr
                325                 330                 335

Thr Glu His Gly Thr Thr Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser
            340                 345                 350

Glu Ile Gln Leu Thr Asp Tyr Gly Ala Leu Thr Leu Asp Cys Ser Pro
        355                 360                 365

Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Thr Met Glu Asn
    370                 375                 380

Lys Ser Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro
385                 390                 395                 400

Trp Thr Ser Gly Ala Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln Asp
                405                 410                 415

Leu Leu Val Thr Phe Lys Thr Ala His Ala Lys Lys Gln Glu Val Val
            420                 425                 430

Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala
        435                 440                 445

Thr Glu Ile Gln Thr Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu
    450                 455                 460

Lys Cys Arg Leu Lys Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr
465                 470                 475                 480

Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr
                485                 490                 495

Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala
            500                 505                 510

Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln
        515                 520                 525

Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys
    530                 535                 540

Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val
545                 550                 555                 560

Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly
                565                 570                 575
```

```
Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg
            580                 585                 590

Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
        595                 600                 605

Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala
    610                 615                 620

Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile
625                 630                 635                 640

Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu
                645                 650                 655

Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val
            660                 665                 670

Met Val Gln Ala
        675
```

<210> 5
<211> 3770
<212> DNA
<213> Dengue virus

<220>
<221> misc_feature
<223> DENV1 capsid K85A_K86A mutant

<220>
<221> CDS
<222> (1046)..(1345)

<400> 5

```
tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca      60

cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg     120

ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc     180

accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc     240

attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat     300

tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt     360

tttcccagtc acgacgttgt aaaacgacgg ccagtgaatt gacgcgtttg acattgatta     420

ttgactagtt attaatagta atcaattacg gggtcattag ttcatagccc atatatggag     480

ttccgcgtta cataacttac ggtaaatggc ccgcctggct gaccgcccaa cgacccccgc     540

ccattgacgt caataatgac gtatgttccc atagtaacgc caatagggac tttccattga     600

cgtcaatggg tggagtattt acggtaaact gcccacttgg cagtacatca agtgtatcat     660

atgccaagta cgcccccctat tgacgtcaat gacggtaaat ggcccgcctg gcattatgcc     720
```

```
cagtacatga ccttatggga ctttcctact tggcagtaca tctacgtatt agtcatcgct      780

attaccatgg tgatgcggtt ttggcagtac atcaatgggc gtggatagcg gtttgactca      840

cggggatttc caagtctcca ccccattgac gtcaatggga gtttgttttg gcaccaaaat      900

caacgggact ttccaaaatg tcgtaacaac tccgccccat tgacgcaaat gggcggtagg      960

cgtgtacggt gggaggtcta tataagcaga gctcgtttag tgaaccgtca gataactgca     1020

ggtcgacgat atcgcggccg ccacc atg aac aac caa cgg aaa aag acg ggt        1072
                              Met Asn Asn Gln Arg Lys Lys Thr Gly
                              1               5

cga ccg tct ttc aat atg ctg aaa cgc gcg aga aac cgc gtg tca act        1120
Arg Pro Ser Phe Asn Met Leu Lys Arg Ala Arg Asn Arg Val Ser Thr
10                  15                  20                  25

gtt tca cag ttg gcg aag aga ttc tca aaa gga ttg ctt tca ggc caa        1168
Val Ser Gln Leu Ala Lys Arg Phe Ser Lys Gly Leu Leu Ser Gly Gln
                30                  35                  40

gga ccc atg aaa ttg gtg atg gct ttt ata gca ttc cta aga ttt cta        1216
Gly Pro Met Lys Leu Val Met Ala Phe Ile Ala Phe Leu Arg Phe Leu
            45                  50                  55

gcc ata cct cca aca gca gga att ttg gct aga tgg ggc tca ttc aag        1264
Ala Ile Pro Pro Thr Ala Gly Ile Leu Ala Arg Trp Gly Ser Phe Lys
        60                  65                  70

aag aat gga gcg atc aaa gtg tta cgg ggt ttc gcg gca gaa atc tca        1312
Lys Asn Gly Ala Ile Lys Val Leu Arg Gly Phe Ala Ala Glu Ile Ser
    75                  80                  85

aac atg ttg aac ata atg aac agg agg aaa aga taataaagat ctgctgtgcc      1365
Asn Met Leu Asn Ile Met Asn Arg Arg Lys Arg
90                  95                  100

ttctagttgc cagccatctg ttgtttgccc ctcccccgtg ccttccttga ccctggaagg      1425

tgccactccc actgtccttt cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag      1485

gtgtcattct attctggggg gtggggtggg gcaggacagc aaggggggagg attgggaaga     1545

caatagcagg catgctgggg atgcggtggg ctctatggct cgagcatggt catagctgtt      1605

tcctgtgtga aattgttatc cgctcacaat tccacacaac atacgagccg gaagcataaa      1665

gtgtaaagcc tggggtgcct aatgagtgag ctaactcaca ttaattgcgt tgcgctcact      1725

gcccgctttc cagtcgggaa acctgtcgtg ccagctgcat taatgaatcg gccaacgcgc      1785

ggggagaggc ggtttgcgta ttgggcgctc ttccgcttcc tcgctcactg actcgctgcg      1845

ctcggtcgtt cggctgcggc gagcggtatc agctcactca aaggcggtaa tacggttatc      1905

cacagaatca ggggataacg caggaaagaa catgtgagca aaaggccagc aaaaggccag      1965

gaaccgtaaa aaggccgcgt tgctggcgtt tttccatagg ctccgccccc ctgacgagca      2025

tcacaaaaat cgacgctcaa gtcagaggtg gcgaaacccg acaggactat aaagatacca      2085

ggcgtttccc cctggaagct ccctcgtgcg ctctcctgtt ccgaccctgc cgcttaccgg      2145

atacctgtcc gcctttctcc cttcgggaag cgtggcgctt tctcatagct cacgctgtag      2205

gtatctcagt tcggtgtagg tcgttcgctc caagctgggc tgtgtgcacg aacccccccgt     2265
```

tcagcccgac cgctgcgcct tatccggtaa ctatcgtctt gagtccaacc cggtaagaca 2325

cgacttatcg ccactggcag cagccactgg taacaggatt agcagagcga ggtatgtagg 2385

cggtgctaca gagttcttga agtggtggcc taactacggc tacactagaa gaacagtatt 2445

tggtatctgc gctctgctga agccagttac cttcggaaaa agagttggta gctcttgatc 2505

cggcaaacaa accaccgctg gtagcggtgg ttttttttgtt tgcaagcagc agattacgcg 2565

cagaaaaaaa ggatctcaag aagatccttt gatcttttct acggggtctg acgctcagtg 2625

gaacgaaaac tcacgttaag ggattttggt catgagatta tcaaaaagga tcttcaccta 2685

gatcctttta aattaaaaat gaagttttaa atcaatctaa agtatatatg agtaaacttg 2745

gtctgacagt tagaaaaact catcgagcat caaatgaaac tgcaatttat tcatatcagg 2805

attatcaata ccatattttt gaaaaagccg tttctgtaat gaaggagaaa actcaccgag 2865

gcagttccat aggatggcaa gatcctggta tcggtctgcg attccgactc gtccaacatc 2925

aatacaacct attaatttcc cctcgtcaaa aataaggtta tcaagtgaga aatcaccatg 2985

agtgacgact gaatccggtg agaatggcaa aagtttatgc atttctttcc agacttgttc 3045

aacaggccag ccattacgct cgtcatcaaa atcactcgca tcaaccaaac cgttattcat 3105

tcgtgattgc gcctgagcga gacgaaatac gcgatcgctg ttaaaaggac aattacaaac 3165

aggaatcgaa tgcaaccggc gcaggaacac tgccagcgca tcaacaatat tttcacctga 3225

atcaggatat tcttctaata cctggaatgc tgttttccca gggatcgcag tggtgagtaa 3285

ccatgcatca tcaggagtac ggataaaatg cttgatggtc ggaagaggca taaattccgt 3345

cagccagttt agtctgacca tctcatctgt aacatcattg gcaacgctac ctttgccatg 3405

tttcagaaac aactctggcg catcgggctt cccatacaat cgatagattg tcgcacctga 3465

ttgcccgaca ttatcgcgag cccatttata cccatataaa tcagcatcca tgttggaatt 3525

taatcgcggc ctagagcaag acgtttcccg ttgaatatgg ctcatactct tccttttca 3585

atattattga agcatttatc agggttattg tctcatgagc ggatacatat ttgaatgtat 3645

ttagaaaaat aaacaaatag gggttccgcg cacatttccc cgaaaagtgc cacctgacgt 3705

ctaagaaacc attattatca tgacattaac ctataaaaat aggcgtatca cgaggccctt 3765

tcgtc 3770

<210> 6
<211> 100
<212> PRT
<213> Dengue virus

<400> 6

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 Ala Ala Glu Ile Ser Asn Met Leu Asn Ile Met Asn
85 90 95

Arg Arg Lys Arg
100

<210> 7
<211> 6679
<212> DNA
<213> Dengue virus

<220>
<221> misc_feature
<223> Chimera DENV2 prM E_chimeric DENV1 E

<220>
<221> CDS
<222> (906)..(2933)

<220>
<221> misc_feature
<222> (906)..(2336)
<223> DENV2 prM E region

<220>
<221> misc_feature
<222> (2337)..(2933)
<223> DENV1 E region

<400> 7
gaattcccat tgcatacgtt gtatccatat cataatatgt acatttatat tggctcatgt 60

ccaacattac cgccatgttg acattgatta ttgactagtt attaatagta atcaattacg 120

gggtcattag ttcatagccc atatatggag ttccgcgtta cataacttac ggtaaatggc 180

ccgcctggct gaccgcccaa cgacccccgc ccattgacgt caataatgac gtatgttccc 240

atagtaacgc caatagggac tttccattga cgtcaatggg tggagtattt acggtaaact 300

gcccacttgg cagtacatca agtgtatcat atgccaagta cgcccccta tgacgtcaat 360

gacggtaaat ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact 420

tggcagtaca tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac 480

atcaatgggc gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac 540

gtcaatggga gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac 600

tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta tataagcaga 660

gctcgtttag tgaaccgtca gatcgcctgg agacgccatc cacgctgttt gacctccat 720

```
agaagacacc gggaccgatc cagcctccgt taacggtgga gggcagtgta gtctgagcag      780

tactcgttgc tgccgcgcgc gccaccagac ataatagctg acagactaac agactgttcc      840

tttccatggg tcttttctgc agtcaccgtc gtcgacacgt gtgatcagat atcgcggccg      900

ccacc atg act gca ggc atg atc atc atg ctg att cca aca gtg atg gcg      950
      Met Thr Ala Gly Met Ile Ile Met Leu Ile Pro Thr Val Met Ala
      1               5                  10                  15

ttt cat ctg acc aca cgc aac gga gaa cca cac atg atc gtc agt aga       998
Phe His Leu Thr Thr Arg Asn Gly Glu Pro His Met Ile Val Ser Arg
                  20                  25                  30

caa gaa aaa ggg aaa agc ctt ctg ttt aag aca aag gac ggc acg aac      1046
Gln Glu Lys Gly Lys Ser Leu Leu Phe Lys Thr Lys Asp Gly Thr Asn
              35                  40                  45

atg tgt acc ctc atg gcc atg gac ctt ggt gag ttg tgt gaa gac aca      1094
Met Cys Thr Leu Met Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr
          50                  55                  60

atc acg tat aaa tgt ccc ttt ctc aag cag aac gaa cca gaa gac ata      1142
Ile Thr Tyr Lys Cys Pro Phe Leu Lys Gln Asn Glu Pro Glu Asp Ile
      65                  70                  75

gat tgt tgg tgc aac tcc acg tcc aca tgg gta act tat ggg aca tgt      1190
Asp Cys Trp Cys Asn Ser Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys
80                  85                  90                  95

acc acc aca gga gag cac aga aga gaa aaa aga tca gtg gcg ctt gtt      1238
Thr Thr Thr Gly Glu His Arg Arg Glu Lys Arg Ser Val Ala Leu Val
                 100                 105                 110

cca cac gtg gga atg gga ttg gag aca cga act gaa aca tgg atg tca      1286
Pro His Val Gly Met Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser
             115                 120                 125

tca gaa ggg gcc tgg aaa cat gcc cag aga att gaa act tgg att ctg      1334
Ser Glu Gly Ala Trp Lys His Ala Gln Arg Ile Glu Thr Trp Ile Leu
         130                 135                 140

aga cat cca ggc ttt acc ata atg gcc gca atc ctg gca tac acc ata      1382
Arg His Pro Gly Phe Thr Ile Met Ala Ala Ile Leu Ala Tyr Thr Ile
     145                 150                 155

gga acg acg cat ttc caa aga gtc ctg ata ttc atc cta ctg aca gcc      1430
Gly Thr Thr His Phe Gln Arg Val Leu Ile Phe Ile Leu Leu Thr Ala
160                 165                 170                 175

atc gct cct tca atg aca atg cgc tgc ata gga ata tca aat agg gac      1478
Ile Ala Pro Ser Met Thr Met Arg Cys Ile Gly Ile Ser Asn Arg Asp
                 180                 185                 190

ttt gtg gaa gga gtg tca gga ggg agt tgg gtt gac ata gtt tta gaa      1526
Phe Val Glu Gly Val Ser Gly Gly Ser Trp Val Asp Ile Val Leu Glu
             195                 200                 205

cat gga agt tgt gtg acg acg atg gca aaa aat aaa cca aca ctg gac      1574
His Gly Ser Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp
         210                 215                 220

ttt gaa ctg ata aaa aca gaa gcc aaa caa ccc gcc acc tta agg aag      1622
Phe Glu Leu Ile Lys Thr Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys
     225                 230                 235

tac tgt ata gag gct aaa ctg acc aac acg aca aca gac tcg cgc tgc      1670
```

```
Tyr Cys Ile Glu Ala Lys Leu Thr Asn Thr Thr Thr Asp Ser Arg Cys
240                 245                 250                 255

cca aca caa ggg gaa ccc acc ctg aat gaa gag cag gac aaa agg ttt      1718
Pro Thr Gln Gly Glu Pro Thr Leu Asn Glu Glu Gln Asp Lys Arg Phe
                260                 265                 270

gtc tgc aaa cat tcc atg gta gac aga gga tgg gga aat gga tgt gga      1766
Val Cys Lys His Ser Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly
            275                 280                 285

tta ttt gga aaa gga ggc atc gtg acc tgt gcc atg ttc aca tgc aaa      1814
Leu Phe Gly Lys Gly Gly Ile Val Thr Cys Ala Met Phe Thr Cys Lys
        290                 295                 300

aag aac atg gag gga aaa att gtg cag cca gaa aac ctg gaa tac act      1862
Lys Asn Met Glu Gly Lys Ile Val Gln Pro Glu Asn Leu Glu Tyr Thr
    305                 310                 315

gtc gtt ata aca cct cat tca ggg gaa gaa cat gca gtc gga aat gac      1910
Val Val Ile Thr Pro His Ser Gly Glu Glu His Ala Val Gly Asn Asp
320                 325                 330                 335

aca gga aaa cat ggt aaa gaa gtc aag ata aca cca cag agc tcc atc      1958
Thr Gly Lys His Gly Lys Glu Val Lys Ile Thr Pro Gln Ser Ser Ile
                340                 345                 350

aca gag gcg gaa ctg aca ggc tat ggc act gtt acg atg gag tgc tct      2006
Thr Glu Ala Glu Leu Thr Gly Tyr Gly Thr Val Thr Met Glu Cys Ser
            355                 360                 365

cca aga acg ggc ctc gac ttc aat gag atg gtg ttg ctg caa atg aaa      2054
Pro Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Gln Met Lys
        370                 375                 380

gac aaa gct tgg ctg gtg cac aga caa tgg ttc cta gac cta ccg ttg      2102
Asp Lys Ala Trp Leu Val His Arg Gln Trp Phe Leu Asp Leu Pro Leu
    385                 390                 395

cca tgg ctg ccc gga gca gac aca caa gga tca aat tgg ata cag aaa      2150
Pro Trp Leu Pro Gly Ala Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys
400                 405                 410                 415

gag aca ctg gtc acc ttc aaa aat ccc cat gcg aaa aaa cag gat gtt      2198
Glu Thr Leu Val Thr Phe Lys Asn Pro His Ala Lys Lys Gln Asp Val
                420                 425                 430

gtt gtc tta ggc tcc caa gag ggg gcc atg cat aca gca ctc aca ggg      2246
Val Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly
            435                 440                 445

gct acg gaa atc cag atg tca tca gga aac ctg ctg ttc aca gga cat      2294
Ala Thr Glu Ile Gln Met Ser Ser Gly Asn Leu Leu Phe Thr Gly His
        450                 455                 460

ctt aag tgc agg ctg aga atg gac aaa tta caa ctt aaa ggg atg tca      2342
Leu Lys Cys Arg Leu Arg Met Asp Lys Leu Gln Leu Lys Gly Met Ser
    465                 470                 475

tat gta atg tgc aca ggg tca ttc aag tta gag aag gaa gtg gct gag      2390
Tyr Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu
480                 485                 490                 495

acc cag cat gga act gtt cta gtg cag gtt aaa tac gaa gga aca gat      2438
Thr Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp
                500                 505                 510

gca cca tgc aag atc ccc ttc tcg tcc caa gat gag aag gga gta acc      2486
```

```
Ala Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr
            515                 520                 525

cag aat ggg aga ttg ata aca gcc aac ccc ata gtc act gac aaa gaa      2534
Gln Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu
        530                 535                 540

aaa cca gtc aac att gaa gcg gag cca cct ttt ggt gag agc tac att      2582
Lys Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile
    545                 550                 555

gtg gta gga gca ggt gaa aaa gct ttg aaa cta agc tgg ttc aag aag      2630
Val Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys
560                 565                 570                 575

gga agc agt ata ggg aaa atg ttt gaa gca act gcc cgt gga gca cga      2678
Gly Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg
                580                 585                 590

agg atg gcc atc ctg gga gac act gca tgg gac ttc ggt tct ata gga      2726
Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly
            595                 600                 605

ggg gtg ttc acg tct gtg gga aaa ctg ata cac cag att ttt ggg act      2774
Gly Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr
        610                 615                 620

gcg tat gga gtt ttg ttc agc ggt gtt tct tgg acc atg aag ata gga      2822
Ala Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly
    625                 630                 635

ata ggg att ctg ctg aca tgg cta gga tta aac tca agg agc acg tcc      2870
Ile Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser
640                 645                 650                 655

ctt tca atg acg tgt atc gca gtt ggc atg gtc acg ctg tac cta gga      2918
Leu Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly
                660                 665                 670

gtc atg gtt cag gcg taataaagat ctgctgtgcc ttctagttgc cagccatctg      2973
Val Met Val Gln Ala
            675

ttgtttgccc ctcccccgtg ccttccttga ccctggaagg tgccactccc actgtccttt     3033

cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag gtgtcattct attctggggg     3093

gtggggtggg gcaggacagc aaggggggagg attgggaaga caatagcagg catgctgggg     3153

atgcggtggg ctctatgggt acccaggtgc tgaagaattg acccggttcc tcctgggcca     3213

gaaagaagca ggcacatccc cttctctgtg acacaccctg tccacgcccc tggttcttag     3273

ttccagcccc actcatagga cactcatagc tcaggagggc tccgccttca atcccacccg     3333

ctaaagtact tggagcggtc tctccctccc tcatcagccc accaaaccaa acctagcctc     3393

caagagtggg aagaaattaa agcaagatag gctattaagt gcagagggag agaaaatgcc     3453

tccaacatgt gaggaagtaa tgagagaaat catagaattt taaggccatg atttaaggcc     3513

atcatggcct aagcttgaaa ggagatagga tcaaagcttg gcgtaatcat ggtcatagct     3573

gtttcctgtg tgaaattgtt atccgctcac aattccacac aacatacgag ccggaagcat     3633

aaagtgtaaa gcctggggtg cctaatgagt gagctaactc acattaattg cgttgcgctc     3693

actgcccgct ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa tcggccaacg     3753
```

cgcggggaga ggcggtttgc gtattgggcg ctcttccgct tcctcgctca ctgactcgct 3813

gcgctcggtc gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg taatacggtt 3873

atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc 3933

caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc cccctgacga 3993

gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata 4053

ccaggcgttt ccccctggaa gctccctcgt gcgctctcct gttccgaccc tgccgcttac 4113

cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcata gctcacgctg 4173

taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc 4233

cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggtaag 4293

acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt 4353

aggcggtgct acagagttct tgaagtggtg gcctaactac ggctacacta gaagaacagt 4413

atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg 4473

atccggcaaa caaaccaccg ctggtagcgg tggtttttttt gtttgcaagc agcagattac 4533

gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca 4593

gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac 4653

ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac 4713

ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt 4773

tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt 4833

accatctggc cccagtgctg caatgatacc gcgagaacca cgctcaccgg ctccagattt 4893

atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc 4953

cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa 5013

tagtttgcgc aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg 5073

tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt 5133

gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc 5193

agtgttatca ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt 5253

aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg 5313

gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac 5373

tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc 5433

gctgttgaga tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt 5493

tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg 5553

aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag 5613

catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5673

acaaataggg gttccgcgca catttccccg aaaagtgcca cctgacgtct aagaaaccat 5733

tattatcatg acattaacct ataaaaatag gcgtatcacg aggccctttc gggtcgcgcg 5793

tttcggtgat gacggtgaaa acctctgaca catgcagctc ccgttgacgg tcacagcttg 5853

tctgtaagcg gatgccggga gcagacaagc ccgtcagggc gcgtcagcgg gtgttggcgg 5913

gtgtcggggc tggcttaact atgcggcatc agagcagatt gtactgagag tgcaccataa 5973

aattgtaaac gttaatattt tgttaaaatt cgcgttaaat ttttgttaaa tcagctcatt 6033

ttttaaccaa taggccgaaa tcggcaaaat cccttataaa tcaaaagaat agcccgagat 6093

agggttgagt gttgttccag tttggaacaa gagtccacta ttaaagaacg tggactccaa 6153

cgtcaaaggg cgaaaaaccg tctatcaggg cgatggccca ctacgtgaac catcacccaa 6213

atcaagtttt ttggggtcga ggtgccgtaa agcactaaat cggaacccta aagggagccc 6273

ccgatttaga gcttgacggg gaaagccggc gaacgtggcg agaaaggaag ggaagaaagc 6333

gaaaggagcg ggcgctaggg cgctggcaag tgtagcggtc acgctgcgcg taaccaccac 6393

acccgccgcg cttaatgcgc cgctacaggg cgcgtactat ggttgctttg acgtatgcgg 6453

tgtgaaatac cgcacagatg cgtaaggaga aaataccgca tcaggcgcca ttcgccattc 6513

aggctgcgca actgttggga agggcgatcg gtgcgggcct cttcgctatt acgccagctg 6573

gcgaaagggg gatgtgctgc aaggcgatta agttgggtaa cgccagggtt ttcccagtca 6633

cgacgttgta aaacgacggc cagtgaattc catggtctca actttc 6679

<210> 8
<211> 676
<212> PRT
<213> Dengue virus

<400> 8

Met Thr Ala Gly Met Ile Ile Met Leu Ile Pro Thr Val Met Ala Phe
1 5 10 15

His Leu Thr Thr Arg Asn Gly Glu Pro His Met Ile Val Ser Arg Gln
20 25 30

Glu Lys Gly Lys Ser Leu Leu Phe Lys Thr Lys Asp Gly Thr Asn Met
35 40 45

Cys Thr Leu Met Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile
50 55 60

Thr Tyr Lys Cys Pro Phe Leu Lys Gln Asn Glu Pro Glu Asp Ile Asp
65 70 75 80

Cys Trp Cys Asn Ser Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr
85 90 95

Thr Thr Gly Glu His Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro
100 105 110

His Val Gly Met Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser

115 120 125

Glu Gly Ala Trp Lys His Ala Gln Arg Ile Glu Thr Trp Ile Leu Arg
130 135 140

His Pro Gly Phe Thr Ile Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly
145 150 155 160

Thr Thr His Phe Gln Arg Val Leu Ile Phe Ile Leu Leu Thr Ala Ile
165 170 175

Ala Pro Ser Met Thr Met Arg Cys Ile Gly Ile Ser Asn Arg Asp Phe
180 185 190

Val Glu Gly Val Ser Gly Gly Ser Trp Val Asp Ile Val Leu Glu His
195 200 205

Gly Ser Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe
210 215 220

Glu Leu Ile Lys Thr Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr
225 230 235 240

Cys Ile Glu Ala Lys Leu Thr Asn Thr Thr Thr Asp Ser Arg Cys Pro
245 250 255

Thr Gln Gly Glu Pro Thr Leu Asn Glu Glu Gln Asp Lys Arg Phe Val
260 265 270

Cys Lys His Ser Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
275 280 285

Phe Gly Lys Gly Gly Ile Val Thr Cys Ala Met Phe Thr Cys Lys Lys
290 295 300

Asn Met Glu Gly Lys Ile Val Gln Pro Glu Asn Leu Glu Tyr Thr Val
305 310 315 320

Val Ile Thr Pro His Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr
325 330 335

Gly Lys His Gly Lys Glu Val Lys Ile Thr Pro Gln Ser Ser Ile Thr
340 345 350

Glu Ala Glu Leu Thr Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro
355 360 365

Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Gln Met Lys Asp
370 375 380

Lys Ala Trp Leu Val His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro

385 390 395 400

Trp Leu Pro Gly Ala Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu
405 410 415

Thr Leu Val Thr Phe Lys Asn Pro His Ala Lys Lys Gln Asp Val Val
420 425 430

Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala
435 440 445

Thr Glu Ile Gln Met Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu
450 455 460

Lys Cys Arg Leu Arg Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr
465 470 475 480

Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr
485 490 495

Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala
500 505 510

Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln
515 520 525

Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys
530 535 540

Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val
545 550 555 560

Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly
565 570 575

Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg
580 585 590

Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
595 600 605

Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala
610 615 620

Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile
625 630 635 640

Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu
645 650 655

Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val

660 665 670

Met Val Gln Ala
675

<210> 9
<211> 6679
<212> DNA
<213> Dengue virus

<220>
<221> misc_feature
<223> Chimera DENV2 prM E (Env F108A)_chimeric DENV1 E

<220>
<221> CDS
<222> (906)..(2933)

<220>
<221> misc_feature
<222> (906)..(2336)
<223> DENV2 prM E region

<220>
<221> misc_feature
<222> (2337)..(2933)
<223> DENV1 region (F108A)

<400> 9
gaattcccat tgcatacgtt gtatccatat cataatatgt acatttatat tggctcatgt 60

ccaacattac cgccatgttg acattgatta ttgactagtt attaatagta atcaattacg 120

gggtcattag ttcatagccc atatatggag ttccgcgtta cataacttac ggtaaatggc 180

ccgcctggct gaccgcccaa cgacccccgc ccattgacgt caataatgac gtatgttccc 240

atagtaacgc caatagggac tttccattga cgtcaatggg tggagtattt acggtaaact 300

gcccacttgg cagtacatca agtgtatcat atgccaagta cgcccccta tgacgtcaat 360

gacggtaaat ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact 420

tggcagtaca tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac 480

atcaatgggc gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac 540

gtcaatggga gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac 600

tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta tataagcaga 660

gctcgtttag tgaaccgtca gatcgcctgg agacgccatc cacgctgttt tgacctccat 720

agaagacacc gggaccgatc cagcctccgt taacggtgga gggcagtgta gtctgagcag 780

tactcgttgc tgccgcgcgc gccaccagac ataatagctg acagactaac agactgttcc 840

tttccatggg tcttttctgc agtcaccgtc gtcgacacgt gtgatcagat atcgcggccg 900

ccacc atg act gca ggc atg atc atc atg ctg att cca aca gtg atg gcg 950
Met Thr Ala Gly Met Ile Ile Met Leu Ile Pro Thr Val Met Ala
1 5 10 15

ttt cat ctg acc aca cgc aac gga gaa cca cac atg atc gtc agt aga 998
Phe His Leu Thr Thr Arg Asn Gly Glu Pro His Met Ile Val Ser Arg

```
                    20                  25                  30

caa gaa aaa ggg aaa agc ctt ctg ttt aag aca aag gac ggc acg aac      1046
Gln Glu Lys Gly Lys Ser Leu Leu Phe Lys Thr Lys Asp Gly Thr Asn
            35                  40                  45

atg tgt acc ctc atg gcc atg gac ctt ggt gag ttg tgt gaa gac aca      1094
Met Cys Thr Leu Met Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr
        50                  55                  60

atc acg tat aaa tgt ccc ttt ctc aag cag aac gaa cca gaa gac ata      1142
Ile Thr Tyr Lys Cys Pro Phe Leu Lys Gln Asn Glu Pro Glu Asp Ile
    65                  70                  75

gat tgt tgg tgc aac tcc acg tcc aca tgg gta act tat ggg aca tgt      1190
Asp Cys Trp Cys Asn Ser Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys
80                  85                  90                  95

acc acc aca gga gag cac aga aga gaa aaa aga tca gtg gcg ctt gtt      1238
Thr Thr Thr Gly Glu His Arg Arg Glu Lys Arg Ser Val Ala Leu Val
                100                 105                 110

cca cac gtg gga atg gga ttg gag aca cga act gaa aca tgg atg tca      1286
Pro His Val Gly Met Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser
            115                 120                 125

tca gaa ggg gcc tgg aaa cat gcc cag aga att gaa act tgg att ctg      1334
Ser Glu Gly Ala Trp Lys His Ala Gln Arg Ile Glu Thr Trp Ile Leu
        130                 135                 140

aga cat cca ggc ttt acc ata atg gcc gca atc ctg gca tac acc ata      1382
Arg His Pro Gly Phe Thr Ile Met Ala Ala Ile Leu Ala Tyr Thr Ile
    145                 150                 155

gga acg acg cat ttc caa aga gtc ctg ata ttc atc cta ctg aca gcc      1430
Gly Thr Thr His Phe Gln Arg Val Leu Ile Phe Ile Leu Leu Thr Ala
160                 165                 170                 175

atc gct cct tca atg aca atg cgc tgc ata gga ata tca aat agg gac      1478
Ile Ala Pro Ser Met Thr Met Arg Cys Ile Gly Ile Ser Asn Arg Asp
                180                 185                 190

ttt gtg gaa gga gtg tca gga ggg agt tgg gtt gac ata gtt tta gaa      1526
Phe Val Glu Gly Val Ser Gly Gly Ser Trp Val Asp Ile Val Leu Glu
            195                 200                 205

cat gga agt tgt gtg acg acg atg gca aaa aat aaa cca aca ctg gac      1574
His Gly Ser Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp
        210                 215                 220

ttt gaa ctg ata aaa aca gaa gcc aaa caa ccc gcc acc tta agg aag      1622
Phe Glu Leu Ile Lys Thr Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys
    225                 230                 235

tac tgt ata gag gct aaa ctg acc aac acg aca aca gac tcg cgc tgc      1670
Tyr Cys Ile Glu Ala Lys Leu Thr Asn Thr Thr Thr Asp Ser Arg Cys
240                 245                 250                 255

cca aca caa ggg gaa ccc acc ctg aat gaa gag cag gac aaa agg ttt      1718
Pro Thr Gln Gly Glu Pro Thr Leu Asn Glu Glu Gln Asp Lys Arg Phe
                260                 265                 270

gtc tgc aaa cat tcc atg gta gac aga gga tgg gga aat gga tgt gga      1766
Val Cys Lys His Ser Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly
            275                 280                 285

tta gct gga aaa gga ggc atc gtg acc tgt gcc atg ttc aca tgc aaa      1814
Leu Ala Gly Lys Gly Gly Ile Val Thr Cys Ala Met Phe Thr Cys Lys
```

```
        290                 295                 300

aag aac atg gag gga aaa att gtg cag cca gaa aac ctg gaa tac act      1862
Lys Asn Met Glu Gly Lys Ile Val Gln Pro Glu Asn Leu Glu Tyr Thr
    305                 310                 315

gtc gtt ata aca cct cat tca ggg gaa gaa cat gca gtc gga aat gac      1910
Val Val Ile Thr Pro His Ser Gly Glu Glu His Ala Val Gly Asn Asp
320                 325                 330                 335

aca gga aaa cat ggt aaa gaa gtc aag ata aca cca cag agc tcc atc      1958
Thr Gly Lys His Gly Lys Glu Val Lys Ile Thr Pro Gln Ser Ser Ile
                340                 345                 350

aca gag gcg gaa ctg aca ggc tat ggc act gtt acg atg gag tgc tct      2006
Thr Glu Ala Glu Leu Thr Gly Tyr Gly Thr Val Thr Met Glu Cys Ser
            355                 360                 365

cca aga acg ggc ctc gac ttc aat gag atg gtg ttg ctg caa atg aaa      2054
Pro Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Gln Met Lys
        370                 375                 380

gac aaa gct tgg ctg gtg cac aga caa tgg ttc cta gac cta ccg ttg      2102
Asp Lys Ala Trp Leu Val His Arg Gln Trp Phe Leu Asp Leu Pro Leu
    385                 390                 395

cca tgg ctg ccc gga gca gac aca caa gga tca aat tgg ata cag aaa      2150
Pro Trp Leu Pro Gly Ala Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys
400                 405                 410                 415

gag aca ctg gtc acc ttc aaa aat ccc cat gcg aaa aaa cag gat gtt      2198
Glu Thr Leu Val Thr Phe Lys Asn Pro His Ala Lys Lys Gln Asp Val
                420                 425                 430

gtt gtc tta ggc tcc caa gag ggg gcc atg cat aca gca ctc aca ggg      2246
Val Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly
            435                 440                 445

gct acg gaa atc cag atg tca tca gga aac ctg ctg ttc aca gga cat      2294
Ala Thr Glu Ile Gln Met Ser Ser Gly Asn Leu Leu Phe Thr Gly His
        450                 455                 460

ctt aag tgc agg ctg aga atg gac aaa tta caa ctt aaa ggg atg tca      2342
Leu Lys Cys Arg Leu Arg Met Asp Lys Leu Gln Leu Lys Gly Met Ser
    465                 470                 475

tat gta atg tgc aca ggg tca ttc aag tta gag aag gaa gtg gct gag      2390
Tyr Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu
480                 485                 490                 495

acc cag cat gga act gtt cta gtg cag gtt aaa tac gaa gga aca gat      2438
Thr Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp
                500                 505                 510

gca cca tgc aag atc ccc ttc tcg tcc caa gat gag aag gga gta acc      2486
Ala Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr
            515                 520                 525

cag aat ggg aga ttg ata aca gcc aac ccc ata gtc act gac aaa gaa      2534
Gln Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu
        530                 535                 540

aaa cca gtc aac att gaa gcg gag cca cct ttt ggt gag agc tac att      2582
Lys Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile
    545                 550                 555

gtg gta gga gca ggt gaa aaa gct ttg aaa cta agc tgg ttc aag aag      2630
Val Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys
```

```
560                 565                 570                 575

gga agc agt ata ggg aaa atg ttt gaa gca act gcc cgt gga gca cga      2678
Gly Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg
                580                 585                 590

agg atg gcc atc ctg gga gac act gca tgg gac ttc ggt tct ata gga      2726
Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly
            595                 600                 605

ggg gtg ttc acg tct gtg gga aaa ctg ata cac cag att ttt ggg act      2774
Gly Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr
        610                 615                 620

gcg tat gga gtt ttg ttc agc ggt gtt tct tgg acc atg aag ata gga      2822
Ala Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly
    625                 630                 635

ata ggg att ctg ctg aca tgg cta gga tta aac tca agg agc acg tcc      2870
Ile Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser
640                 645                 650                 655

ctt tca atg acg tgt atc gca gtt ggc atg gtc acg ctg tac cta gga      2918
Leu Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly
                660                 665                 670

gtc atg gtt cag gcg taataaagat ctgctgtgcc ttctagttgc cagccatctg      2973
Val Met Val Gln Ala
            675

ttgtttgccc ctcccccgtg ccttccttga ccctggaagg tgccactccc actgtccttt     3033

cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag gtgtcattct attctggggg     3093

gtggggtggg gcaggacagc aaggggggagg attgggaaga caatagcagg catgctgggg     3153

atgcggtggg ctctatgggt acccaggtgc tgaagaattg acccggttcc tcctgggcca     3213

gaaagaagca ggcacatccc cttctctgtg acacaccctg tccacgcccc tggttcttag     3273

ttccagcccc actcatagga cactcatagc tcaggagggc tccgccttca atcccacccg     3333

ctaaagtact tggagcggtc tctccctccc tcatcagccc accaaaccaa acctagcctc     3393

caagagtggg aagaaattaa agcaagatag gctattaagt gcagagggag agaaaatgcc     3453

tccaacatgt gaggaagtaa tgagagaaat catagaattt taaggccatg atttaaggcc     3513

atcatggcct aagcttgaaa ggagatagga tcaaagcttg gcgtaatcat ggtcatagct     3573

gtttcctgtg tgaaattgtt atccgctcac aattccacac aacatacgag ccggaagcat     3633

aaagtgtaaa gcctggggtg cctaatgagt gagctaactc acattaattg cgttgcgctc     3693

actgcccgct ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa tcggccaacg     3753

cgcggggaga ggcggtttgc gtattgggcg ctcttccgct tcctcgctca ctgactcgct     3813

gcgctcggtc gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg taatacggtt     3873

atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc     3933

caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc cccctgacga     3993

gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata     4053

ccaggcgttt ccccctggaa gctccctcgt gcgctctcct gttccgaccc tgccgcttac     4113
```

cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcata gctcacgctg 4173

taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc 4233

cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggtaag 4293

acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt 4353

aggcggtgct acagagttct tgaagtggtg gcctaactac ggctacacta gaagaacagt 4413

atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg 4473

atccggcaaa caaaccaccg ctggtagcgg tggtttttt gtttgcaagc agcagattac 4533

gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca 4593

gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac 4653

ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac 4713

ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt 4773

tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt 4833

accatctggc cccagtgctg caatgatacc gcgagaacca cgctcaccgg ctccagattt 4893

atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc 4953

cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa 5013

tagtttgcgc aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg 5073

tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt 5133

gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc 5193

agtgttatca ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt 5253

aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg 5313

gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac 5373

tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc 5433

gctgttgaga tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt 5493

tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg 5553

aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag 5613

catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5673

acaaataggg gttccgcgca catttccccg aaaagtgcca cctgacgtct aagaaaccat 5733

tattatcatg acattaacct ataaaaatag gcgtatcacg aggccctttc gggtcgcgcg 5793

tttcggtgat gacggtgaaa acctctgaca catgcagctc ccgttgacgg tcacagcttg 5853

tctgtaagcg gatgccggga gcagacaagc ccgtcagggc gcgtcagcgg gtgttggcgg 5913

gtgtcggggc tggcttaact atgcggcatc agagcagatt gtactgagag tgcaccataa 5973

aattgtaaac gttaatattt tgttaaaatt cgcgttaaat ttttgttaaa tcagctcatt 6033

ttttaaccaa taggccgaaa tcggcaaaat cccttataaa tcaaaagaat agcccgagat 6093

agggttgagt gttgttccag tttggaacaa gagtccacta ttaaagaacg tggactccaa 6153

cgtcaaaggg cgaaaaaccg tctatcaggg cgatggccca ctacgtgaac catcacccaa 6213

atcaagtttt ttggggtcga ggtgccgtaa agcactaaat cggaacccta aagggagccc 6273

ccgatttaga gcttgacggg gaaagccggc gaacgtggcg agaaaggaag ggaagaaagc 6333

gaaaggagcg ggcgctaggg cgctggcaag tgtagcggtc acgctgcgcg taaccaccac 6393

acccgccgcg cttaatgcgc cgctacaggg cgcgtactat ggttgctttg acgtatgcgg 6453

tgtgaaatac cgcacagatg cgtaaggaga aaataccgca tcaggcgcca ttcgccattc 6513

aggctgcgca actgttggga agggcgatcg gtgcgggcct cttcgctatt acgccagctg 6573

gcgaaagggg gatgtgctgc aaggcgatta agttgggtaa cgccagggtt ttcccagtca 6633

cgacgttgta aaacgacggc cagtgaattc catggtctca actttc 6679

<210> 10
<211> 676
<212> PRT
<213> Dengue virus

<400> 10

Met Thr Ala Gly Met Ile Ile Met Leu Ile Pro Thr Val Met Ala Phe
1 5 10 15

His Leu Thr Thr Arg Asn Gly Glu Pro His Met Ile Val Ser Arg Gln
20 25 30

Glu Lys Gly Lys Ser Leu Leu Phe Lys Thr Lys Asp Gly Thr Asn Met
35 40 45

Cys Thr Leu Met Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile
50 55 60

Thr Tyr Lys Cys Pro Phe Leu Lys Gln Asn Glu Pro Glu Asp Ile Asp
65 70 75 80

Cys Trp Cys Asn Ser Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr
85 90 95

Thr Thr Gly Glu His Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro
100 105 110

His Val Gly Met Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser
115 120 125

Glu Gly Ala Trp Lys His Ala Gln Arg Ile Glu Thr Trp Ile Leu Arg
130 135 140

His Pro Gly Phe Thr Ile Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly
145 150 155 160

Thr Thr His Phe Gln Arg Val Leu Ile Phe Ile Leu Leu Thr Ala Ile
165 170 175

```
Ala Pro Ser Met Thr Met Arg Cys Ile Gly Ile Ser Asn Arg Asp Phe
            180                 185                 190

Val Glu Gly Val Ser Gly Gly Ser Trp Val Asp Ile Val Leu Glu His
        195                 200                 205

Gly Ser Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe
    210                 215                 220

Glu Leu Ile Lys Thr Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr
225                 230                 235                 240

Cys Ile Glu Ala Lys Leu Thr Asn Thr Thr Thr Asp Ser Arg Cys Pro
                245                 250                 255

Thr Gln Gly Glu Pro Thr Leu Asn Glu Glu Gln Asp Lys Arg Phe Val
            260                 265                 270

Cys Lys His Ser Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
        275                 280                 285

Ala Gly Lys Gly Gly Ile Val Thr Cys Ala Met Phe Thr Cys Lys Lys
    290                 295                 300

Asn Met Glu Gly Lys Ile Val Gln Pro Glu Asn Leu Glu Tyr Thr Val
305                 310                 315                 320

Val Ile Thr Pro His Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr
                325                 330                 335

Gly Lys His Gly Lys Glu Val Lys Ile Thr Pro Gln Ser Ser Ile Thr
            340                 345                 350

Glu Ala Glu Leu Thr Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro
        355                 360                 365

Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Gln Met Lys Asp
    370                 375                 380

Lys Ala Trp Leu Val His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro
385                 390                 395                 400

Trp Leu Pro Gly Ala Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu
                405                 410                 415

Thr Leu Val Thr Phe Lys Asn Pro His Ala Lys Lys Gln Asp Val Val
            420                 425                 430

Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala
        435                 440                 445
```

```
Thr Glu Ile Gln Met Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu
    450                 455                 460

Lys Cys Arg Leu Arg Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr
465                 470                 475                 480

Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr
                485                 490                 495

Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala
            500                 505                 510

Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln
        515                 520                 525

Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys
    530                 535                 540

Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val
545                 550                 555                 560

Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly
                565                 570                 575

Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg
            580                 585                 590

Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
        595                 600                 605

Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala
    610                 615                 620

Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile
625                 630                 635                 640

Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu
                645                 650                 655

Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val
            660                 665                 670

Met Val Gln Ala
        675
```

<210> 11
<211> 3770
<212> DNA
<213> Dengue virus

<220>
<221> misc_feature
<223> DENV2 capsid R85A K86A mutant

<220>
<221> CDS
<222> (1046)..(1345)

<400> 11
tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60

cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120

ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180

accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240

attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat 300

tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360

tttcccagtc acgacgttgt aaaacgacgg ccagtgaatt gacgcgtttg acattgatta 420

ttgactagtt attaatagta atcaattacg gggtcattag ttcatagccc atatatggag 480

ttccgcgtta cataacttac ggtaaatggc ccgcctggct gaccgcccaa cgacccccgc 540

ccattgacgt caataatgac gtatgttccc atagtaacgc caatagggac tttccattga 600

cgtcaatggg tggagtattt acggtaaact gcccacttgg cagtacatca agtgtatcat 660

atgccaagta cgcccccctat tgacgtcaat gacggtaaat ggcccgcctg gcattatgcc 720

cagtacatga ccttatggga ctttcctact tggcagtaca tctacgtatt agtcatcgct 780

attaccatgg tgatgcggtt ttggcagtac atcaatgggc gtggatagcg gtttgactca 840

cggggatttc caagtctcca ccccattgac gtcaatggga gtttgttttg gcaccaaaat 900

caacgggact ttccaaaatg tcgtaacaac tccgccccat tgacgcaaat gggcggtagg 960

cgtgtacggt gggaggtcta tataagcaga gctcgtttag tgaaccgtca gataactgca 1020

ggtcgacgat atcgcggccg ccacc atg aat gac caa cgg aaa aag gcg aga 1072
Met Asn Asp Gln Arg Lys Lys Ala Arg
1 5

aac acg cct ttc aat atg ctg aaa cgc gag aga aac cgc gtg tca act 1120
Asn Thr Pro Phe Asn Met Leu Lys Arg Glu Arg Asn Arg Val Ser Thr
10 15 20 25

gta caa cag ttg aca aag aga ttc tca ctt gga atg ctg cag gga cga 1168
Val Gln Gln Leu Thr Lys Arg Phe Ser Leu Gly Met Leu Gln Gly Arg
30 35 40

gga cca cta aaa ttg ttc atg gcc ctg gtg gca ttc ctt cgt ttc cta 1216
Gly Pro Leu Lys Leu Phe Met Ala Leu Val Ala Phe Leu Arg Phe Leu
45 50 55

aca atc cca cca aca gca ggg ata tta aaa aga tgg gga aca att aaa 1264
Thr Ile Pro Pro Thr Ala Gly Ile Leu Lys Arg Trp Gly Thr Ile Lys
60 65 70

aaa tca aag gct att aat gtt ctg aga ggc ttc gcg gca gag att gga 1312
Lys Ser Lys Ala Ile Asn Val Leu Arg Gly Phe Ala Ala Glu Ile Gly
75 80 85

agg atg ctg aat atc tta aac agg aga cgt aga taataaagat ctgctgtgcc 1365

Arg Met Leu Asn Ile Leu Asn Arg Arg Arg Arg
90 95 100

ttctagttgc cagccatctg ttgtttgccc ctcccccgtg ccttccttga ccctggaagg 1425

tgccactccc actgtccttt cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag 1485

gtgtcattct attctggggg gtggggtggg gcaggacagc aaggggggagg attgggaaga 1545

caatagcagg catgctgggg atgcggtggg ctctatggct cgagcatggt catagctgtt 1605

tcctgtgtga aattgttatc cgctcacaat tccacacaac atacgagccg gaagcataaa 1665

gtgtaaagcc tggggtgcct aatgagtgag ctaactcaca ttaattgcgt tgcgctcact 1725

gcccgctttc cagtcgggaa acctgtcgtg ccagctgcat taatgaatcg gccaacgcgc 1785

ggggagaggc ggtttgcgta ttgggcgctc ttccgcttcc tcgctcactg actcgctgcg 1845

ctcggtcgtt cggctgcggc gagcggtatc agctcactca aaggcggtaa tacggttatc 1905

cacagaatca ggggataacg caggaaagaa catgtgagca aaaggccagc aaaaggccag 1965

gaaccgtaaa aaggccgcgt tgctggcgtt tttccatagg ctccgccccc ctgacgagca 2025

tcacaaaaat cgacgctcaa gtcagaggtg gcgaaacccg acaggactat aaagatacca 2085

ggcgtttccc cctggaagct ccctcgtgcg ctctcctgtt ccgaccctgc cgcttaccgg 2145

atacctgtcc gcctttctcc cttcgggaag cgtggcgctt tctcatagct cacgctgtag 2205

gtatctcagt tcggtgtagg tcgttcgctc caagctgggc tgtgtgcacg aacccccgt 2265

tcagcccgac cgctgcgcct tatccggtaa ctatcgtctt gagtccaacc cggtaagaca 2325

cgacttatcg ccactggcag cagccactgg taacaggatt agcagagcga ggtatgtagg 2385

cggtgctaca gagttcttga agtggtggcc taactacggc tacactagaa gaacagtatt 2445

tggtatctgc gctctgctga agccagttac cttcggaaaa agagttggta gctcttgatc 2505

cggcaaacaa accaccgctg gtagcggtgg ttttttttgtt tgcaagcagc agattacgcg 2565

cagaaaaaaa ggatctcaag aagatccttt gatcttttct acggggtctg acgctcagtg 2625

gaacgaaaac tcacgttaag ggattttggt catgagatta tcaaaaagga tcttcaccta 2685

gatccttta aattaaaaat gaagttttaa atcaatctaa agtatatatg agtaaacttg 2745

gtctgacagt tagaaaaact catcgagcat caaatgaaac tgcaatttat tcatatcagg 2805

attatcaata ccatattttt gaaaaagccg tttctgtaat gaaggagaaa actcaccgag 2865

gcagttccat aggatggcaa gatcctggta tcggtctgcg attccgactc gtccaacatc 2925

aatacaacct attaatttcc cctcgtcaaa aataaggtta tcaagtgaga aatcaccatg 2985

agtgacgact gaatccggtg agaatggcaa aagtttatgc atttctttcc agacttgttc 3045

aacaggccag ccattacgct cgtcatcaaa atcactcgca tcaaccaaac cgttattcat 3105

tcgtgattgc gcctgagcga gacgaaatac gcgatcgctg ttaaaaggac aattacaaac 3165

aggaatcgaa tgcaaccggc gcaggaacac tgccagcgca tcaacaatat tttcacctga 3225

atcaggatat tcttctaata cctggaatgc tgttttccca gggatcgcag tggtgagtaa 3285

ccatgcatca tcaggagtac ggataaaatg cttgatggtc ggaagaggca taaattccgt 3345

cagccagttt agtctgacca tctcatctgt aacatcattg gcaacgctac ctttgccatg 3405

tttcagaaac aactctggcg catcgggctt cccatacaat cgatagattg tcgcacctga 3465

ttgcccgaca ttatcgcgag cccatttata cccatataaa tcagcatcca tgttggaatt 3525

taatcgcggc ctagagcaag acgtttcccg ttgaatatgg ctcatactct tccttttca 3585

atattattga agcatttatc agggttattg tctcatgagc ggatacatat ttgaatgtat 3645

ttagaaaaat aaacaaatag gggttccgcg cacatttccc cgaaaagtgc cacctgacgt 3705

ctaagaaacc attattatca tgacattaac ctataaaaat aggcgtatca cgaggccctt 3765

tcgtc 3770

<210> 12
<211> 100
<212> PRT
<213> Dengue virus

<400> 12

Met Asn Asp Gln Arg Lys Lys Ala Arg Asn Thr Pro Phe Asn Met Leu
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 Ala Ala Glu Ile Gly Arg Met Leu Asn Ile Leu Asn
85 90 95

Arg Arg Arg Arg
100

<210> 13
<211> 6910
<212> DNA
<213> Dengue virus

<220>
<221> misc_feature
<223> DENV1 prM E (F108A K246M)

<220>
<221> CDS
<222> (1137)..(3164)

<400> 13

```
gaattcccat tgcatacgtt gtatccatat cataatatgt acatttatat tggctcatgt       60

ccaacattac cgccatgttg acattgatta ttgactagtt attaatagta atcaattacg      120

gggtcattag ttcatagccc atatatggag ttccgcgtta cataacttac ggtaaatggc      180

ccgcctggct gaccgcccaa cgacccccgc ccattgacgt caataatgac gtatgttccc      240

atagtaacgc caatagggac tttccattga cgtcaatggg tggagtattt acggtaaact      300

gcccacttgg cagtacatca agtgtatcat atgccaagta cgccccctat tgacgtcaat      360

gacggtaaat ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact      420

tggcagtaca tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac      480

atcaatgggc gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac      540

gtcaatggga gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac      600

tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta tataagcaga      660

gctcgtttag tgaaccgtca gatcgcctgg agacgccatc cacgctgttt tgacctccat      720

agaagacacc gggaccgatc cagcctccat cggctcgcat ctctccttca cgcgcccgcc      780

gccctacctg aggccgccat ccacgccggt tgagtcgcgt tctgccgcct cccgcctgtg      840

gtgcctcctg aactgcgtcc gccgtctagg taagtttaaa gctcaggtcg agaccgggcc      900

tttgtccggc gctcccttgg agcctaccta gactcagccg gctctccacg ctttgcctga      960

ccctgcttgc tcaactctag ttaacggtgg agggcagtgt agtctgagca gtactcgttg     1020

ctgccgcgcg cgccaccaga cataatagct gacagactaa cagactgttc ctttccatgg     1080

gtcttttctg cagtcaccgt cgtcgacacg tgtgatcaga tatcgcggcc gccacc atg     1139
                                                                 Met
                                                                  1

tcg gtg acc atg ctc ctc atg ctg ctg ccc aca gcc ctg gcg ttc cat     1187
Ser Val Thr Met Leu Leu Met Leu Leu Pro Thr Ala Leu Ala Phe His
            5                  10                  15

ctg acc acc cga ggg gga gag ccg cac atg ata gtt agc aag cag gaa     1235
Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val Ser Lys Gln Glu
        20                  25                  30

aga gga aaa tca ctt ttg ttt aag acc tct gca ggt gtc aac atg tgc     1283
Arg Gly Lys Ser Leu Leu Phe Lys Thr Ser Ala Gly Val Asn Met Cys
    35                  40                  45

acc ctt att gca atg gat ttg gga gag tta tgt gag gac aca atg acc     1331
Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Met Thr
50                  55                  60                  65

tac aaa tgc ccc cgg atc act gag acg gaa cca gat gac gtt gac tgt     1379
Tyr Lys Cys Pro Arg Ile Thr Glu Thr Glu Pro Asp Asp Val Asp Cys
                70                  75                  80

tgg tgc aat gcc acg gag aca tgg gtg acc tat gga aca tgt tct caa     1427
Trp Cys Asn Ala Thr Glu Thr Trp Val Thr Tyr Gly Thr Cys Ser Gln
            85                  90                  95

act ggt gaa cac cga cga gac aaa cgt tcc gtc gca ctg gca cca cac     1475
Thr Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala Pro His
        100                 105                 110
```

```
gta ggg ctt ggt cta gaa aca aga acc gaa acg tgg atg tcc tct gaa       1523
Val Gly Leu Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu
    115                 120                 125

ggc gct tgg aaa caa ata caa aaa gtg gag acc tgg gct ctg aga cac       1571
Gly Ala Trp Lys Gln Ile Gln Lys Val Glu Thr Trp Ala Leu Arg His
130                 135                 140                 145

cca gga ttc acg gtg ata gcc ctt ttt cta gca cat gcc ata gga aca       1619
Pro Gly Phe Thr Val Ile Ala Leu Phe Leu Ala His Ala Ile Gly Thr
                150                 155                 160

tcc atc acc cag aaa ggg atc att ttt att ttg ctg atg ctg gta act       1667
Ser Ile Thr Gln Lys Gly Ile Ile Phe Ile Leu Leu Met Leu Val Thr
            165                 170                 175

cca tcc atg gcc atg cgg tgc gtg gga ata ggc aac aga gac ttc gtg       1715
Pro Ser Met Ala Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe Val
        180                 185                 190

gaa gga ctg tca gga gct acg tgg gtg gat gtg gta ctg gag cat gga       1763
Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu His Gly
    195                 200                 205

agt tgc gtc act acc atg gca aaa gac aaa cca aca ctg gac att gaa       1811
Ser Cys Val Thr Thr Met Ala Lys Asp Lys Pro Thr Leu Asp Ile Glu
210                 215                 220                 225

ctc ttg aag acg gag gtc aca aac cct gcc gtc ctg cgc aaa ctg tgc       1859
Leu Leu Lys Thr Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu Cys
                230                 235                 240

att gaa gct aaa ata tca aac acc acc acc gat tcg aga tgt cca aca       1907
Ile Glu Ala Lys Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro Thr
            245                 250                 255

caa gga gaa gcc acg ctg gtg gaa gaa cag gac acg aac ttt gtg tgt       1955
Gln Gly Glu Ala Thr Leu Val Glu Glu Gln Asp Thr Asn Phe Val Cys
        260                 265                 270

cga cga acg ttc gtg gac aga ggc tgg ggc aat ggt tgt ggg cta gcc       2003
Arg Arg Thr Phe Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Ala
    275                 280                 285

gga aaa ggt agc tta ata acg tgt gct aag ttt aag tgt gtg aca aaa       2051
Gly Lys Gly Ser Leu Ile Thr Cys Ala Lys Phe Lys Cys Val Thr Lys
290                 295                 300                 305

ctg gaa gga aag ata gtc caa tat gaa aac tta aaa tat tca gtg ata       2099
Leu Glu Gly Lys Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser Val Ile
                310                 315                 320

gtc acc gta cac act gga gac cag cac caa gtt gga aat gag acc aca       2147
Val Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr Thr
            325                 330                 335

gaa cat gga aca act gca acc ata aca cct caa gct ccc acg tcg gaa       2195
Glu His Gly Thr Thr Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser Glu
        340                 345                 350

ata cag ctg aca gac tac gga gct cta aca ttg gat tgt tca cct aga       2243
Ile Gln Leu Thr Asp Tyr Gly Ala Leu Thr Leu Asp Cys Ser Pro Arg
    355                 360                 365

aca ggg cta gac ttt aat gag atg gtg ttg ttg aca atg gaa aat aaa       2291
Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Thr Met Glu Asn Lys
370                 375                 380                 385
```

```
tca tgg ctc gtc cac aaa caa tgg ttt cta gac tta cca ctg cct tgg        2339
Ser Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp
                390                 395                 400

acc tcg ggg gct tca aca tcc caa gag act tgg aat aga caa gac ttg        2387
Thr Ser Gly Ala Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln Asp Leu
            405                 410                 415

ctg gtc aca ttt aag aca gct cat gca aaa aag cag gaa gta gtc gta        2435
Leu Val Thr Phe Lys Thr Ala His Ala Lys Lys Gln Glu Val Val Val
        420                 425                 430

cta gga tca caa gaa gga gca atg cac act gcg ttg act gga gcg aca        2483
Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr
    435                 440                 445

gaa atc caa acg tct gga acg aca aca att ttt gca gga cac ctg aaa        2531
Glu Ile Gln Thr Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu Lys
450                 455                 460                 465

tgc aga cta aaa atg gat aaa ctg act tta aaa ggg atg tca tat gta        2579
Cys Arg Leu Lys Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr Val
                470                 475                 480

atg tgc aca ggg tca ttc aag tta gag aag gaa gtg gct gag acc cag        2627
Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr Gln
            485                 490                 495

cat gga act gtt cta gtg cag gtt aaa tac gaa gga aca gat gca cca        2675
His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala Pro
        500                 505                 510

tgc aag atc ccc ttc tcg tcc caa gat gag aag gga gta acc cag aat        2723
Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln Asn
    515                 520                 525

ggg aga ttg ata aca gcc aac ccc ata gtc act gac aaa gaa aaa cca        2771
Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys Pro
530                 535                 540                 545

gtc aac att gaa gcg gag cca cct ttt ggt gag agc tac att gtg gta        2819
Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val Val
                550                 555                 560

gga gca ggt gaa aaa gct ttg aaa cta agc tgg ttc aag aag gga agc        2867
Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly Ser
            565                 570                 575

agt ata ggg aaa atg ttt gaa gca act gcc cgt gga gca cga agg atg        2915
Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg Met
        580                 585                 590

gcc atc ctg gga gac act gca tgg gac ttc ggt tct ata gga ggg gtg        2963
Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val
    595                 600                 605

ttc acg tct gtg gga aaa ctg ata cac cag att ttt ggg act gcg tat        3011
Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala Tyr
610                 615                 620                 625

gga gtt ttg ttc agc ggt gtt tct tgg acc atg aag ata gga ata ggg        3059
Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile Gly
                630                 635                 640

att ctg ctg aca tgg cta gga tta aac tca agg agc acg tcc ctt tca        3107
Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu Ser
            645                 650                 655
```

atg acg tgt atc gca gtt ggc atg gtc acg ctg tac cta gga gtc atg 3155
Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val Met
660 665 670

gtt cag gcg taataaagat ctgctgtgcc ttctagttgc cagccatctg 3204
Val Gln Ala
675

ttgtttgccc ctcccccgtg ccttccttga ccctggaagg tgccactccc actgtccttt 3264

cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag gtgtcattct attctggggg 3324

gtggggtggg gcaggacagc aagggggagg attgggaaga caatagcagg catgctgggg 3384

atgcggtggg ctctatgggt acccaggtgc tgaagaattg acccggttcc tcctgggcca 3444

gaaagaagca ggcacatccc cttctctgtg acacaccctg tccacgcccc tggttcttag 3504

ttccagcccc actcatagga cactcatagc tcaggagggc tccgccttca atcccacccg 3564

ctaaagtact tggagcggtc tctccctccc tcatcagccc accaaaccaa acctagcctc 3624

caagagtggg aagaaattaa agcaagatag gctattaagt gcagagggag agaaaatgcc 3684

tccaacatgt gaggaagtaa tgagagaaat catagaattt taaggccatg atttaaggcc 3744

atcatggcct aagcttgaaa ggagatagga tcaaagcttg gcgtaatcat ggtcatagct 3804

gtttcctgtg tgaaattgtt atccgctcac aattccacac aacatacgag ccggaagcat 3864

aaagtgtaaa gcctggggtg cctaatgagt gagctaactc acattaattg cgttgcgctc 3924

actgcccgct ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa tcggccaacg 3984

cgcggggaga ggcggtttgc gtattgggcg ctcttccgct tcctcgctca ctgactcgct 4044

gcgctcggtc gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg taatacggtt 4104

atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc 4164

caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc cccctgacga 4224

gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata 4284

ccaggcgttt cccccctggaa gctccctcgt gcgctctcct gttccgaccc tgccgcttac 4344

cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcata gctcacgctg 4404

taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc 4464

cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggtaag 4524

acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt 4584

aggcggtgct acagagttct tgaagtggtg gcctaactac ggctacacta gaagaacagt 4644

atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg 4704

atccggcaaa caaaccaccg ctggtagcgg tggttttttt gtttgcaagc agcagattac 4764

gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca 4824

gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac 4884

ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac 4944

ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt 5004

tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt 5064

accatctggc cccagtgctg caatgatacc gcgagaacca cgctcaccgg ctccagattt 5124

atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc 5184

cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa 5244

tagtttgcgc aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg 5304

tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt 5364

gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc 5424

agtgttatca ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt 5484

aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg 5544

gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac 5604

tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc 5664

gctgttgaga tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt 5724

tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg 5784

aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag 5844

catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5904

acaaataggg gttccgcgca catttccccg aaaagtgcca cctgacgtct aagaaaccat 5964

tattatcatg acattaacct ataaaaatag gcgtatcacg aggccctttc gggtcgcgcg 6024

tttcggtgat gacggtgaaa acctctgaca catgcagctc ccgttgacgg tcacagcttg 6084

tctgtaagcg gatgccggga gcagacaagc ccgtcagggc gcgtcagcgg gtgttggcgg 6144

gtgtcggggc tggcttaact atgcggcatc agagcagatt gtactgagag tgcaccataa 6204

aattgtaaac gttaatattt tgttaaaatt cgcgttaaat ttttgttaaa tcagctcatt 6264

ttttaaccaa taggccgaaa tcggcaaaat cccttataaa tcaaaagaat agcccgagat 6324

agggttgagt gttgttccag tttggaacaa gagtccacta ttaaagaacg tggactccaa 6384

cgtcaaaggg cgaaaaaccg tctatcaggg cgatggccca ctacgtgaac catcacccaa 6444

atcaagtttt ttggggtcga ggtgccgtaa agcactaaat cggaacccta aagggagccc 6504

ccgatttaga gcttgacggg gaaagccggc gaacgtggcg agaaaggaag ggaagaaagc 6564

gaaaggagcg ggcgctaggg cgctggcaag tgtagcggtc acgctgcgcg taaccaccac 6624

acccgccgcg cttaatgcgc cgctacaggg cgcgtactat ggttgctttg acgtatgcgg 6684

tgtgaaatac cgcacagatg cgtaaggaga aaataccgca tcaggcgcca ttcgccattc 6744

aggctgcgca actgttggga agggcgatcg gtgcgggcct cttcgctatt acgccagctg 6804

gcgaaagggg gatgtgctgc aaggcgatta agttgggtaa cgccagggtt ttcccagtca 6864

cgacgttgta aaacgacggc cagtgaattc catggtctca actttc 6910

<210> 14
<211> 676
<212> PRT

<213> Dengue virus

<400> 14

```
Met Ser Val Thr Met Leu Leu Met Leu Leu Pro Thr Ala Leu Ala Phe
1               5                  10                  15

His Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val Ser Lys Gln
            20                  25                  30

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

Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Met
    50                  55                  60

Thr Tyr Lys Cys Pro Arg Ile Thr Glu Thr Glu Pro Asp Asp Val Asp
65                  70                  75                  80

Cys Trp Cys Asn Ala Thr Glu Thr Trp Val Thr Tyr Gly Thr Cys Ser
                85                  90                  95

Gln Thr Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala Pro
            100                 105                 110

His Val Gly Leu Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser
        115                 120                 125

Glu Gly Ala Trp Lys Gln Ile Gln Lys Val Glu Thr Trp Ala Leu Arg
    130                 135                 140

His Pro Gly Phe Thr Val Ile Ala Leu Phe Leu Ala His Ala Ile Gly
145                 150                 155                 160

Thr Ser Ile Thr Gln Lys Gly Ile Ile Phe Ile Leu Leu Met Leu Val
                165                 170                 175

Thr Pro Ser Met Ala Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe
            180                 185                 190

Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu His
        195                 200                 205

Gly Ser Cys Val Thr Thr Met Ala Lys Asp Lys Pro Thr Leu Asp Ile
    210                 215                 220

Glu Leu Leu Lys Thr Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu
225                 230                 235                 240

Cys Ile Glu Ala Lys Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro
                245                 250                 255
```

```
Thr Gln Gly Glu Ala Thr Leu Val Glu Glu Gln Asp Thr Asn Phe Val
            260                 265                 270

Cys Arg Arg Thr Phe Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
        275                 280                 285

Ala Gly Lys Gly Ser Leu Ile Thr Cys Ala Lys Phe Lys Cys Val Thr
    290                 295                 300

Lys Leu Glu Gly Lys Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser Val
305                 310                 315                 320

Ile Val Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr
                325                 330                 335

Thr Glu His Gly Thr Thr Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser
            340                 345                 350

Glu Ile Gln Leu Thr Asp Tyr Gly Ala Leu Thr Leu Asp Cys Ser Pro
        355                 360                 365

Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Thr Met Glu Asn
    370                 375                 380

Lys Ser Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro
385                 390                 395                 400

Trp Thr Ser Gly Ala Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln Asp
                405                 410                 415

Leu Leu Val Thr Phe Lys Thr Ala His Ala Lys Lys Gln Glu Val Val
            420                 425                 430

Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala
        435                 440                 445

Thr Glu Ile Gln Thr Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu
    450                 455                 460

Lys Cys Arg Leu Lys Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr
465                 470                 475                 480

Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr
                485                 490                 495

Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala
            500                 505                 510

Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln
        515                 520                 525
```

Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys
530 535 540

Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val
545 550 555 560

Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly
565 570 575

Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg
580 585 590

Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
595 600 605

Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala
610 615 620

Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile
625 630 635 640

Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu
645 650 655

Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val
660 665 670

Met Val Gln Ala
675

<210> 15
<211> 6910
<212> DNA
<213> Dengue virus

<220>
<221> misc_feature
<223> DENV1 prM E (F108A K203N) VLP D01

<220>
<221> CDS
<222> (1137)..(3164)

<400> 15
gaattcccat tgcatacgtt gtatccatat cataatatgt acatttatat tggctcatgt 60

ccaacattac cgccatgttg acattgatta ttgactagtt attaatagta atcaattacg 120

gggtcattag ttcatagccc atatatggag ttccgcgtta cataacttac ggtaaatggc 180

ccgcctggct gaccgcccaa cgacccccgc ccattgacgt caataatgac gtatgttccc 240

atagtaacgc caatagggac tttccattga cgtcaatggg tggagtattt acggtaaact 300

gcccacttgg cagtacatca agtgtatcat atgccaagta cgcccccctat tgacgtcaat 360

gacggtaaat ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact 420

```
tggcagtaca tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac      480

atcaatgggc gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac      540

gtcaatggga gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac      600

tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta tataagcaga      660

gctcgtttag tgaaccgtca gatcgcctgg agacgccatc cacgctgttt tgacctccat      720

agaagacacc gggaccgatc cagcctccat cggctcgcat ctctccttca cgcgcccgcc      780

gccctacctg aggccgccat ccacgccggt tgagtcgcgt tctgccgcct cccgcctgtg      840

gtgcctcctg aactgcgtcc gccgtctagg taagtttaaa gctcaggtcg agaccgggcc      900

tttgtccggc gctcccttgg agcctaccta gactcagccg gctctccacg ctttgcctga      960

ccctgcttgc tcaactctag ttaacggtgg agggcagtgt agtctgagca gtactcgttg     1020

ctgccgcgcg cgccaccaga cataatagct gacagactaa cagactgttc ctttccatgg     1080

gtcttttctg cagtcaccgt cgtcgacacg tgtgatcaga tatcgcggcc gccacc atg     1139
                                                              Met
                                                               1

tcg gtg acc atg ctc ctc atg ctg ctg ccc aca gcc ctg gcg ttc cat      1187
Ser Val Thr Met Leu Leu Met Leu Leu Pro Thr Ala Leu Ala Phe His
            5                  10                  15

ctg acc acc cga ggg gga gag ccg cac atg ata gtt agc aag cag gaa      1235
Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val Ser Lys Gln Glu
        20                  25                  30

aga gga aaa tca ctt ttg ttt aag acc tct gca ggt gtc aac atg tgc      1283
Arg Gly Lys Ser Leu Leu Phe Lys Thr Ser Ala Gly Val Asn Met Cys
    35                  40                  45

acc ctt att gca atg gat ttg gga gag tta tgt gag gac aca atg acc      1331
Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Met Thr
50                  55                  60                  65

tac aaa tgc ccc cgg atc act gag acg gaa cca gat gac gtt gac tgt      1379
Tyr Lys Cys Pro Arg Ile Thr Glu Thr Glu Pro Asp Asp Val Asp Cys
                70                  75                  80

tgg tgc aat gcc acg gag aca tgg gtg acc tat gga aca tgt tct caa      1427
Trp Cys Asn Ala Thr Glu Thr Trp Val Thr Tyr Gly Thr Cys Ser Gln
            85                  90                  95

act ggt gaa cac cga cga gac aaa cgt tcc gtc gca ctg gca cca cac      1475
Thr Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala Pro His
        100                 105                 110

gta ggg ctt ggt cta gaa aca aga acc gaa acg tgg atg tcc tct gaa      1523
Val Gly Leu Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu
    115                 120                 125

ggc gct tgg aaa caa ata caa aaa gtg gag acc tgg gct ctg aga cac      1571
Gly Ala Trp Lys Gln Ile Gln Lys Val Glu Thr Trp Ala Leu Arg His
130                 135                 140                 145

cca gga ttc acg gtg ata gcc ctt ttt cta gca cat gcc ata gga aca      1619
Pro Gly Phe Thr Val Ile Ala Leu Phe Leu Ala His Ala Ile Gly Thr
                150                 155                 160

tcc atc acc cag aaa ggg atc att ttt att ttg ctg atg ctg gta act      1667
```

```
Ser Ile Thr Gln Lys Gly Ile Ile Phe Ile Leu Leu Met Leu Val Thr
            165                 170                 175

cca tcc atg gcc atg cgg tgc gtg gga ata ggc aac aga gac ttc gtg       1715
Pro Ser Met Ala Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe Val
        180                 185                 190

gaa gga ctg tca gga gct acg tgg gtg gat gtg gta ctg gag cat gga       1763
Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu His Gly
    195                 200                 205

agt tgc gtc act acc atg gca aaa gac aaa cca aca ctg gac att gaa       1811
Ser Cys Val Thr Thr Met Ala Lys Asp Lys Pro Thr Leu Asp Ile Glu
210                 215                 220                 225

ctc ttg aag acg gag gtc aca aac cct gcc gtc ctg cgc aaa ctg tgc       1859
Leu Leu Lys Thr Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu Cys
                230                 235                 240

att gaa gct aaa ata tca aac acc acc acc gat tcg aga tgt cca aca       1907
Ile Glu Ala Lys Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro Thr
            245                 250                 255

caa gga gaa gcc acg ctg gtg gaa gaa cag gac acg aac ttt gtg tgt       1955
Gln Gly Glu Ala Thr Leu Val Glu Glu Gln Asp Thr Asn Phe Val Cys
        260                 265                 270

cga cga acg ttc gtg gac aga ggc tgg ggc aat ggt tgt ggg cta gcc       2003
Arg Arg Thr Phe Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Ala
    275                 280                 285

gga aaa ggt agc tta ata acg tgt gct aag ttt aag tgt gtg aca aaa       2051
Gly Lys Gly Ser Leu Ile Thr Cys Ala Lys Phe Lys Cys Val Thr Lys
290                 295                 300                 305

ctg gaa gga aag ata gtc caa tat gaa aac tta aaa tat tca gtg ata       2099
Leu Glu Gly Lys Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser Val Ile
                310                 315                 320

gtc acc gta cac act gga gac cag cac caa gtt gga aat gag acc aca       2147
Val Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr Thr
            325                 330                 335

gaa cat gga aca act gca acc ata aca cct caa gct ccc acg tcg gaa       2195
Glu His Gly Thr Thr Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser Glu
        340                 345                 350

ata cag ctg aca gac tac gga gct cta aca ttg gat tgt tca cct aga       2243
Ile Gln Leu Thr Asp Tyr Gly Ala Leu Thr Leu Asp Cys Ser Pro Arg
    355                 360                 365

aca ggg cta gac ttt aat gag atg gtg ttg ttg aca atg gaa aaa aaa       2291
Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Thr Met Glu Lys Lys
370                 375                 380                 385

tca tgg ctc gtc cac aaa caa tgg ttt cta gac tta cca ctg cct tgg       2339
Ser Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp
                390                 395                 400

acc tcg ggg gct tca aca tcc caa gag act tgg aat aga caa gac ttg       2387
Thr Ser Gly Ala Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln Asp Leu
            405                 410                 415

ctg gtc aca ttt aag aca gct cat gca atg aag cag gaa gta gtc gta       2435
Leu Val Thr Phe Lys Thr Ala His Ala Met Lys Gln Glu Val Val Val
        420                 425                 430

cta gga tca caa gaa gga gca atg cac act gcg ttg act gga gcg aca       2483
```

```
Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr
    435                 440                 445

gaa atc caa acg tct gga acg aca aca att ttt gca gga cac ctg aaa      2531
Glu Ile Gln Thr Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu Lys
450                 455                 460                 465

tgc aga cta aaa atg gat aaa ctg act tta aaa ggg atg tca tat gta      2579
Cys Arg Leu Lys Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr Val
                470                 475                 480

atg tgc aca ggg tca ttc aag tta gag aag gaa gtg gct gag acc cag      2627
Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr Gln
            485                 490                 495

cat gga act gtt cta gtg cag gtt aaa tac gaa gga aca gat gca cca      2675
His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala Pro
        500                 505                 510

tgc aag atc ccc ttc tcg tcc caa gat gag aag gga gta acc cag aat      2723
Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln Asn
    515                 520                 525

ggg aga ttg ata aca gcc aac ccc ata gtc act gac aaa gaa aaa cca      2771
Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys Pro
530                 535                 540                 545

gtc aac att gaa gcg gag cca cct ttt ggt gag agc tac att gtg gta      2819
Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val Val
                550                 555                 560

gga gca ggt gaa aaa gct ttg aaa cta agc tgg ttc aag aag gga agc      2867
Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly Ser
            565                 570                 575

agt ata ggg aaa atg ttt gaa gca act gcc cgt gga gca cga agg atg      2915
Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg Met
        580                 585                 590

gcc atc ctg gga gac act gca tgg gac ttc ggt tct ata gga ggg gtg      2963
Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val
    595                 600                 605

ttc acg tct gtg gga aaa ctg ata cac cag att ttt ggg act gcg tat      3011
Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala Tyr
610                 615                 620                 625

gga gtt ttg ttc agc ggt gtt tct tgg acc atg aag ata gga ata ggg      3059
Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile Gly
                630                 635                 640

att ctg ctg aca tgg cta gga tta aac tca agg agc acg tcc ctt tca      3107
Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu Ser
            645                 650                 655

atg acg tgt atc gca gtt ggc atg gtc acg ctg tac cta gga gtc atg      3155
Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val Met
        660                 665                 670

gtt cag gcg taataaagat ctgctgtgcc ttctagttgc agccatctg              3204
Val Gln Ala
    675

ttgtttgccc ctcccccgtg ccttccttga ccctggaagg tgccactccc actgtccttt    3264

cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag gtgtcattct attctggggg    3324

gtggggtggg gcaggacagc aaggggggagg attgggaaga caatagcagg catgctgggg   3384
```

atgcggtggg ctctatgggt acccaggtgc tgaagaattg acccggttcc tcctgggcca 3444
gaaagaagca ggcacatccc cttctctgtg acacaccctg tccacgcccc tggttcttag 3504
ttccagcccc actcatagga cactcatagc tcaggagggc tccgccttca atcccacccg 3564
ctaaagtact tggagcggtc tctccctccc tcatcagccc accaaaccaa acctagcctc 3624
caagagtggg aagaaattaa agcaagatag gctattaagt gcagagggag agaaaatgcc 3684
tccaacatgt gaggaagtaa tgagagaaat catagaattt taaggccatg atttaaggcc 3744
atcatggcct aagcttgaaa ggagatagga tcaaagcttg gcgtaatcat ggtcatagct 3804
gtttcctgtg tgaaattgtt atccgctcac aattccacac aacatacgag ccggaagcat 3864
aaagtgtaaa gcctggggtg cctaatgagt gagctaactc acattaattg cgttgcgctc 3924
actgcccgct ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa tcggccaacg 3984
cgcggggaga ggcggtttgc gtattgggcg ctcttccgct tcctcgctca ctgactcgct 4044
gcgctcggtc gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg taatacggtt 4104
atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc 4164
caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc cccctgacga 4224
gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata 4284
ccaggcgttt ccccctggaa gctccctcgt gcgctctcct gttccgaccc tgccgcttac 4344
cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcata gctcacgctg 4404
taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc 4464
cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggtaag 4524
acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt 4584
aggcggtgct acagagttct tgaagtggtg gcctaactac ggctacacta gaagaacagt 4644
atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg 4704
atccggcaaa caaaccaccg ctggtagcgg tggttttttt gtttgcaagc agcagattac 4764
gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca 4824
gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac 4884
ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac 4944
ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt 5004
tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt 5064
accatctggc cccagtgctg caatgatacc gcgagaacca cgctcaccgg ctccagattt 5124
atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc 5184
cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa 5244
tagtttgcgc aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg 5304
tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt 5364
gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc 5424

agtgttatca ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt 5484

aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg 5544

gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac 5604

tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc 5664

gctgttgaga tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt 5724

tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg 5784

aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag 5844

catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5904

acaaataggg gttccgcgca catttccccg aaaagtgcca cctgacgtct aagaaaccat 5964

tattatcatg acattaacct ataaaaatag gcgtatcacg aggccctttc gggtcgcgcg 6024

tttcggtgat gacggtgaaa acctctgaca catgcagctc ccgttgacgg tcacagcttg 6084

tctgtaagcg gatgccggga gcagacaagc ccgtcagggc gcgtcagcgg gtgttggcgg 6144

gtgtcggggc tggcttaact atgcggcatc agagcagatt gtactgagag tgcaccataa 6204

aattgtaaac gttaatattt tgttaaaatt cgcgttaaat ttttgttaaa tcagctcatt 6264

ttttaaccaa taggccgaaa tcggcaaaat cccttataaa tcaaaagaat agcccgagat 6324

agggttgagt gttgttccag tttggaacaa gagtccacta ttaaagaacg tggactccaa 6384

cgtcaaaggg cgaaaaaccg tctatcaggg cgatggccca ctacgtgaac catcacccaa 6444

atcaagtttt ttggggtcga ggtgccgtaa agcactaaat cggaacccta aagggagccc 6504

ccgatttaga gcttgacggg gaaagccggc gaacgtggcg agaaaggaag ggaagaaagc 6564

gaaaggagcg ggcgctaggg cgctggcaag tgtagcggtc acgctgcgcg taaccaccac 6624

acccgccgcg cttaatgcgc cgctacaggg cgcgtactat ggttgctttg acgtatgcgg 6684

tgtgaaatac cgcacagatg cgtaaggaga aaataccgca tcaggcgcca ttcgccattc 6744

aggctgcgca actgttggga agggcgatcg gtgcgggcct cttcgctatt acgccagctg 6804

gcgaaagggg gatgtgctgc aaggcgatta agttgggtaa cgccagggtt ttcccagtca 6864

cgacgttgta aaacgacggc cagtgaattc catggtctca actttc 6910

<210> 16
<211> 676
<212> PRT
<213> Dengue virus

<400> 16

Met Ser Val Thr Met Leu Leu Met Leu Leu Pro Thr Ala Leu Ala Phe
1 5 10 15

His Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val Ser Lys Gln
20 25 30

Glu Arg Gly Lys Ser Leu Leu Phe Lys Thr Ser Ala Gly Val Asn Met

35 40 45

Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Met
50 55 60

Thr Tyr Lys Cys Pro Arg Ile Thr Glu Thr Glu Pro Asp Asp Val Asp
65 70 75 80

Cys Trp Cys Asn Ala Thr Glu Thr Trp Val Thr Tyr Gly Thr Cys Ser
85 90 95

Gln Thr Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala Pro
100 105 110

His Val Gly Leu Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser
115 120 125

Glu Gly Ala Trp Lys Gln Ile Gln Lys Val Glu Thr Trp Ala Leu Arg
130 135 140

His Pro Gly Phe Thr Val Ile Ala Leu Phe Leu Ala His Ala Ile Gly
145 150 155 160

Thr Ser Ile Thr Gln Lys Gly Ile Ile Phe Ile Leu Leu Met Leu Val
165 170 175

Thr Pro Ser Met Ala Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe
180 185 190

Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu His
195 200 205

Gly Ser Cys Val Thr Thr Met Ala Lys Asp Lys Pro Thr Leu Asp Ile
210 215 220

Glu Leu Leu Lys Thr Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu
225 230 235 240

Cys Ile Glu Ala Lys Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro
245 250 255

Thr Gln Gly Glu Ala Thr Leu Val Glu Glu Gln Asp Thr Asn Phe Val
260 265 270

Cys Arg Arg Thr Phe Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
275 280 285

Ala Gly Lys Gly Ser Leu Ile Thr Cys Ala Lys Phe Lys Cys Val Thr
290 295 300

Lys Leu Glu Gly Lys Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser Val

305 310 315 320

Ile Val Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr
325 330 335

Thr Glu His Gly Thr Thr Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser
340 345 350

Glu Ile Gln Leu Thr Asp Tyr Gly Ala Leu Thr Leu Asp Cys Ser Pro
355 360 365

Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Thr Met Glu Lys
370 375 380

Lys Ser Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro
385 390 395 400

Trp Thr Ser Gly Ala Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln Asp
405 410 415

Leu Leu Val Thr Phe Lys Thr Ala His Ala Met Lys Gln Glu Val Val
420 425 430

Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala
435 440 445

Thr Glu Ile Gln Thr Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu
450 455 460

Lys Cys Arg Leu Lys Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr
465 470 475 480

Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr
485 490 495

Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala
500 505 510

Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln
515 520 525

Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys
530 535 540

Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val
545 550 555 560

Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly
565 570 575

Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg

580 585 590

Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
595 600 605

Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala
610 615 620

Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile
625 630 635 640

Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu
645 650 655

Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val
660 665 670

Met Val Gln Ala
675

<210> 17
<211> 14
<212> PRT
<213> Dengue virus

<220>
<221> SIGNAL
<222> (1)..(14)

<400> 17

Ser Val Thr Met Leu Leu Met Leu Leu Pro Thr Ala Leu Ala
1 5 10

<210> 18
<211> 91
<212> PRT
<213> Dengue virus

<220>
<221> misc_feature
<222> (1)..(91)
<223> pr sequence

<220>
<221> misc_feature
<222> (1)..(91)
<223> DENV1 pr sequence

<400> 18

Phe His Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val Ser Lys
1 5 10 15

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

```
Met Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr
        35                  40                  45

Met Thr Tyr Lys Cys Pro Arg Ile Thr Glu Thr Glu Pro Asp Asp Val
    50                  55                  60

Asp Cys Trp Cys Asn Ala Thr Glu Thr Trp Val Thr Tyr Gly Thr Cys
65                  70                  75                  80

Ser Gln Thr Gly Glu His Arg Arg Asp Lys Arg
                85                  90
```

<210> 19
<211> 75
<212> PRT
<213> Dengue virus

<220>
<221> MISC_FEATURE
<222> (1)..(75)
<223> M sequence

<220>
<221> MISC_FEATURE
<222> (1)..(75)
<223> DENV1 M sequence

<400> 19

```
Ser Val Ala Leu Ala Pro His Val Gly Leu Gly Leu Glu Thr Arg Thr
1               5                   10                  15

Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys Gln Ile Gln Lys Val
            20                  25                  30

Glu Thr Trp Ala Leu Arg His Pro Gly Phe Thr Val Ile Ala Leu Phe
        35                  40                  45

Leu Ala His Ala Ile Gly Thr Ser Ile Thr Gln Lys Gly Ile Ile Phe
    50                  55                  60

Ile Leu Leu Met Leu Val Thr Pro Ser Met Ala
65                  70                  75
```

<210> 20
<211> 495
<212> PRT
<213> Dengue virus

<220>
<221> MISC_FEATURE
<222> (1)..(495)
<223> DENV1 Envelope sequence

<400> 20

```
Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe Val Glu Gly Leu Ser
1               5                  10                  15

Gly Ala Thr Trp Val Asp Val Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30

Thr Met Ala Lys Asp Lys Pro Thr Leu Asp Ile Glu Leu Leu Lys Thr
        35                  40                  45

Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu Cys Ile Glu Ala Lys
    50                  55                  60

Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65                  70                  75                  80

Thr Leu Val Glu Glu Gln Asp Thr Asn Phe Val Cys Arg Arg Thr Phe
                85                  90                  95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
            100                 105                 110

Leu Ile Thr Cys Ala Lys Phe Lys Cys Val Thr Lys Leu Glu Gly Lys
        115                 120                 125

Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser Val Ile Val Thr Val His
    130                 135                 140

Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr Thr Glu His Gly Thr
145                 150                 155                 160

Thr Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser Glu Ile Gln Leu Thr
                165                 170                 175

Asp Tyr Gly Ala Leu Thr Leu Asp Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

Phe Asn Glu Met Val Leu Leu Thr Met Glu Lys Lys Ser Trp Leu Val
        195                 200                 205

His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Thr Ser Gly Ala
    210                 215                 220

Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln Asp Leu Leu Val Thr Phe
225                 230                 235                 240

Lys Thr Ala His Ala Lys Lys Gln Glu Val Val Val Leu Gly Ser Gln
                245                 250                 255

Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Thr
            260                 265                 270
```

```
Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu Lys Cys Arg Leu Lys
        275                 280                 285

Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr Val Met Cys Thr Gly
    290                 295                 300

Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr Gln His Gly Thr Val
305                 310                 315                 320

Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala Pro Cys Lys Ile Pro
                325                 330                 335

Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln Asn Gly Arg Leu Ile
            340                 345                 350

Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys Pro Val Asn Ile Glu
        355                 360                 365

Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val Val Gly Ala Gly Glu
    370                 375                 380

Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly Ser Ser Ile Gly Lys
385                 390                 395                 400

Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg Met Ala Ile Leu Gly
                405                 410                 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Thr Ser Val
            420                 425                 430

Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala Tyr Gly Val Leu Phe
        435                 440                 445

Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile Gly Ile Leu Leu Thr
    450                 455                 460

Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu Ser Met Thr Cys Ile
465                 470                 475                 480

Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
                485                 490                 495


<210>  21
<211>  676
<212>  PRT
<213>  Dengue virus


<220>
<221>  INIT_MET
<222>  (1)..(1)

<220>
<221>  SIGNAL
```

<222> (2)..(15)

<220>
<221> MISC_FEATURE
<222> (16)..(106)

<220>
<221> MISC_FEATURE
<222> (107)..(181)
<223> DENV1 M sequence

<220>
<221> MISC_FEATURE
<222> (182)..(676)
<223> DENV1 Envelope sequence

<400> 21

```
Met Ser Val Thr Met Leu Leu Met Leu Leu Pro Thr Ala Leu Ala Phe
1               5                  10                  15

His Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val Ser Lys Gln
            20                  25                  30

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

Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Met
    50                  55                  60

Thr Tyr Lys Cys Pro Arg Ile Thr Glu Thr Glu Pro Asp Asp Val Asp
65                  70                  75                  80

Cys Trp Cys Asn Ala Thr Glu Thr Trp Val Thr Tyr Gly Thr Cys Ser
                85                  90                  95

Gln Thr Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala Pro
            100                 105                 110

His Val Gly Leu Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser
        115                 120                 125

Glu Gly Ala Trp Lys Gln Ile Gln Lys Val Glu Thr Trp Ala Leu Arg
    130                 135                 140

His Pro Gly Phe Thr Val Ile Ala Leu Phe Leu Ala His Ala Ile Gly
145                 150                 155                 160

Thr Ser Ile Thr Gln Lys Gly Ile Ile Phe Ile Leu Leu Met Leu Val
                165                 170                 175

Thr Pro Ser Met Ala Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe
            180                 185                 190

Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu His
        195                 200                 205
```

```
Gly Ser Cys Val Thr Thr Met Ala Lys Asp Lys Pro Thr Leu Asp Ile
    210                 215                 220

Glu Leu Leu Lys Thr Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu
225                 230                 235                 240

Cys Ile Glu Ala Lys Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro
                245                 250                 255

Thr Gln Gly Glu Ala Thr Leu Val Glu Glu Gln Asp Thr Asn Phe Val
            260                 265                 270

Cys Arg Arg Thr Phe Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
        275                 280                 285

Phe Gly Lys Gly Ser Leu Ile Thr Cys Ala Lys Phe Lys Cys Val Thr
    290                 295                 300

Lys Leu Glu Gly Lys Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser Val
305                 310                 315                 320

Ile Val Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr
                325                 330                 335

Thr Glu His Gly Thr Thr Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser
            340                 345                 350

Glu Ile Gln Leu Thr Asp Tyr Gly Ala Leu Thr Leu Asp Cys Ser Pro
        355                 360                 365

Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Thr Met Glu Lys
    370                 375                 380

Lys Ser Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro
385                 390                 395                 400

Trp Thr Ser Gly Ala Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln Asp
                405                 410                 415

Leu Leu Val Thr Phe Lys Thr Ala His Ala Lys Lys Gln Glu Val Val
            420                 425                 430

Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala
        435                 440                 445

Thr Glu Ile Gln Thr Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu
    450                 455                 460

Lys Cys Arg Leu Lys Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr
465                 470                 475                 480
```

```
Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr
                485                 490                 495

Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala
            500                 505                 510

Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln
        515                 520                 525

Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys
    530                 535                 540

Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val
545                 550                 555                 560

Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly
                565                 570                 575

Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg
            580                 585                 590

Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
        595                 600                 605

Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala
    610                 615                 620

Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile
625                 630                 635                 640

Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu
                645                 650                 655

Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val
            660                 665                 670

Met Val Gln Ala
        675
```

<210> 22
<211> 676
<212> PRT
<213> Dengue virus

<220>
<221> MISC_FEATURE
<223> DEN2 prM E (F108A)_3' DEN1

<220>
<221> MISC_FEATURE
<222> (182)..(477)
<223> DEN2 prM E (F108A)

<220>
<221> MISC_FEATURE
<222> (182)..(477)
<223> DEV2 prM E (F108A)

<220>
<221> MISC_FEATURE
<222> (478)..(676)
<223> 3' DEV1

<400> 22

```
Met Thr Ala Gly Met Ile Ile Met Leu Ile Pro Thr Val Met Ala Phe
1               5                  10                  15

His Leu Thr Thr Arg Asn Gly Glu Pro His Met Ile Val Ser Arg Gln
            20                  25                  30

Glu Lys Gly Lys Ser Leu Leu Phe Lys Thr Lys Asp Gly Thr Asn Met
        35                  40                  45

Cys Thr Leu Met Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile
    50                  55                  60

Thr Tyr Lys Cys Pro Phe Leu Lys Gln Asn Glu Pro Glu Asp Ile Asp
65                  70                  75                  80

Cys Trp Cys Asn Ser Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr
                85                  90                  95

Thr Thr Gly Glu His Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro
            100                 105                 110

His Val Gly Met Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser
        115                 120                 125

Glu Gly Ala Trp Lys His Ala Gln Arg Ile Glu Thr Trp Ile Leu Arg
    130                 135                 140

His Pro Gly Phe Thr Ile Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly
145                 150                 155                 160

Thr Thr His Phe Gln Arg Val Leu Ile Phe Ile Leu Leu Thr Ala Ile
                165                 170                 175

Ala Pro Ser Met Thr Met Arg Cys Ile Gly Ile Ser Asn Arg Asp Phe
            180                 185                 190

Val Glu Gly Val Ser Gly Gly Ser Trp Val Asp Ile Val Leu Glu His
        195                 200                 205

Gly Ser Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe
    210                 215                 220
```

```
Glu Leu Ile Lys Thr Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr
225                 230                 235                 240

Cys Ile Glu Ala Lys Leu Thr Asn Thr Thr Thr Asp Ser Arg Cys Pro
                245                 250                 255

Thr Gln Gly Glu Pro Thr Leu Asn Glu Glu Gln Asp Lys Arg Phe Val
            260                 265                 270

Cys Lys His Ser Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
        275                 280                 285

Ala Gly Lys Gly Gly Ile Val Thr Cys Ala Met Phe Thr Cys Lys Lys
    290                 295                 300

Asn Met Glu Gly Lys Ile Val Gln Pro Glu Asn Leu Glu Tyr Thr Val
305                 310                 315                 320

Val Ile Thr Pro His Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr
                325                 330                 335

Gly Lys His Gly Lys Glu Val Lys Ile Thr Pro Gln Ser Ser Ile Thr
            340                 345                 350

Glu Ala Glu Leu Thr Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro
        355                 360                 365

Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Gln Met Lys Asp
    370                 375                 380

Lys Ala Trp Leu Val His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro
385                 390                 395                 400

Trp Leu Pro Gly Ala Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu
                405                 410                 415

Thr Leu Val Thr Phe Lys Asn Pro His Ala Lys Lys Gln Asp Val Val
            420                 425                 430

Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala
        435                 440                 445

Thr Glu Ile Gln Met Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu
    450                 455                 460

Lys Cys Arg Leu Arg Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr
465                 470                 475                 480

Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr
                485                 490                 495
```

```
Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala
            500                 505                 510

Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln
        515                 520                 525

Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys
    530                 535                 540

Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val
545                 550                 555                 560

Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly
                565                 570                 575

Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg
            580                 585                 590

Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
        595                 600                 605

Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala
    610                 615                 620

Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile
625                 630                 635                 640

Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu
                645                 650                 655

Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val
            660                 665                 670

Met Val Gln Ala
        675


<210>  23
<211>  674
<212>  PRT
<213>  Dengue virus


<220>
<221>  misc_feature
<223>  DEV3 prM E (F108A)_3'DEV1

<220>
<221>  misc_feature
<222>  (182)..(475)
<223>  DEV3 prM E (F108A)

<220>
<221>  misc_feature
<222>  (476)..(676)
<223>  3' DEV1
```

<400> 23

Met Thr Ser Leu Cys Leu Met Met Ile Leu Pro Ala Thr Leu Ala Phe
1 5 10 15

His Leu Thr Ser Arg Asp Gly Glu Pro Arg Met Ile Val Gly Lys Asn
20 25 30

Glu Arg Gly Lys Ser Leu Leu Phe Lys Thr Ala Ser Gly Ile Asn Met
35 40 45

Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Met Cys Asp Asp Thr Val
50 55 60

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

Cys Trp Cys Asn Leu Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Asn
85 90 95

Gln Ala Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala Pro
100 105 110

His Val Gly Met Gly Leu Asp Thr Arg Thr Gln Thr Trp Met Ser Ala
115 120 125

Glu Gly Ala Trp Arg Gln Val Glu Lys Val Glu Thr Trp Ala Leu Arg
130 135 140

His Pro Gly Phe Thr Ile Leu Ala Leu Phe Leu Ala His Tyr Ile Gly
145 150 155 160

Thr Ser Leu Thr Gln Lys Val Val Ile Phe Ile Leu Leu Met Leu Val
165 170 175

Thr Pro Ser Met Thr Met Arg Cys Val Gly Val Gly Asn Arg Asp Phe
180 185 190

Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu His
195 200 205

Gly Gly Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Ile
210 215 220

Glu Leu Gln Lys Thr Glu Ala Thr Gln Leu Ala Thr Leu Arg Lys Leu
225 230 235 240

Cys Ile Glu Gly Lys Ile Thr Asn Ile Thr Thr Asp Ser Arg Cys Pro
245 250 255

Thr Gln Gly Glu Ala Ile Leu Pro Glu Glu Gln Asp Gln Asn Tyr Val

260 265 270

Cys Lys His Thr Tyr Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
275 280 285

Ala Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Gln Cys Leu Glu
290 295 300

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

Ile Ile Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Asp Thr
325 330 335

Gln Gly Val Thr Val Glu Ile Thr Pro Gln Ala Ser Thr Val Glu Ala
340 345 350

Ile Leu Pro Glu Tyr Gly Thr Leu Gly Leu Glu Cys Ser Pro Arg Thr
355 360 365

Gly Leu Asp Phe Asn Glu Met Ile Leu Leu Thr Met Lys Asn Lys Ala
370 375 380

Trp Met Val His Arg Gln Trp Phe Phe Asp Leu Pro Leu Pro Trp Thr
385 390 395 400

Ser Gly Ala Thr Thr Glu Ala Pro Thr Trp Asn Arg Lys Glu Leu Leu
405 410 415

Val Thr Phe Lys Asn Ala His Ala Lys Lys Gln Glu Val Val Val Leu
420 425 430

Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu
435 440 445

Ile Gln Asn Ser Gly Gly Thr Ser Ile Phe Ala Gly His Leu Lys Cys
450 455 460

Arg Leu Lys Met Asp Lys Leu Glu Leu Lys Gly Met Ser Tyr Val Met
465 470 475 480

Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr Gln His
485 490 495

Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala Pro Cys
500 505 510

Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln Asn Gly
515 520 525

Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys Pro Val

530 535 540

Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val Val Gly
545 550 555 560

Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly Ser Ser
565 570 575

Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg Met Ala
580 585 590

Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe
595 600 605

Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala Tyr Gly
610 615 620

Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile Gly Ile
625 630 635 640

Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu Ser Met
645 650 655

Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val Met Val
660 665 670

Gln Ala

<210> 24
<211> 676
<212> PRT
<213> Dengue virus

<220>
<221> MISC_FEATURE
<223> DEV4 prM E (F108A)_3'DEV1

<220>
<221> MISC_FEATURE
<222> (1)..(477)
<223> DEV4 prM E (F108A)

<220>
<221> MISC_FEATURE
<222> (478)..(676)
<223> 3' DEV1

<400> 24

Met Ser Thr Val Thr Leu Leu Cys Leu Ile Pro Thr Val Met Ala Phe
1 5 10 15

His Leu Ser Thr Arg Asp Gly Glu Pro Leu Met Ile Val Ala Lys His
20 25 30

```
Glu Arg Gly Arg Pro Leu Leu Phe Lys Thr Thr Glu Gly Ile Asn Lys
        35                  40                  45

Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Met Cys Glu Asp Thr Val
    50                  55                  60

Thr Tyr Lys Cys Pro Leu Leu Val Asn Thr Glu Pro Glu Asp Ile Asp
65                  70                  75                  80

Cys Trp Cys Asn Leu Thr Ser Thr Trp Val Met Tyr Gly Thr Cys Thr
                85                  90                  95

Gln Asn Gly Glu Arg Arg Arg Glu Lys Arg Ser Val Ala Leu Thr Pro
            100                 105                 110

His Ser Gly Met Gly Leu Glu Thr Arg Ala Glu Thr Trp Met Ser Ser
        115                 120                 125

Glu Gly Ala Trp Lys His Ala Gln Arg Val Glu Ser Trp Ile Leu Arg
    130                 135                 140

Asn Pro Gly Phe Ala Leu Leu Ala Gly Phe Met Ala Tyr Met Ile Gly
145                 150                 155                 160

Gln Thr Gly Ile Gln Arg Thr Val Phe Phe Val Leu Met Met Leu Val
                165                 170                 175

Ala Pro Ser Tyr Gly Met Arg Cys Ile Gly Val Gly Asn Arg Asp Phe
            180                 185                 190

Val Glu Gly Val Ser Gly Gly Ala Trp Val Asp Leu Val Leu Glu His
        195                 200                 205

Gly Gly Cys Val Thr Thr Met Ala Gln Gly Lys Pro Thr Leu Asp Phe
    210                 215                 220

Glu Leu Ile Lys Thr Thr Ala Lys Glu Val Ala Leu Leu Arg Thr Tyr
225                 230                 235                 240

Cys Ile Glu Ala Ser Ile Ser Asn Ile Thr Thr Ala Thr Arg Cys Pro
                245                 250                 255

Thr Gln Gly Glu Pro Tyr Leu Lys Glu Glu Gln Asp Gln Gln Tyr Ile
            260                 265                 270

Cys Arg Arg Asp Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
        275                 280                 285

Ala Gly Lys Gly Gly Val Val Thr Cys Ala Lys Phe Ser Cys Ser Gly
    290                 295                 300
```

```
Lys Ile Thr Gly Asn Leu Val Gln Ile Glu Asn Leu Glu Tyr Thr Val
305                 310                 315                 320

Val Val Thr Val His Asn Gly Asp Thr His Ala Val Gly Asn Asp Thr
                325                 330                 335

Ser Asn His Gly Val Thr Ala Thr Ile Thr Pro Arg Ser Pro Ser Val
            340                 345                 350

Glu Val Glu Leu Pro Asp Tyr Gly Glu Leu Ser Leu Asp Cys Glu Pro
        355                 360                 365

Arg Ser Gly Ile Asp Phe Asn Glu Met Ile Leu Met Lys Met Glu Lys
    370                 375                 380

Lys Thr Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro
385                 390                 395                 400

Trp Thr Ala Gly Ala Asp Thr Ser Glu Val His Trp Asn His Lys Glu
                405                 410                 415

Arg Met Val Thr Phe Lys Val Pro His Ala Lys Arg Gln Asp Val Thr
            420                 425                 430

Val Leu Gly Ser Gln Glu Gly Ala Met His Ser Ala Leu Thr Gly Ala
        435                 440                 445

Thr Glu Val Asp Ser Gly Asp Gly Asn His Met Phe Ala Gly His Leu
    450                 455                 460

Lys Cys Lys Val Arg Met Glu Lys Leu Arg Ile Lys Gly Met Ser Tyr
465                 470                 475                 480

Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr
                485                 490                 495

Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala
            500                 505                 510

Pro Cys Lys Ile Pro Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln
        515                 520                 525

Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys
    530                 535                 540

Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val
545                 550                 555                 560

Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly
                565                 570                 575
```

```
Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg
            580                 585                 590

Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
        595                 600                 605

Val Phe Thr Ser Val Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala
    610                 615                 620

Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile
625                 630                 635                 640

Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu
                645                 650                 655

Ser Met Thr Cys Ile Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val
            660                 665                 670

Met Val Gln Ala
        675
```