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CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> RECOMBINANT MEASLES VIRUS EXPRESSING ZIKA VIRUS PROTEINS AND THEIR APPLICATIONS

<130> B12291A/AD/DP/KN

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<170> PatentIn version 3.5

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<223> Signal peptide from the fusion protein of MV (MVsp)

<400> 14

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His
20 25

<210> 15
<211> 81
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of modified signal peptide from the fusion protein of MV (MVsp')

<400> 15
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact 60

ctccaaacac ccaccggtca a 81

<210> 16
<211> 81
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of modified signal peptide from the fusion protein of MV (MVsp')

<400> 16
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca g 81

<210> 17
<211> 27
<212> PRT
<213> Artificial sequence

<220>
<223> Modified signal peptide from the fusion protein of MV (MVsp’)

<400> 17

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln
20 25

<210> 18
<211> 504
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of precursor of membrane (prM) protein of ZIKV

<400> 18
gcggaggtca ctagacgtgg gagtgcatac tatatgtact tggacagaaa cgatgctggg 60

gaggccatat cttttccaac cacattgggg atgaataagt gttatataca gatcatggat 120

cttggacaca tgtgtgatgc caccatgagc tatgaatgcc ctatgctgga tgaggggtg 180

gaaccagatg acgtcgattg ttggtgcaac acgacgtcaa cttgggttgt gtacggaacc 240

tgccatcaca aaaaaggtga agcacggaga tctagaagag ctgtgacgct cccctcccat 300

tccactagga agctgcaaac gcggtcgcaa acctggttgg aatcaagaga atacacaaag 360

cacttgatta gagtcgaaaa ttggatattc aggaaccctg gcttcgcgtt agcagcagct 420

gccatcgctt ggcttttggg aagctcaacg agccaaaaag tcatatactt ggtcatgata 480

ctgctgattg ccccggcata cagc 504

<210> 19
<211> 505
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of precursor of membrane (prM) protein of ZIKV

<400> 19
gcagaggtga ccaggagagg aagcgcctac tatatgtacc tggacaggaa tgatgccggc 60

gaggccatct ccttcccaac cacactgggc atgaacaagt gctacatcca gatcatggac 120

ctgggccaca tgtgcgatgc caccatgtcc tatgagtgtc caatgctgga cgagggcgtg 180

gagcccgacg atgtggattg ctggtgtaat accacatcta catgggtggt gtacggcacc 240

tgtcaccaca agaagggaga ggcccggcgg agccggcggg ccgtgacact gccttcccac 300

tctaccagga agctgcagac acgcagccag acctggctgg agtccagaga gtataccaag 360

cacctgatca gggtggagaa ctggatcttt cgcaatccag gattcgcact ggcagcagca 420

gcaatcgcat ggctgctggg aagctccacc agccagaaag tgatctacct ggtcatgatc 480

ctgctgatcg ctcctgccta ttcta 505

<210> 20
<211> 168
<212> PRT
<213> Artificial sequence

<220>
<223> Precursor of membrane (prM) protein of ZIKV

<400> 20

Ala Glu Val Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg
1   5   10   15

Asn Asp Ala Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn
            20   25   30

Lys Cys Tyr Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr
        35   40   45

Met Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp
    50   55   60

```
Val Asp Cys Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr
65                  70                  75                  80

Cys His His Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr
                85                  90                  95

Leu Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp
            100                 105                 110

Leu Glu Ser Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp
        115                 120                 125

Ile Phe Arg Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp
    130                 135                 140

Leu Leu Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile
145                 150                 155                 160

Leu Leu Ile Ala Pro Ala Tyr Ser
                165
```

<210> 21
<211> 1512
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of full-length E protein of ZIKV

<400> 21

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atcaggtgca taggagtcag caatagggac tttgtggaag gtatgtcagg tgggacttgg       60

gttgatgttg tcttggaaca tggaggttgt gtcaccgtaa tggcacagga caaaccgact      120

gtcgacatag agctggttac aacaacagtc agcaacatgg cggaggtaag atcctactgc      180

tatgaggcat caatatcaga catggcttcg gacagccgct gcccaacaca aggtgaagcc      240

taccttgaca agcaatcaga cactcaatat gtctgcaaaa gaacgttagt ggacagaggc      300

tggggaaatg gatgtggact ttttggcaaa gggagcctgg tgacatgcgc taagtttgca      360
```

tgctccaaga aaatgaccgg gaagagcatc cagccagaga atctggagta ccggataatg 420

ctgtcagttc atggctccca gcacagtggg atgatcgtta atgacacagg acatgaaact 480

gatgagaata gagcgaaggt tgagataacg cccaattcac caagagccga agccaccctg 540

gggggttttg gaagcctagg acttgattgt gaaccgagga caggccttga cttttcagat 600

ttgtattact tgactatgaa taacaagcac tggttggttc acaaggagtg gttccacgac 660

attccattac cttggcacgc tggggcagac accggaactc cacactggaa caacaaagaa 720

gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt tctagggagt 780

caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat ggatggtgca 840

aagggaaggc tgtcctctgg ccacttgaaa tgtcgcctga aaatggataa acttagattg 900

aagggcgtgt catactcctt gtgtaccgca gcgttcacat tcaccaagat cccggctgaa 960

acactgcacg ggacagtcac agtggaggta cagtacgcag ggacagatgg accttgcaag 1020

gttccagctc agatggcggt ggacatgcaa actctgaccc cagttgggag gttgataacc 1080

gctaaccccg taatcactga aagcactgag aactctaaga tgatgctgga acttgatcca 1140

ccatttgggg actcttacat tgtcatagga gtcggggaga agaagatcac ccaccactgg 1200

cacaggagtg gcagcaccat tggaaaagca tttgaagcca ctgtgagagg tgccaagaga 1260

atggcagtct tgggagacac agcctgggac tttggatcag ttggaggcgc tctcaactca 1320

ttgggcaagg gcatccatca aatttttgga gcagctttca aatcattgtt tggaggaatg 1380

tcctggttct cacaaattct cattggaacg ttgctgatgt ggttgggtct gaacacaaag 1440

aatggatcta tttcccttat gtgcttggcc ttaggggggag tgttgatctt cttatccaca 1500

gccgtctctg ct 1512

<210> 22
<211> 1511
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of full-length E protein of ZIKV

<400> 22

tccggtgcat cggcgtgagc aatagagact tcgtggaggg aatgtccgga ggaacctggg 60

tggatgtggt gctggagcac ggcggctgcg tgacagtgat ggcccaggac aagccaaccg 120

tggatatcga gctggtgacc acaaccgtgt ccaacatggc cgaggtgagg tcttactgct 180

atgaggccag catctccgac atggcctctg atagcaggtg tccaacccag ggagaggcat 240

acctggacaa gcagtccgat acacagtacg tgtgcaagcg gaccctggtg gacagaggct 300

ggggcaatgg ctgtggcctg tttggcaagg gctctctggt gacatgcgcc aagttcgcct 360

gtagcaagaa gatgaccggc aagtccatcc agccagagaa cctggagtac cggatcatgc 420

tgtctgtgca cggctcccag cactctggca tgatcgtgaa cgacacaggc cacgagacag 480

atgagaatcg ggccaaggtg gagatcacac ctaactctcc aagagccgag gccaccctgg 540

gaggatttgg ctctctgggc ctggactgcg agcctagaac aggcctggac ttctccgatc 600

tgtactatct gaccatgaac aataagcact ggctggtgca caaggagtgg tttcacgaca 660

tcccactgcc atggcacgca ggagcagata caggaacacc acactggaac aataaggagg 720

ccctggtgga gttcaaggat gcccacgcca agcggcagac agtggtggtg ctgggcagcc 780

aggagggagc agtgcacacc gccctggcag gcgccctgga ggcagagatg gacggagcta 840

agggcagact gtctagcggc cacctgaagt gcaggctgaa gatggataag ctgcgcctga 900

agggcgtgtc ctactctctg tgcacagccg ccttcacctt caccaagatc cctgccgaga 960

cactgcacgg cacagtgacc gtggaggtgc agtatgccgg cacagacgga ccctgtaagg 1020

tgcctgccca gatggccgtg gatatgcaga cactgacacc tgtgggcagg ctgatcaccg 1080

ccaatccagt gatcacagag tctaccgaga acagcaagat gatgctggag ctggacccac 1140

catttggcga tagctatatc gtgatcggcg tgggcgagaa gaagatcaca caccactggc 1200

accgcagcgg ctccacaatc ggcaaggcct ttgaggcaac cgtgcgcgga gcaaagagaa 1260

tggccgtgct gggcgacacc gcatgggatt tcggatctgt gggaggcgcc ctgaacagcc 1320

tgggcaaggg catccaccag atcttcggcg ccgcctttaa gtccctgttc ggcggcatga 1380

gctggttctc acagatcctg atcggcacac tgctgatgtg gctgggcctg aacaccaaga 1440

atggctctat cagcctgatg tgcctggccc tgggaggcgt gctgatcttc ctgtccaccg 1500

ccgtgtctgc c 1511

<210> 23
<211> 504
<212> PRT
<213> Artificial sequence

<220>
<223> Full-length E protein of ZIKV

<400> 23

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

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

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

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

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

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

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

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr

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145                 150                 155                 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
                165                 170                 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
            180                 185                 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
        195                 200                 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
    210                 215                 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225                 230                 235                 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
                245                 250                 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
            260                 265                 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
        275                 280                 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
    290                 295                 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305                 310                 315                 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
                325                 330                 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
            340                 345                 350
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Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
        355                 360                 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
    370                 375                 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385                 390                 395                 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
                405                 410                 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
            420                 425                 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
        435                 440                 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
    450                 455                 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
465                 470                 475                 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
                485                 490                 495

Phe Leu Ser Thr Ala Val Ser Ala
            500
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<210> 24
<211> 1368
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of E protein of ZIKV truncated at amino acid position x (Edx)

<400> 24
atcaggtgca taggagtcag caatagggac tttgtggaag gtatgtcagg tgggacttgg 60

gttgatgttg tcttggaaca tggaggttgt gtcaccgtaa tggcacagga caaaccgact 120

gtcgacatag agctggttac aacaacagtc agcaacatgg cggaggtaag atcctactgc 180

tatgaggcat caatatcaga catggcttcg gacagccgct gcccaacaca aggtgaagcc 240

taccttgaca agcaatcaga cactcaatat gtctgcaaaa gaacgttagt ggacagaggc 300

tggggaaatg gatgtggact ttttggcaaa gggagcctgg tgacatgcgc taagtttgca 360

tgctccaaga aaatgaccgg gaagagcatc cagccagaga atctggagta ccggataatg 420

ctgtcagttc atggctccca gcacagtggg atgatcgtta atgacacagg acatgaaact 480

gatgagaata gagcgaaggt tgagataacg cccaattcac caagagccga agccaccctg 540

gggggttttg gaagcctagg acttgattgt gaaccgagga caggccttga cttttcagat 600

ttgtattact tgactatgaa taacaagcac tggttggttc acaaggagtg gttccacgac 660

attccattac cttggcacgc tggggcagac accggaactc cacactggaa caacaaagaa 720

gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt tctagggagt 780

caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat ggatggtgca 840

aagggaaggc tgtcctctgg ccacttgaaa tgtcgcctga aaatggataa acttagattg 900

aagggcgtgt catactcctt gtgtaccgca gcgttcacat tcaccaagat cccggctgaa 960

acactgcacg ggacagtcac agtggaggta cagtacgcag ggacagatgg accttgcaag 1020

gttccagctc agatggcggt ggacatgcaa actctgaccc cagttgggag gttgataacc 1080

gctaaccccg taatcactga aagcactgag aactctaaga tgatgctgga acttgatcca 1140

ccatttgggg actcttacat tgtcatagga gtcggggaga agaagatcac ccaccactgg 1200

cacaggagtg gcagcaccat tggaaaagca tttgaagcca ctgtgagagg tgccaagaga 1260

atggcagtct tgggagacac agcctgggac tttggatcag ttggaggcgc tctcaactca 1320

ttgggcaagg gcatccatca aatttttgga gcagctttca aatcattg 1368

<210> 25
<211> 1367

<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E protein of ZIKV truncated at amino acid position x (Edx)

<400> 25
tccggtgcat cggcgtgagc aatagagact tcgtggaggg aatgtccgga ggaacctggg 60

tggatgtggt gctggagcac ggcggctgcg tgacagtgat ggcccaggac aagccaaccg 120

tggatatcga gctggtgacc acaaccgtgt ccaacatggc cgaggtgagg tcttactgct 180

atgaggccag catctccgac atggcctctg atagcaggtg tccaacccag ggagaggcat 240

acctggacaa gcagtccgat acacagtacg tgtgcaagcg gaccctggtg gacagaggct 300

ggggcaatgg ctgtggcctg tttggcaagg gctctctggt gacatgcgcc aagttcgcct 360

gtagcaagaa gatgaccggc aagtccatcc agccagagaa cctggagtac cggatcatgc 420

tgtctgtgca cggctcccag cactctggca tgatcgtgaa cgacacaggc cacgagacag 480

atgagaatcg ggccaaggtg gagatcacac ctaactctcc aagagccgag gccaccctgg 540

gaggatttgg ctctctgggc ctggactgcg agcctagaac aggcctggac ttctccgatc 600

tgtactatct gaccatgaac aataagcact ggctggtgca caaggagtgg tttcacgaca 660

tcccactgcc atggcacgca ggagcagata caggaacacc acactggaac aataaggagg 720

ccctggtgga gttcaaggat gcccacgcca agcggcagac agtggtggtg ctgggcagcc 780

aggagggagc agtgcacacc gccctggcag gcgccctgga ggcagagatg gacggagcta 840

agggcagact gtctagcggc cacctgaagt gcaggctgaa gatggataag ctgcgcctga 900

agggcgtgtc ctactctctg tgcacagccg ccttcacctt caccaagatc cctgccgaga 960

cactgcacgg cacagtgacc gtggaggtgc agtatgccgg cacagacgga ccctgtaagg 1020

tgcctgccca gatggccgtg gatatgcaga cactgacacc tgtgggcagg ctgatcaccg 1080

ccaatccagt gatcacagag tctaccgaga acagcaagat gatgctggag ctggacccac 1140

catttggcga tagctatatc gtgatcggcg tgggcgagaa gaagatcaca caccactggc 1200

accgcagcgg ctccacaatc ggcaaggcct ttgaggcaac cgtgcgcgga gcaaagagaa 1260

tggccgtgct gggcgacacc gcatgggatt tcggatctgt gggaggcgcc ctgaacagcc 1320

tgggcaaggg catccaccag atcttcggcg ccgcctttaa gtccctg 1367

<210> 26
<211> 456
<212> PRT
<213> Artificial sequence

<220>
<223> E protein of ZIKV truncated at amino acid position x (Edx)

<400> 26

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

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

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

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

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

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

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

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

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


Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
                165                 170                 175


Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
            180                 185                 190


Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
        195                 200                 205


Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
    210                 215                 220


Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225                 230                 235                 240


Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
                245                 250                 255


Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
            260                 265                 270


Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
        275                 280                 285


Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
    290                 295                 300


Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305                 310                 315                 320


Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
                325                 330                 335


Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
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            340                 345                 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
        355                 360                 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
    370                 375                 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385                 390                 395                 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
                405                 410                 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
            420                 425                 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
        435                 440                 445

Phe Gly Ala Ala Phe Lys Ser Leu
    450                 455
```

<210> 27
<211> 1335
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of E protein of ZIKV truncated at amino acid position 411 (Ed411)

<400> 27
atcaggtgca taggagtcag caatagggac tttgtggaag gtatgtcagg tgggacttgg 60

gttgatgttg tcttggaaca tggaggttgt gtcaccgtaa tggcacagga caaaccgact 120

gtcgacatag agctggttac aacaacagtc agcaacatgg cggaggtaag atcctactgc 180

tatgaggcat caatatcaga catggcttcg gacagccgct gcccaacaca aggtgaagcc 240

taccttgaca agcaatcaga cactcaatat gtctgcaaaa gaacgttagt ggacagaggc 300

tggggaaatg gatgtggact ttttggcaaa gggagcctgg tgacatgcgc taagtttgca 360

tgctccaaga aaatgaccgg gaagagcatc cagccagaga atctggagta ccggataatg 420

ctgtcagttc atggctccca gcacagtggg atgatcgtta atgacacagg acatgaaact 480

gatgagaata gagcgaaggt tgagataacg cccaattcac caagagccga agccaccctg 540

gggggttttg gaagcctagg acttgattgt gaaccgagga caggccttga cttttcagat 600

ttgtattact tgactatgaa taacaagcac tggttggttc acaaggagtg gttccacgac 660

attccattac cttggcacgc tggggcagac accggaactc cacactggaa caacaaagaa 720

gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt tctagggagt 780

caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat ggatggtgca 840

aagggaaggc tgtcctctgg ccacttgaaa tgtcgcctga aaatggataa acttagattg 900

aagggcgtgt catactcctt gtgtaccgca gcgttcacat tcaccaagat cccggctgaa 960

acactgcacg ggacagtcac agtggaggta cagtacgcag ggacagatgg accttgcaag 1020

gttccagctc agatggcggt ggacatgcaa actctgaccc cagttgggag gttgataacc 1080

gctaaccccg taatcactga aagcactgag aactctaaga tgatgctgga acttgatcca 1140

ccatttgggg actcttacat tgtcatagga gtcggggaga agaagatcac ccaccactgg 1200

cacaggagtg gcagcaccat tggaaaagca tttgaagcca ctgtgagagg tgccaagaga 1260

atggcagtct tgggagacac agcctgggac tttggatcag ttggaggcgc tctcaactca 1320

ttgggcaagg gcatc 1335

<210> 28
<211> 1334
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E protein of ZIKV truncated at amino acid position 411 (Ed411)

<400> 28
tccggtgcat cggcgtgagc aatagagact tcgtggaggg aatgtccgga ggaacctggg 60

tggatgtggt gctggagcac ggcggctgcg tgacagtgat ggcccaggac aagccaaccg 120

tggatatcga gctggtgacc acaaccgtgt ccaacatggc cgaggtgagg tcttactgct 180

atgaggccag catctccgac atggcctctg atagcaggtg tccaacccag ggagaggcat 240

acctggacaa gcagtccgat acacagtacg tgtgcaagcg gaccctggtg gacagaggct 300

ggggcaatgg ctgtggcctg tttggcaagg gctctctggt gacatgcgcc aagttcgcct 360

gtagcaagaa gatgaccggc aagtccatcc agccagagaa cctggagtac cggatcatgc 420

tgtctgtgca cggctcccag cactctggca tgatcgtgaa cgacacaggc cacgagacag 480

atgagaatcg ggccaaggtg gagatcacac ctaactctcc aagagccgag gccaccctgg 540

gaggatttgg ctctctgggc ctggactgcg agcctagaac aggcctggac ttctccgatc 600

tgtactatct gaccatgaac aataagcact ggctggtgca caaggagtgg tttcacgaca 660

tcccactgcc atggcacgca ggagcagata caggaacacc acactggaac aataaggagg 720

ccctggtgga gttcaaggat gcccacgcca agcggcagac agtggtggtg ctgggcagcc 780

aggagggagc agtgcacacc gccctggcag gcgccctgga ggcagagatg gacggagcta 840

agggcagact gtctagcggc cacctgaagt gcaggctgaa gatggataag ctgcgcctga 900

agggcgtgtc ctactctctg tgcacagccg ccttcacctt caccaagatc cctgccgaga 960

cactgcacgg cacagtgacc gtggaggtgc agtatgccgg cacagacgga ccctgtaagg 1020

tgcctgccca gatggccgtg gatatgcaga cactgacacc tgtgggcagg ctgatcaccg 1080

ccaatccagt gatcacagag tctaccgaga acagcaagat gatgctggag ctggacccac 1140

catttggcga tagctatatc gtgatcggcg tgggcgagaa gaagatcaca caccactggc 1200

accgcagcgg ctccacaatc ggcaaggcct ttgaggcaac cgtgcgcgga gcaaagagaa 1260

tggccgtgct gggcgacacc gcatgggatt tcggatctgt gggaggcgcc ctgaacagcc 1320

tgggcaaggg catc 1334

<210> 29
<211> 445
<212> PRT
<213> Artificial sequence

<220>
<223> E protein of ZIKV truncated at amino acid position 411 (Ed411)

<400> 29

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


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


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


Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
    50                  55                  60


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


Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
                85                  90                  95


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


Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
        115                 120                 125


Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
    130                 135                 140


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


Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
                165                 170                 175


Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
```

```
            180                 185                 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
        195                 200                 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
    210                 215                 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225                 230                 235                 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
                245                 250                 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
            260                 265                 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
        275                 280                 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
    290                 295                 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305                 310                 315                 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
                325                 330                 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
            340                 345                 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
        355                 360                 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
    370                 375                 380
```

```
Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385                 390                 395                 400


His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
                405                 410                 415


Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
            420                 425                 430


Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
        435                 440                 445
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<210> 30
<211> 1212
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of E protein of ZIKV truncated at amino acid position 395 (Ed395)

<400> 30

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atcaggtgca taggagtcag caatagggac tttgtggaag gtatgtcagg tgggacttgg       60

gttgatgttg tcttggaaca tggaggttgt gtcaccgtaa tggcacagga caaaccgact      120

gtcgacatag agctggttac aacaacagtc agcaacatgg cggaggtaag atcctactgc      180

tatgaggcat caatatcaga catggcttcg gacagccgct gcccaacaca aggtgaagcc      240

taccttgaca agcaatcaga cactcaatat gtctgcaaaa gaacgttagt ggacagaggc      300

tggggaaatg gatgtggact ttttggcaaa gggagcctgg tgacatgcgc taagtttgca      360

tgctccaaga aaatgaccgg gaagagcatc cagccagaga atctggagta ccggataatg      420

ctgtcagttc atggctccca gcacagtggg atgatcgtta atgacacagg acatgaaact      480

gatgagaata gagcgaaggt tgagataacg cccaattcac caagagccga agccaccctg      540

gggggttttg gaagcctagg acttgattgt gaaccgagga caggccttga cttttcagat      600

ttgtattact tgactatgaa taacaagcac tggttggttc acaaggagtg gttccacgac      660

attccattac cttggcacgc tggggcagac accggaactc cacactggaa caacaaagaa      720
```

gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt tctagggagt 780

caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat ggatggtgca 840

aagggaaggc tgtcctctgg ccacttgaaa tgtcgcctga aaatggataa acttagattg 900

aagggcgtgt catactcctt gtgtaccgca gcgttcacat tcaccaagat cccggctgaa 960

acactgcacg ggacagtcac agtggaggta cagtacgcag ggacagatgg accttgcaag 1020

gttccagctc agatggcggt ggacatgcaa actctgaccc cagttgggag gttgataacc 1080

gctaaccccg taatcactga aagcactgag aactctaaga tgatgctgga acttgatcca 1140

ccatttgggg actcttacat tgtcatagga gtcggggaga agaagatcac ccaccactgg 1200

cacaggagtg gc 1212

<210> 31
<211> 1211
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E protein of ZIKV truncated at amino acid position 395 (Ed395)

<400> 31
tccggtgcat cggcgtgagc aatagagact tcgtggaggg aatgtccgga ggaacctggg 60

tggatgtggt gctggagcac ggcggctgcg tgacagtgat ggcccaggac aagccaaccg 120

tggatatcga gctggtgacc acaaccgtgt ccaacatggc cgaggtgagg tcttactgct 180

atgaggccag catctccgac atggcctctg atagcaggtg tccaacccag ggagaggcat 240

acctggacaa gcagtccgat acacagtacg tgtgcaagcg gaccctggtg gacagaggct 300

ggggcaatgg ctgtggcctg tttggcaagg gctctctggt gacatgcgcc aagttcgcct 360

gtagcaagaa gatgaccggc aagtccatcc agccagagaa cctggagtac cggatcatgc 420

tgtctgtgca cggctcccag cactctggca tgatcgtgaa cgacacaggc cacgagacag 480

atgagaatcg ggccaaggtg gagatcacac ctaactctcc aagagccgag gccaccctgg 540

gaggatttgg ctctctgggc ctggactgcg agcctagaac aggcctggac ttctccgatc 600

tgtactatct gaccatgaac aataagcact ggctggtgca caaggagtgg tttcacgaca 660

tcccactgcc atggcacgca ggagcagata caggaacacc acactggaac aataaggagg 720

ccctggtgga gttcaaggat gcccacgcca agcggcagac agtggtggtg ctgggcagcc 780

aggagggagc agtgcacacc gccctggcag gcgccctgga ggcagagatg gacggagcta 840

agggcagact gtctagcggc cacctgaagt gcaggctgaa gatggataag ctgcgcctga 900

agggcgtgtc ctactctctg tgcacagccg ccttcacctt caccaagatc cctgccgaga 960

cactgcacgg cacagtgacc gtggaggtgc agtatgccgg cacagacgga ccctgtaagg 1020

tgcctgccca gatggccgtg gatatgcaga cactgacacc tgtgggcagg ctgatcaccg 1080

ccaatccagt gatcacagag tctaccgaga acagcaagat gatgctggag ctggacccac 1140

catttggcga tagctatatc gtgatcggcg tgggcgagaa gaagatcaca caccactggc 1200

accgcagcgg c 1211

<210> 32
<211> 404
<212> PRT
<213> Artificial sequence

<220>
<223> E protein of ZIKV truncated at amino acid position 395 (Ed395)

<400> 32

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

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

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

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala

```
65                  70                  75                  80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
                85                  90                  95

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

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
        115                 120                 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
    130                 135                 140

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

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
                165                 170                 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
            180                 185                 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
        195                 200                 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
    210                 215                 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225                 230                 235                 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
                245                 250                 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
            260                 265                 270
```

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly

<210> 33
<211> 156
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of E stem region of ZIKV

<400> 33
agcaccattg gaaaagcatt tgaagccact gtgagaggtg ccaagagaat ggcagtcttg 60

ggagacacag cctgggactt tggatcagtt ggaggcgctc tcaactcatt gggcaagggc 120

atccatcaaa tttttggagc agctttcaaa tcattg 156

<210> 34
<211> 156
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E stem region of ZIKV

<400> 34
tccacaatcg gcaaggcctt tgaggcaacc gtgcgcggag caaagagaat ggccgtgctg 60

ggcgacaccg catgggattt cggatctgtg ggaggcgccc tgaacagcct gggcaagggc 120

atccaccaga tcttcggcgc cgcctttaag tccctg 156

<210> 35
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> E stem region of ZIKV

<400> 35

Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg
1 5 10 15

Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
20 25 30

Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala
35 40 45

Phe Lys Ser Leu
50

<210> 36
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of intermediate domain between E stem and E anchor regions of ZIKV

<400> 36
tttggaggaa tgtcctggtt ctca 24

<210> 37
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of intermediate domain between E stem and E anchor regions of ZIKV

<400> 37
ttcggcggca tgagctggtt ctcacagatc ctga 34

<210> 38
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Intermediate domain between E stem and E anchor regions of ZIKV

<400> 38

Phe Gly Gly Met Ser Trp Phe Ser
1 5

<210> 39
<211> 120
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of E anchor region of ZIKV

<400> 39
caaattctca ttggaacgtt gctgatgtgg ttgggtctga acacaaagaa tggatctatt 60

tcccttatgt gcttggcctt agggggagtg ttgatcttct tatccacagc cgtctctgct 120

<210> 40

<211> 110
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E anchor region of ZIKV

<400> 40
tcggcacact gctgatgtgg ctgggcctga acaccaagaa tggctctatc agcctgatgt 60

gcctggccct gggaggcgtg ctgatcttcc tgtccaccgc cgtgtctgcc 110

<210> 41
<211> 40
<212> PRT
<213> Artificial sequence

<220>
<223> E anchor region of ZIKV

<400> 41

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
1 5 10 15

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
20 25 30

Phe Leu Ser Thr Ala Val Ser Ala
35 40

<210> 42
<211> 192
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of transmembrane (TM) and intracytoplasmic tail of MV F protein

<400> 42
atgaaaggtt tatcgagcac tagcatagtc tacatcctga ttgcagtgtg tcttggaggg 60

ttgataggga tccccgcttt aatatgttgc tgcaggggggc gttgtaacaa aaagggagaa 120

caagttggta tgtcaagacc aggcctaaag cctgatctta cgggaacatc aaaatcctat 180

gtaaggtcgc tc 192

<210> 43
<211> 192
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of transmembrane (TM) and intracytoplasmic tail of MV F protein

<400> 43
atgaagggcc tgtcctctac ctctatcgtg tacatcctga tcgccgtgtg cctgggaggc 60

ctgatcggaa tcccagccct gatctgctgt tgcagaggcc gctgcaacaa gaagggagag 120

caagtgggaa tgtctcggcc aggcctgaag ccagacctga caggcacctc caagtcttat 180

gtgagaagcc tg 192

<210> 44
<211> 64
<212> PRT
<213> Artificial sequence

<220>
<223> Transmembrane (TM) and intracytoplasmic tail of MV F protein

<400> 44

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

Cys Leu Gly Gly Leu Ile Gly Ile Pro Ala Leu Ile Cys Cys Cys Arg
20 25 30

Gly Arg Cys Asn Lys Lys Gly Glu Gln Val Gly Met Ser Arg Pro Gly
35 40 45

Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys Ser Tyr Val Arg Ser Leu
50 55 60

<210> 45

<211> 2094
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaprME protein (A1)

<400> 45
atggagaaga agagacgagg cgcagatact agtgtcggaa ttgttggcct cctgctgacc 60

acagctatgg cagcggaggt cactagacgt gggagtgcat actatatgta cttggacaga 120

aacgatgctg gggaggccat atcttttcca accacattgg ggatgaataa gtgttatata 180

cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt 300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg 360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga 420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg 480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac 540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat 600

agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga 660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

agcatccagc cagagaatct ggagtaccgg ataatgctgt cagttcatgg ctcccagcac 1020

agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag 1080

ataacgccca attcaccaag agccgaagcc accctggggg gttttggaag cctaggactt 1140

gattgtgaac cgaggacagg ccttgacttt tcagatttgt attacttgac tatgaataac 1200

aagcactggt tggttcacaa ggagtggttc cacgacattc cattaccttg gcacgctggg 1260

gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca 1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt 1500

accgcagcgt tcacattcac caagatcccg gctgaaacac tgcacgggac agtcacagtg 1560

gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac 1620

atgcaaactc tgaccccagt tgggaggttg ataaccgcta accccgtaat cactgaaagc 1680

actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ccatcaaatt 1920

tttggagcag ctttcaaatc attgtttgga ggaatgtcct ggttctcaca aattctcatt 1980

ggaacgttgc tgatgtggtt gggtctgaac acaaagaatg gatctatttc ccttatgtgc 2040

ttggccttag ggggagtgtt gatcttctta tccacagccg tctctgcttg atga 2094

<210> 46
<211> 2094
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaprME protein (A1)

<400> 46
atggagaaga agcggagagg agcagacaca agcgtgggaa tcgtgggcct gctgctgacc 60

acagcaatgg cagcagaggt gaccaggaga ggaagcgcct actatatgta cctggacagg 120

aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

agagacttcg tggagggaat gtccggagga acctgggtgg atgtggtgct ggagcacggc 660

ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt 900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag 960

tccatccagc cagagaacct ggagtaccgg atcatgctgt ctgtgcacgg ctcccagcac 1020

tctggcatga tcgtgaacga cacaggccac gagacagatg agaatcgggc caaggtggag 1080

atcacaccta actctccaag agccgaggcc accctgggag gatttggctc tctgggcctg 1140

gactgcgagc ctagaacagg cctggacttc tccgatctgt actatctgac catgaacaat 1200

aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

ctgaagtgca ggctgaagat ggataagctg cgcctgaagg gcgtgtccta ctctctgtgc 1500

acagccgcct tcaccttcac caagatccct gccgagacac tgcacggcac agtgaccgtg 1560

gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

atgcagacac tgacacctgt gggcaggctg atcaccgcca atccagtgat cacagagtct 1680

accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctc cacaatcggc 1800

aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

tgggatttcg gatctgtggg aggcgccctg aacagcctgg gcaagggcat ccaccagatc 1920

ttcggcgccg cctttaagtc cctgttcggc ggcatgagct ggttctcaca gatcctgatc 1980

ggcacactgc tgatgtggct gggcctgaac accaagaatg gctctatcag cctgatgtgc 2040

ctggccctgg gaggcgtgct gatcttcctg tccaccgccg tgtctgcctg atga 2094

<210> 47
<211> 696
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaprME protein (A1)

<400> 47

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

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
35 40 45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
50 55 60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65 70 75 80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
85 90 95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
100 105 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
115 120 125

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Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
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                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
        435                 440                 445

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525
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Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595                 600                 605

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610                 615                 620

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
625                 630                 635                 640

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
                645                 650                 655

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
            660                 665                 670

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
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Phe Leu Ser Thr Ala Val Ser Ala
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<210> 48
<211> 1950
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_Zika_prME_no_Anchor protein (A2)

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aacgatgctg gggaggccat atcttttcca accacattgg ggatgaataa gtgttatata 180

cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt 300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg 360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga 420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg 480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac 540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat 600

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ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

agcatccagc cagagaatct ggagtaccgg ataatgctgt cagttcatgg ctcccagcac 1020

agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag 1080

ataacgccca attcaccaag agccgaagcc accctggggg gttttggaag cctaggactt 1140

gattgtgaac cgaggacagg ccttgacttt tcagatttgt attacttgac tatgaataac 1200

aagcactggt tggttcacaa ggagtggttc cacgacattc cattaccttg gcacgctggg 1260

gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca 1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt 1500

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gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac 1620

atgcaaactc tgaccccagt tgggaggttg ataaccgcta accccgtaat cactgaaagc 1680

actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ccatcaaatt 1920

tttggagcag ctttcaaatc attgtgatga 1950

<210> 49
<211> 1950
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_Zika_prME_no_Anchor protein (A2)

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aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

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ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt 900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag 960

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gactgcgagc ctagaacagg cctggacttc tccgatctgt actatctgac catgaacaat 1200

aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

ctgaagtgca ggctgaagat ggataagctg cgcctgaagg gcgtgtccta ctctctgtgc 1500

acagccgcct tcaccttcac caagatccct gccgagacac tgcacggcac agtgaccgtg 1560

gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

atgcagacac tgacacctgt gggcaggctg atcaccgcca atccagtgat cacagagtct 1680

accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctc cacaatcggc 1800

aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

tgggatttcg gatctgtggg aggcgccctg aacagcctgg gcaagggcat ccaccagatc 1920

ttcggcgccg cctttaagtc cctgtgatga 1950

<210> 50
<211> 648

<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_Zika_prME_no_Anchor protein (A2)

<400> 50

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

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
        35   40   45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50   55   60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65   70   75   80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85   90   95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100   105   110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115   120   125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130   135   140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145   150   155   160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165   170   175

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Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
        355                 360                 365
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Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
        435                 440                 445

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575
```

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
580 585 590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
595 600 605

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
610 615 620

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
625 630 635 640

Phe Gly Ala Ala Phe Lys Ser Leu
645

<210> 51
<211> 1914
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_Zika_prME411 protein (A3)

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cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt 300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg 360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga 420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg 480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac 540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat 600

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ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

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catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

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ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ctga 1914

<210> 52
<211> 1914
<212> DNA
<213> Artificial sequence

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<223> Codon-optimized nucleotide sequence of Zikasp_Zika_prME411 protein (A3)

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aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

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gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

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ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

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gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

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aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

tgggatttcg gatctgtggg aggcgccctg aacagcctgg gcaagggcat ctga 1914

<210> 53
<211> 637
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_Zika_prME411 protein (A3)

<400> 53

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20 25 30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
35 40 45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
50 55 60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65 70 75 80

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Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85                  90                  95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285
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Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
        435                 440                 445

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480
```

```
Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595                 600                 605

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610                 615                 620

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625                 630                 635
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<210> 54
<211> 1794
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_Zika_prME395 protein (A4)

<400> 54
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acagctatgg cagcggaggt cactagacgt gggagtgcat actatatgta cttggacaga 120

aacgatgctg gggaggccat atcttttcca accacattgg ggatgaataa gtgttatata 180

cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt 300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg 360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga 420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg 480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac 540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat 600

agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga 660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

agcatccagc cagagaatct ggagtaccgg ataatgctgt cagttcatgg ctcccagcac 1020

agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag 1080

ataacgccca attcaccaag agccgaagcc accctggggg gttttggaag cctaggactt 1140

gattgtgaac cgaggacagg ccttgacttt tcagatttgt attacttgac tatgaataac 1200

aagcactggt tggttcacaa ggagtggttc cacgacattc cattaccttg gcacgctggg 1260

gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca 1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt 1500

accgcagcgt tcacattcac caagatcccg gctgaaacac tgcacgggac agtcacagtg 1560

gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac 1620

atgcaaactc tgaccccagt tgggaggttg ataaccgcta accccgtaat cactgaaagc 1680

actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggctg atga 1794

<210> 55
<211> 1794
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_Zika_prME395 protein (A4)

<400> 55
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acagcaatgg cagcagaggt gaccaggaga ggaagcgcct actatatgta cctggacagg 120

aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

agagacttcg tggagggaat gtccggagga acctgggtgg atgtggtgct ggagcacggc 660

ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt 900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag 960

tccatccagc cagagaacct ggagtaccgg atcatgctgt ctgtgcacgg ctcccagcac 1020

tctggcatga tcgtgaacga cacaggccac gagacagatg agaatcgggc caaggtggag 1080

atcacaccta actctccaag agccgaggcc accctgggag gatttggctc tctgggcctg 1140

gactgcgagc ctagaacagg cctggacttc tccgatctgt actatctgac catgaacaat 1200

aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

ctgaagtgca ggctgaagat ggataagctg cgcctgaagg gcgtgtccta ctctctgtgc 1500

acagccgcct tcaccttcac caagatccct gccgagacac tgcacggcac agtgaccgtg 1560

gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

atgcagacac tgacacctgt gggcaggctg atcaccgcca atccagtgat cacagagtct 1680

accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctg atga 1794

<210> 56
<211> 596
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_Zika_prME395 protein (A4)

<400> 56

Met Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile Val Gly
1 5 10 15

Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg Gly Ser
20 25 30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
35 40 45

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Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50                  55                  60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65                  70                  75                  80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85                  90                  95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

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

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
        435                 440                 445
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```
Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590

His Arg Ser Gly
        595
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<210> 57
<211> 1590
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaE protein (A5)

<400> 57
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acagctatgg caatcaggtg cataggagtc agcaataggg actttgtgga aggtatgtca 120

ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag 180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta 240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tgggggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg 1140

aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg 1200

gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc 1260

acccaccact ggcacaggag tggcagcacc attggaaaag catttgaagc cactgtgaga 1320

ggtgccaaga gaatggcagt cttgggagac acagcctggg actttggatc agttggaggc 1380

gctctcaact cattgggcaa gggcatccat caaatttttg gagcagcttt caaatcattg 1440

tttggaggaa tgtcctggtt ctcacaaatt ctcattggaa cgttgctgat gtggttgggt 1500

ctgaacacaa agaatggatc tatttccctt atgtgcttgg ccttaggggg agtgttgatc 1560

ttcttatcca cagccgtctc tgcttgatga 1590

<210> 58
<211> 1590
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaE protein (A5)

<400> 58
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acagcaatgg caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc 120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc 300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc 420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca 540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc 600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag 900

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gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc 1320

ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc 1380

gccctgaaca gcctgggcaa gggcatccac cagatcttcg gcgccgcctt taagtccctg 1440

ttcggcggca tgagctggtt ctcacagatc ctgatcggca cactgctgat gtggctgggc 1500

ctgaacacca agaatggctc tatcagcctg atgtgcctgg ccctgggagg cgtgctgatc 1560

ttcctgtcca ccgccgtgtc tgcctgatga 1590

<210> 59
<211> 528
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaE protein (A5)

<400> 59

Met Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile Val Gly
1 5 10 15

Leu Leu Leu Thr Thr Ala Met Ala Ile Arg Cys Ile Gly Val Ser Asn
20 25 30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
35 40 45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
50 55 60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65 70 75 80

```
Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285
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Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

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

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420                 425                 430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435                 440                 445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
    450                 455                 460

Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465                 470                 475                 480
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Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu
485 490 495

Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu Met Cys
500 505 510

Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
515 520 525

<210> 60
<211> 1446
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaE_no_Anchor protein (A6)

<400> 60
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acagctatgg caatcaggtg cataggagtc agcaataggg actttgtgga aggtatgtca 120

ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag 180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta 240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tgggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg 1140

aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg 1200

gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc 1260

acccaccact ggcacaggag tggcagcacc attggaaaag catttgaagc cactgtgaga 1320

ggtgccaaga gaatggcagt cttgggagac acagcctggg actttggatc agttggaggc 1380

gctctcaact cattgggcaa gggcatccat caaatttttg gagcagcttt caaatcattg 1440

tgatga 1446

<210> 61
<211> 1446
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaE_no_Anchor protein (A6)

<400> 61
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acagcaatgg caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc 120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc 300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc 420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca 540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc 600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag 900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat 960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag 1020

atccctgccg agacactgca cggcacagtg accgtggagg tgcagtatgc cggcacagac 1080

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aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg 1200

gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc 1320

ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc 1380

gccctgaaca gcctgggcaa gggcatccac cagatcttcg gcgccgcctt taagtccctg 1440

tgatga 1446

<210> 62
<211> 480
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaE_no_Anchor protein (A6)

<400> 62

Met Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile Val Gly
1 5 10 15

Leu Leu Leu Thr Thr Ala Met Ala Ile Arg Cys Ile Gly Val Ser Asn
20 25 30

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Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35                  40                  45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50                  55                  60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65                  70                  75                  80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
```

```
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

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

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420                 425                 430
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Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
435 440 445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
450 455 460

Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465 470 475 480

<210> 63
<211> 1410
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaE411 protein (A7)

<400> 63
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acagctatgg caatcaggtg cataggagtc agcaataggg actttgtgga aggtatgtca 120

ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag 180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta 240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tgggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg 1140

aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg 1200

gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc 1260

acccaccact ggcacaggag tggcagcacc attggaaaag catttgaagc cactgtgaga 1320

ggtgccaaga gaatggcagt cttgggagac acagcctggg actttggatc agttggaggc 1380

gctctcaact cattgggcaa gggcatctga 1410

<210> 64
<211> 1410
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaE411 protein (A7)

<400> 64
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acagcaatgg caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc 120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc 300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc 420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca 540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc 600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag 900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat 960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag 1020

atccctgccg agacactgca cggcacagtg accgtggagg tgcagtatgc cggcacagac 1080

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aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg 1200

gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc 1320

ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc 1380

gccctgaaca gcctgggcaa gggcatctga 1410

<210> 65
<211> 469
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaE411 protein (A7)

<400> 65

Met Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile Val Gly
1 5 10 15

Leu Leu Leu Thr Thr Ala Met Ala Ile Arg Cys Ile Gly Val Ser Asn
20 25 30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
35 40 45

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Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50                  55                  60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65                  70                  75                  80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
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                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

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

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420                 425                 430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435                 440                 445
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Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
450 455 460

Leu Gly Lys Gly Ile
465

<210> 66
<211> 1290
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaE395 protein (A8)

<400> 66
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acagctatgg caatcaggtg cataggagtc agcaataggg actttgtgga aggtatgtca 120

ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag 180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta 240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tgggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg 1140

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gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc 1260

acccaccact ggcacaggag tggctgatga 1290

<210> 67
<211> 1290
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaE395 protein (A8)

<400> 67
atggagaaga agcggagagg agcagacaca agcgtgggaa tcgtgggcct gctgctgacc 60

acagcaatgg caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc 120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

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cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc 420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

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ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc 600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

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aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag 1020

atccctgccg agacactgca cggcacagtg accgtggagg tgcagtatgc cggcacagac 1080

ggaccctgta aggtgcctgc ccagatggcc gtggatatgc agacactgac acctgtgggc 1140

aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg 1200

gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctgatga 1290

<210> 68
<211> 428
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaE395 protein (A8)

<400> 68

Met Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile Val Gly
1 5 10 15

Leu Leu Leu Thr Thr Ala Met Ala Ile Arg Cys Ile Gly Val Ser Asn
20 25 30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
35 40 45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
50 55 60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65 70 75 80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
85 90 95

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Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
```

290 295 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305 310 315 320

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

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
340 345 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
355 360 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
370 375 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385 390 395 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
405 410 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly
420 425

<210> 69
<211> 1572
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp’_ZikaE protein (A9)

<400> 69
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tgcataggag tcagcaatag ggactttgtg gaaggtatgt caggtgggac ttgggttgat 120

gttgtcttgg aacatggagg ttgtgtcacc gtaatggcac aggacaaacc gactgtcgac 180

atagagctgg ttacaacaac agtcagcaac atggcggagg taagatccta ctgctatgag 240

gcatcaatat cagacatggc ttcggacagc cgctgcccaa cacaaggtga agcctacctt 300

gacaagcaat cagacactca atatgtctgc aaaagaacgt tagtggacag aggctgggga 360

aatggatgtg gacttttgg caaagggagc ctggtgacat gcgctaagtt tgcatgctcc 420

aagaaaatga ccgggaagag catccagcca gagaatctgg agtaccggat aatgctgtca 480

gttcatggct cccagcacag tgggatgatc gttaatgaca caggacatga aactgatgag 540

aatagagcga aggttgagat aacgcccaat tcaccaagag ccgaagccac cctgggggt 600

tttggaagcc taggacttga ttgtgaaccg aggacaggcc ttgacttttc agatttgtat 660

tacttgacta tgaataacaa gcactggttg gttcacaagg agtggttcca cgacattcca 720

ttaccttggc acgctggggc agacaccgga actccacact ggaacaacaa agaagcactg 780

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gctcagatgg cggtggacat gcaaactctg accccagttg ggaggttgat aaccgctaac 1140

cccgtaatca ctgaaagcac tgagaactct aagatgatgc tggaacttga tccaccattt 1200

ggggactctt acattgtcat aggagtcggg gagaagaaga tcacccacca ctggcacagg 1260

agtggcagca ccattggaaa agcatttgaa gccactgtga gaggtgccaa gagaatggca 1320

gtcttgggag acacagcctg ggactttgga tcagttggag gcgctctcaa ctcattgggc 1380

aagggcatcc atcaaatttt tggagcagct ttcaaatcat tgtttggagg aatgtcctgg 1440

ttctcacaaa ttctcattgg aacgttgctg atgtggttgg gtctgaacac aaagaatgga 1500

tctatttccc ttatgtgctt ggccttaggg ggagtgttga tcttcttatc cacagccgtc 1560

tctgcttgat ga 1572

<210> 70

<211> 1572
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp'_ZikaE protein (A9)

<400> 70
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tgcatcggcg tgagcaatag agacttcgtg gagggaatgt ccggaggaac ctgggtggat 120

gtggtgctgg agcacggcgg ctgcgtgaca gtgatggccc aggacaagcc aaccgtggat 180

atcgagctgg tgaccacaac cgtgtccaac atggccgagg tgaggtctta ctgctatgag 240

gccagcatct ccgacatggc ctctgatagc aggtgtccaa cccagggaga ggcatacctg 300

gacaagcagt ccgatacaca gtacgtgtgc aagcggaccc tggtggacag aggctggggc 360

aatggctgtg gcctgtttgg caagggctct ctggtgacat gcgccaagtt cgcctgtagc 420

aagaagatga ccggcaagtc catccagcca gagaacctgg agtaccggat catgctgtct 480

gtgcacggct cccagcactc tggcatgatc gtgaacgaca caggccacga gacagatgag 540

aatcgggcca aggtggagat cacacctaac tctccaagag ccgaggccac cctgggagga 600

tttggctctc tgggcctgga ctgcgagcct agaacaggcc tggacttctc cgatctgtac 660

tatctgacca tgaacaataa gcactggctg gtgcacaagg agtggtttca cgacatccca 720

ctgccatggc acgcaggagc agatacagga acaccacact ggaacaataa ggaggccctg 780

gtggagttca aggatgccca cgccaagcgg cagacagtgg tggtgctggg cagccaggag 840

ggagcagtgc acaccgccct ggcaggcgcc ctggaggcag agatggacgg agctaagggc 900

agactgtcta gcggccacct gaagtgcagg ctgaagatgg ataagctgcg cctgaagggc 960

gtgtcctact ctctgtgcac agccgccttc accttcacca agatccctgc cgagacactg 1020

cacggcacag tgaccgtgga ggtgcagtat gccggcacag acggaccctg taaggtgcct 1080

gcccagatgg ccgtggatat gcagacactg acacctgtgg gcaggctgat caccgccaat 1140

ccagtgatca cagagtctac cgagaacagc aagatgatgc tggagctgga cccaccattt 1200

ggcgatagct atatcgtgat cggcgtgggc gagaagaaga tcacacacca ctggcaccgc 1260

agcggctcca caatcggcaa ggcctttgag gcaaccgtgc gcggagcaaa gagaatggcc 1320

gtgctgggcg acaccgcatg ggatttcgga tctgtgggag gcgccctgaa cagcctgggc 1380

aagggcatcc accagatctt cggcgccgcc tttaagtccc tgttcggcgg catgagctgg 1440

ttctcacaga tcctgatcgg cacactgctg atgtggctgg gcctgaacac caagaatggc 1500

tctatcagcc tgatgtgcct ggccctggga ggcgtgctga tcttcctgtc caccgccgtg 1560

tctgcctgat ga 1572

<210> 71
<211> 522
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp'_ZikaE protein (A9)

<400> 71

Met Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
1 5 10 15

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
20 25 30

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
35 40 45

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
50 55 60

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
65 70 75 80

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
85 90 95

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
100 105 110

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Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
        115                 120                 125

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
    130                 135                 140

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
145                 150                 155                 160

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
                165                 170                 175

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
            180                 185                 190

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
        195                 200                 205

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
    210                 215                 220

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
225                 230                 235                 240

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
                245                 250                 255

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
            260                 265                 270

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
        275                 280                 285

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
    290                 295                 300

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
```

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305                 310                 315                 320

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
                325                 330                 335

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
            340                 345                 350

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
        355                 360                 365

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
    370                 375                 380

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
385                 390                 395                 400

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
                405                 410                 415

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
            420                 425                 430

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
        435                 440                 445

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
    450                 455                 460

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
465                 470                 475                 480

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
                485                 490                 495

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
            500                 505                 510
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Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
515 520

<210> 72
<211> 1428
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp'_ZikaE_no_anchor protein (A10)

<400> 72
atgcaaaaag tcatatactt ggtcatgata ctgctgattg ccccggcata cagcatcagg 60

tgcataggag tcagcaatag ggactttgtg gaaggtatgt caggtgggac ttgggttgat 120

gttgtcttgg aacatggagg ttgtgtcacc gtaatggcac aggacaaacc gactgtcgac 180

atagagctgg ttacaacaac agtcagcaac atggcggagg taagatccta ctgctatgag 240

gcatcaatat cagacatggc ttcggacagc cgctgcccaa cacaaggtga agcctacctt 300

gacaagcaat cagacactca atatgtctgc aaaagaacgt tagtggacag aggctgggga 360

aatggatgtg gacttttgg caaagggagc ctggtgacat gcgctaagtt tgcatgctcc 420

aagaaaatga ccgggaagag catccagcca gagaatctgg agtaccggat aatgctgtca 480

gttcatggct cccagcacag tgggatgatc gttaatgaca caggacatga aactgatgag 540

aatagagcga aggttgagat aacgcccaat tcaccaagag ccgaagccac cctgggggt 600

tttggaagcc taggacttga ttgtgaaccg aggacaggcc ttgacttttc agatttgtat 660

tacttgacta tgaataacaa gcactggttg gttcacaagg agtggttcca cgacattcca 720

ttaccttggc acgctggggc agacaccgga actccacact ggaacaacaa agaagcactg 780

gtagagttca aggacgcaca tgccaaaagg caaactgtcg tggttctagg gagtcaagaa 840

ggagcagttc acacggccct tgctggagct ctggaggctg agatggatgg tgcaaaggga 900

aggctgtcct ctggccactt gaaatgtcgc ctgaaaatgg ataaacttag attgaagggc 960

gtgtcatact ccttgtgtac cgcagcgttc acattcacca agatcccggc tgaaacactg 1020

cacgggacag tcacagtgga ggtacagtac gcagggacag atggaccttg caaggttcca 1080

gctcagatgg cggtggacat gcaaactctg accccagttg ggaggttgat aaccgctaac 1140

cccgtaatca ctgaaagcac tgagaactct aagatgatgc tggaacttga tccaccattt 1200

ggggactctt acattgtcat aggagtcggg gagaagaaga tcacccacca ctggcacagg 1260

agtggcagca ccattggaaa agcatttgaa gccactgtga gaggtgccaa gagaatggca 1320

gtcttgggag acacagcctg ggactttgga tcagttggag gcgctctcaa ctcattgggc 1380

aagggcatcc atcaaatttt tggagcagct ttcaaatcat tgtgatga 1428

<210> 73
<211> 1428
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp'_ZikaE_no_anchor protein (A10)

<400> 73
atgcagaaag tgatctacct ggtcatgatc ctgctgatcg ctcctgccta ttctatccgg 60

tgcatcggcg tgagcaatag agacttcgtg gagggaatgt ccggaggaac ctgggtggat 120

gtggtgctgg agcacggcgg ctgcgtgaca gtgatggccc aggacaagcc aaccgtggat 180

atcgagctgg tgaccacaac cgtgtccaac atggccgagg tgaggtctta ctgctatgag 240

gccagcatct ccgacatggc ctctgatagc aggtgtccaa cccagggaga ggcatacctg 300

gacaagcagt ccgatacaca gtacgtgtgc aagcggaccc tggtggacag aggctggggc 360

aatggctgtg gcctgtttgg caagggctct ctggtgacat gcgccaagtt cgcctgtagc 420

aagaagatga ccggcaagtc catccagcca gagaacctgg agtaccggat catgctgtct 480

gtgcacggct cccagcactc tggcatgatc gtgaacgaca caggccacga gacagatgag 540

aatcgggcca aggtggagat cacacctaac tctccaagag ccgaggccac cctgggagga 600

tttggctctc tgggcctgga ctgcgagcct agaacaggcc tggacttctc cgatctgtac 660

tatctgacca tgaacaataa gcactggctg gtgcacaagg agtggtttca cgacatccca 720

ctgccatggc acgcaggagc agatacagga acaccacact ggaacaataa ggaggccctg 780

gtggagttca aggatgccca cgccaagcgg cagacagtgg tggtgctggg cagccaggag 840

ggagcagtgc acaccgccct ggcaggcgcc ctggaggcag agatggacgg agctaagggc 900

agactgtcta gcggccacct gaagtgcagg ctgaagatgg ataagctgcg cctgaagggc 960

gtgtcctact ctctgtgcac agccgccttc accttcacca agatccctgc cgagacactg 1020

cacggcacag tgaccgtgga ggtgcagtat gccggcacag acggaccctg taaggtgcct 1080

gcccagatgg ccgtggatat gcagacactg acacctgtgg gcaggctgat caccgccaat 1140

ccagtgatca cagagtctac cgagaacagc aagatgatgc tggagctgga cccaccattt 1200

ggcgatagct atatcgtgat cggcgtgggc gagaagaaga tcacacacca ctggcaccgc 1260

agcggctcca caatcggcaa ggcctttgag gcaaccgtgc gcggagcaaa gagaatggcc 1320

gtgctgggcg acaccgcatg ggatttcgga tctgtgggag gcgccctgaa cagcctgggc 1380

aagggcatcc accagatctt cggcgccgcc tttaagtccc tgtgatga 1428

<210> 74
<211> 474
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp'_ZikaE_no_anchor protein (A10)

<400> 74

Met Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
1 5 10 15

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
20 25 30

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
35 40 45

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
50 55 60

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
65 70 75 80

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Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
                85                  90                  95

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
            100                 105                 110

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
        115                 120                 125

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
    130                 135                 140

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
145                 150                 155                 160

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
                165                 170                 175

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
            180                 185                 190

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
        195                 200                 205

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
    210                 215                 220

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
225                 230                 235                 240

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
                245                 250                 255

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
            260                 265                 270

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
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        275                 280                 285

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
    290                 295                 300

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
305                 310                 315                 320

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
                325                 330                 335

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
            340                 345                 350

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
        355                 360                 365

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
    370                 375                 380

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
385                 390                 395                 400

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
                405                 410                 415

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
            420                 425                 430

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
        435                 440                 445

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
    450                 455                 460

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465                 470
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<210> 75
<211> 1392
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp'_ZikaE411 protein (A11)

<400> 75
atgcaaaaag tcatatactt ggtcatgata ctgctgattg ccccggcata cagcatcagg 60

tgcataggag tcagcaatag ggactttgtg gaaggtatgt caggtgggac ttgggttgat 120

gttgtcttgg aacatggagg ttgtgtcacc gtaatggcac aggacaaacc gactgtcgac 180

atagagctgg ttacaacaac agtcagcaac atggcggagg taagatccta ctgctatgag 240

gcatcaatat cagacatggc ttcggacagc cgctgcccaa cacaaggtga agcctacctt 300

gacaagcaat cagacactca atatgtctgc aaaagaacgt tagtggacag aggctgggga 360

aatggatgtg gacttttgg caaagggagc ctggtgacat gcgctaagtt tgcatgctcc 420

aagaaaatga ccgggaagag catccagcca gagaatctgg agtaccggat aatgctgtca 480

gttcatggct cccagcacag tgggatgatc gttaatgaca caggacatga aactgatgag 540

aatagagcga aggttgagat aacgcccaat tcaccaagag ccgaagccac cctgggggt 600

tttggaagcc taggacttga ttgtgaaccg aggacaggcc ttgacttttc agatttgtat 660

tacttgacta tgaataacaa gcactggttg gttcacaagg agtggttcca cgacattcca 720

ttaccttggc acgctggggc agacaccgga actccacact ggaacaacaa agaagcactg 780

gtagagttca aggacgcaca tgccaaaagg caaactgtcg tggttctagg gagtcaagaa 840

ggagcagttc acacggccct tgctggagct ctggaggctg agatggatgg tgcaaaggga 900

aggctgtcct ctggccactt gaaatgtcgc ctgaaaatgg ataaacttag attgaagggc 960

gtgtcatact ccttgtgtac cgcagcgttc acattcacca agatcccggc tgaaacactg 1020

cacgggacag tcacagtgga ggtacagtac gcagggacag atggaccttg caaggttcca 1080

gctcagatgg cggtggacat gcaaactctg accccagttg ggaggttgat aaccgctaac 1140

cccgtaatca ctgaaagcac tgagaactct aagatgatgc tggaacttga tccaccattt 1200

ggggactctt acattgtcat aggagtcggg gagaagaaga tcacccacca ctggcacagg 1260

agtggcagca ccattggaaa agcatttgaa gccactgtga gaggtgccaa gagaatggca 1320

gtcttgggag acacagcctg ggactttgga tcagttggag gcgctctcaa ctcattgggc 1380

aagggcatct ga 1392

<210> 76
<211> 1392
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp'_ZikaE411 protein (A11)

<400> 76
atgcagaaag tgatctacct ggtcatgatc ctgctgatcg ctcctgccta ttctatccgg 60

tgcatcggcg tgagcaatag agacttcgtg gagggaatgt ccggaggaac ctgggtggat 120

gtggtgctgg agcacggcgg ctgcgtgaca gtgatggccc aggacaagcc aaccgtggat 180

atcgagctgg tgaccacaac cgtgtccaac atggccgagg tgaggtctta ctgctatgag 240

gccagcatct ccgacatggc ctctgatagc aggtgtccaa cccagggaga ggcatacctg 300

gacaagcagt ccgatacaca gtacgtgtgc aagcggaccc tggtggacag aggctggggc 360

aatggctgtg gcctgtttgg caagggctct ctggtgacat gcgccaagtt cgcctgtagc 420

aagaagatga ccggcaagtc catccagcca gagaacctgg agtaccggat catgctgtct 480

gtgcacggct cccagcactc tggcatgatc gtgaacgaca caggccacga gacagatgag 540

aatcgggcca aggtggagat cacacctaac tctccaagag ccgaggccac cctgggagga 600

tttggctctc tgggcctgga ctgcgagcct agaacaggcc tggacttctc cgatctgtac 660

tatctgacca tgaacaataa gcactggctg gtgcacaagg agtggtttca cgacatccca 720

ctgccatggc acgcaggagc agatacagga acaccacact ggaacaataa ggaggccctg 780

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agactgtcta gcggccacct gaagtgcagg ctgaagatgg ataagctgcg cctgaagggc 960

gtgtcctact ctctgtgcac agccgccttc accttcacca agatccctgc cgagacactg 1020

cacggcacag tgaccgtgga ggtgcagtat gccggcacag acggaccctg taaggtgcct 1080

gcccagatgg ccgtggatat gcagacactg acacctgtgg gcaggctgat caccgccaat 1140

ccagtgatca cagagtctac cgagaacagc aagatgatgc tggagctgga cccaccattt 1200

ggcgatagct atatcgtgat cggcgtgggc gagaagaaga tcacacacca ctggcaccgc 1260

agcggctcca caatcggcaa ggcctttgag gcaaccgtgc gcggagcaaa gagaatggcc 1320

gtgctgggcg acaccgcatg ggatttcgga tctgtgggag gcgccctgaa cagcctgggc 1380

aagggcatct ga 1392

<210> 77
<211> 463
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp'_ZikaE411 protein (A11)

<400> 77

Met Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
1 5 10 15

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
20 25 30

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
35 40 45

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
50 55 60

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
65 70 75 80

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
85 90 95

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Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
            100                 105                 110

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
        115                 120                 125

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
    130                 135                 140

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
145                 150                 155                 160

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
                165                 170                 175

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
            180                 185                 190

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
        195                 200                 205

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
    210                 215                 220

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
225                 230                 235                 240

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
                245                 250                 255

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
            260                 265                 270

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
        275                 280                 285

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
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290 295 300

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
305 310 315 320

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
325 330 335

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
340 345 350

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
355 360 365

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
370 375 380

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
385 390 395 400

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
405 410 415

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
420 425 430

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
435 440 445

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
450 455 460

<210> 78
<211> 1266
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp’_ZikaE395 protein (A12)

<400> 78
atgcaaaaag tcatatactt ggtcatgata ctgctgattg ccccggcata cagcatcagg 60

tgcataggag tcagcaatag ggactttgtg gaaggtatgt caggtgggac ttgggttgat 120

gttgtcttgg aacatggagg ttgtgtcacc gtaatggcac aggacaaacc gactgtcgac 180

atagagctgg ttacaacaac agtcagcaac atggcggagg taagatccta ctgctatgag 240

gcatcaatat cagacatggc ttcggacagc cgctgcccaa cacaaggtga agcctacctt 300

gacaagcaat cagacactca atatgtctgc aaaagaacgt tagtggacag aggctgggga 360

aatggatgtg gacttttgg caaagggagc ctggtgacat gcgctaagtt tgcatgctcc 420

aagaaaatga ccgggaagag catccagcca gagaatctgg agtaccggat aatgctgtca 480

gttcatggct cccagcacag tgggatgatc gttaatgaca caggacatga aactgatgag 540

aatagagcga aggttgagat aacgcccaat tcaccaagag ccgaagccac cctgggggt 600

tttggaagcc taggacttga ttgtgaaccg aggacaggcc ttgacttttc agatttgtat 660

tacttgacta tgaataacaa gcactggttg gttcacaagg agtggttcca cgacattcca 720

ttaccttggc acgctggggc agacaccgga actccacact ggaacaacaa agaagcactg 780

gtagagttca aggacgcaca tgccaaaagg caaactgtcg tggttctagg gagtcaagaa 840

ggagcagttc acacggccct tgctggagct ctggaggctg agatggatgg tgcaaaggga 900

aggctgtcct ctggccactt gaaatgtcgc ctgaaaatgg ataaacttag attgaagggc 960

gtgtcatact ccttgtgtac cgcagcgttc acattcacca agatcccggc tgaaacactg 1020

cacgggacag tcacagtgga ggtacagtac gcagggacag atggaccttg caaggttcca 1080

gctcagatgg cggtggacat gcaaactctg accccagttg ggaggttgat aaccgctaac 1140

cccgtaatca ctgaaagcac tgagaactct aagatgatgc tggaacttga tccaccattt 1200

ggggactctt acattgtcat aggagtcggg gagaagaaga tcacccacca ctggcacagg 1260

agtggc 1266

<210> 79
<211> 1272
<212> DNA

<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp'_ZikaE395 protein (A12)

<400> 79
atgcagaaag tgatctacct ggtcatgatc ctgctgatcg ctcctgccta ttctatccgg 60

tgcatcggcg tgagcaatag agacttcgtg gagggaatgt ccggaggaac ctgggtggat 120

gtggtgctgg agcacggcgg ctgcgtgaca gtgatggccc aggacaagcc aaccgtggat 180

atcgagctgg tgaccacaac cgtgtccaac atggccgagg tgaggtctta ctgctatgag 240

gccagcatct ccgacatggc ctctgatagc aggtgtccaa cccagggaga ggcatacctg 300

gacaagcagt ccgatacaca gtacgtgtgc aagcggaccc tggtggacag aggctggggc 360

aatggctgtg gcctgtttgg caagggctct ctggtgacat gcgccaagtt cgcctgtagc 420

aagaagatga ccggcaagtc catccagcca gagaacctgg agtaccggat catgctgtct 480

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<210> 80
<211> 422
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp'_ZikaE395 protein (A12)

<400> 80

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            20                  25                  30


Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
        35                  40                  45


Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
    50                  55                  60


Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
65                  70                  75                  80


Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
                85                  90                  95


Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
            100                 105                 110


Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
        115                 120                 125


Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
    130                 135                 140


Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
145                 150                 155                 160
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Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
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Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
            180                 185                 190

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
        195                 200                 205

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
    210                 215                 220

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
225                 230                 235                 240

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
                245                 250                 255

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
            260                 265                 270

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
        275                 280                 285

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
    290                 295                 300

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
305                 310                 315                 320

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
                325                 330                 335

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
            340                 345                 350

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
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355 360 365

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
370 375 380

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
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Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
405 410 415

His Trp His Arg Ser Gly
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<210> 81
<211> 2094
<212> DNA
<213> Artificial sequence

<220>
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cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

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gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg 480

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gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

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aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ccatcaaatt 1920

tttggagcag ctttcaaatc attgtttgga ggaatgtcct ggttctcaca aattctcatt 1980

ggaacgttgc tgatgtggtt gggtctgaac acaaagaatg gatctatttc ccttatgtgc 2040

ttggccttag ggggagtgtt gatcttctta tccacagccg tctctgcttg atga 2094

<210> 82

<211> 2094
<212> DNA
<213> Artificial sequence

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<223> Codon-optimized nucleotide sequence of JEVsp_ZikaprME protein (B1)

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aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

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gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

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accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

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<210> 83
<211> 696
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_ZikaprME protein (B1)

<400> 83

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20 25 30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
35 40 45

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Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50                  55                  60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65                  70                  75                  80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85                  90                  95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
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                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
        435                 440                 445
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Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595                 600                 605

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610                 615                 620

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
625                 630                 635                 640

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
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645 650 655

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
660 665 670

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
675 680 685

Phe Leu Ser Thr Ala Val Ser Ala
690 695

<210> 84
<211> 1950
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_Zika_prME_no_Anchor protein (B2)

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cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt 300

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caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

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tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ccatcaaatt 1920

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<210> 85
<211> 1950
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_Zika_prME_no_Anchor protein (B2)

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<210> 86
<211> 648
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_Zika_prME_no_Anchor protein (B2)

<400> 86

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20 25 30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
35 40 45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
50 55 60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65 70 75 80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
85 90 95

```
Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285
```

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Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
        435                 440                 445

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495
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Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595                 600                 605

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610                 615                 620

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
625                 630                 635                 640

Phe Gly Ala Ala Phe Lys Ser Leu
                645
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<210> 87
<211> 1914
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_Zika_prME411 protein (B3)

<400> 87
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tgtgcaggag ccgcggaggt cactagacgt gggagtgcat actatatgta cttggacaga 120

aacgatgctg gggaggccat atcttttcca accacattgg ggatgaataa gtgttatata 180

cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt 300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg 360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga 420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg 480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac 540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat 600

agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga 660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

agcatccagc cagagaatct ggagtaccgg ataatgctgt cagttcatgg ctcccagcac 1020

agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag 1080

ataacgccca attcaccaag agccgaagcc accctggggg gttttggaag cctaggactt 1140

gattgtgaac cgaggacagg ccttgacttt tcagatttgt attacttgac tatgaataac 1200

aagcactggt tggttcacaa ggagtggttc cacgacattc cattaccttg gcacgctggg 1260

gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca 1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt 1500

accgcagcgt tcacattcac caagatcccg gctgaaacac tgcacgggac agtcacagtg 1560

gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac 1620

atgcaaactc tgaccccagt tgggaggttg ataaccgcta accccgtaat cactgaaagc 1680

actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ctga 1914

<210> 88
<211> 1914
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_Zika_prME411 protein (B3)

<400> 88
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tgtgcaggag cagcagaggt gaccaggaga ggaagcgcct actatatgta cctggacagg 120

aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

agagacttcg tggagggaat gtccggagga acctgggtgg atgtggtgct ggagcacggc 660

ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt 900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag 960

tccatccagc cagagaacct ggagtaccgg atcatgctgt ctgtgcacgg ctcccagcac 1020

tctggcatga tcgtgaacga cacaggccac gagacagatg agaatcgggc caaggtggag 1080

atcacaccta actctccaag agccgaggcc accctgggag gatttggctc tctgggcctg 1140

gactgcgagc ctagaacagg cctggacttc tccgatctgt actatctgac catgaacaat 1200

aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

ctgaagtgca ggctgaagat ggataagctg cgcctgaagg gcgtgtccta ctctctgtgc 1500

acagccgcct tcaccttcac caagatccct gccgagacac tgcacggcac agtgaccgtg 1560

gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

atgcagacac tgacacctgt gggcaggctg atcaccgcca atccagtgat cacagagtct 1680

accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctc cacaatcggc 1800

aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

tgggatttcg gatctgtggg aggcgccctg aacagcctgg gcaagggcat ctga 1914

<210> 89
<211> 637
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_Zika_prME411 protein (B3)

<400> 89

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1               5                   10                  15

Val Val Ile Ala Cys Ala Gly Ala Ala Glu Val Thr Arg Arg Gly Ser
            20                  25                  30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
        35                  40                  45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50                  55                  60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65                  70                  75                  80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85                  90                  95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205
```

```
Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400
```

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Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
        435                 440                 445

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595                 600                 605
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Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
610 615 620

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625 630 635

<210> 90
<211> 1794
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_Zika_prME395 protein (B4)

<400> 90
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aacgatgctg gggaggccat atcttttcca accacattgg ggatgaataa gtgttatata 180

cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt 300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg 360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga 420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg 480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac 540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat 600

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ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

agcatccagc cagagaatct ggagtaccgg ataatgctgt cagttcatgg ctcccagcac 1020

agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag 1080

ataacgccca attcaccaag agccgaagcc accctggggg gttttggaag cctaggactt 1140

gattgtgaac cgaggacagg ccttgacttt tcagatttgt attacttgac tatgaataac 1200

aagcactggt tggttcacaa ggagtggttc cacgacattc cattaccttg gcacgctggg 1260

gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca 1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt 1500

accgcagcgt tcacattcac caagatcccg gctgaaacac tgcacgggac agtcacagtg 1560

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ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggctg atga 1794

<210> 91
<211> 1794
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_Zika_prME395 protein (B4)

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aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

agagacttcg tggagggaat gtccggagga acctgggtgg atgtggtgct ggagcacggc 660

ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt 900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag 960

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gactgcgagc ctagaacagg cctggacttc tccgatctgt actatctgac catgaacaat 1200

aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

ctgaagtgca ggctgaagat ggataagctg cgcctgaagg gcgtgtccta ctctctgtgc 1500

acagccgcct tcaccttcac caagatccct gccgagacac tgcacggcac agtgaccgtg 1560

gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

atgcagacac tgacacctgt gggcaggctg atcaccgcca atccagtgat cacagagtct 1680

accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctg atga 1794

<210> 92
<211> 596
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_Zika_prME395 protein (B4)

<400> 92

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Val Val Ile Ala Cys Ala Gly Ala Ala Glu Val Thr Arg Arg Gly Ser
            20                  25                  30


Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
        35                  40                  45


Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50                  55                  60


Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65                  70                  75                  80


Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85                  90                  95


Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110


Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125


Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140


His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160
```

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Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
        355                 360                 365
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Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
        435                 440                 445

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560
```

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
565 570 575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
580 585 590

His Arg Ser Gly
595

<210> 93
<211> 1590
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_ZikaE protein (B5)

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ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag 180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta 240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tgggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

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ttcttatcca cagccgtctc tgcttgatga 1590

<210> 94
<211> 1590
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<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_ZikaE protein (B5)

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gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

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cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc 420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

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gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

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atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat 960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag 1020

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gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc 1320

ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc 1380

gccctgaaca gcctgggcaa gggcatccac cagatcttcg gcgccgcctt taagtccctg 1440

ttcggcggca tgagctggtt ctcacagatc ctgatcggca cactgctgat gtggctgggc 1500

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ttcctgtcca ccgccgtgtc tgcctgatga 1590

<210> 95
<211> 528
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_ZikaE protein (B5)

<400> 95

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            20                  25                  30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35                  40                  45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50                  55                  60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65                  70                  75                  80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205
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Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

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

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400
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Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415


Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420                 425                 430


Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435                 440                 445


Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
    450                 455                 460


Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465                 470                 475                 480


Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu
                485                 490                 495


Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu Met Cys
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Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
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<210>  96
<211>  1446
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of JEVsp_ZikaE_no_Anchor protein (B6)

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ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag      180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta      240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca      300
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caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tgggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

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ggtgccaaga gaatggcagt cttgggagac acagcctggg actttggatc agttggaggc 1380

gctctcaact cattgggcaa gggcatccat caaatttttg gagcagcttt caaatcattg 1440

tgatga 1446

<210> 97
<211> 1446
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_ZikaE_no_Anchor protein (B6)

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ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

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taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca 540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc 600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

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gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

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<210> 98
<211> 480
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_ZikaE_no_Anchor protein (B6)

<400> 98

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            20                  25                  30


Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35                  40                  45


Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50                  55                  60


Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65                  70                  75                  80


Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95


Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110


Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125


Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140


Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160
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Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

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

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350
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Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420                 425                 430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435                 440                 445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
    450                 455                 460

Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465                 470                 475                 480
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<210> 99
<211> 1410
<212> DNA
<213> Artificial sequence

<220>
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ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag 180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta 240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

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gaagccaccc tgggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

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aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

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gctctcaact cattgggcaa gggcatctga 1410

<210> 100
<211> 1410
<212> DNA
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<223> Codon-optimized nucleotide sequence of JEVsp_ZikaE411 protein (B7)

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gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

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gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

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aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag 1020

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gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc 1320

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<210> 101
<211> 469

<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_ZikaE411 protein (B7)

<400> 101

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            20                  25                  30


Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35                  40                  45


Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50                  55                  60


Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65                  70                  75                  80


Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95


Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110


Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125


Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140


Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160


Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175
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Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

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

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365
```

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Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420                 425                 430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435                 440                 445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
    450                 455                 460

Leu Gly Lys Gly Ile
465
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<210> 102
<211> 1290
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_ZikaE395 protein (B8)

<400> 102

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tgtgcaggag ccatcaggtg cataggagtc agcaataggg actttgtgga aggtatgtca      120

ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag      180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta      240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca      300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta      360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc      420
```

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tgggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg 1140

aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg 1200

gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc 1260

acccaccact ggcacaggag tggctgatga 1290

<210> 103
<211> 1290
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_ZikaE395 protein (B8)

<400> 103
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tgtgcaggag caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc 120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc 300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc 420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca 540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc 600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag 900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat 960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag 1020

atccctgccg agacactgca cggcacagtg accgtggagg tgcagtatgc cggcacagac 1080

ggaccctgta aggtgcctgc ccagatggcc gtggatatgc agacactgac acctgtgggc 1140

aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg 1200

gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctgatga 1290

<210> 104
<211> 428
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_ZikaE395 protein (B8)

<400> 104

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

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Val Val Ile Ala Cys Ala Gly Ala Ile Arg Cys Ile Gly Val Ser Asn
            20                  25                  30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35                  40                  45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50                  55                  60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65                  70                  75                  80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220
```

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Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

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

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415
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Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly
420 425

<210> 105
<211> 2106
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_ZikaprME (C1)

<400> 105
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ctccaaacac ccaccggtca aatccatgcg gaggtcacta gacgtgggag tgcatactat 120

atgtacttgg acagaaacga tgctggggag gccatatctt ttccaaccac attggggatg 180

aataagtgtt atatacagat catggatctt ggacacatgt gtgatgccac catgagctat 240

gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg 300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct 360

agaagagctg tgacgctccc ctcccattcc actaggaagc tgcaaacgcg gtcgcaaacc 420

tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg 480

aaccctggct tcgcgttagc agcagctgcc atcgcttggc ttttgggaag ctcaacgagc 540

caaaaagtca tatacttggt catgatactg ctgattgccc cggcatacag catcaggtgc 600

ataggagtca gcaataggga ctttgtggaa ggtatgtcag gtgggacttg ggttgatgtt 660

gtcttggaac atggaggttg tgtcaccgta atggcacagg acaaaccgac tgtcgacata 720

gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca 780

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac 840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat 900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag 960

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt 1020

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat 1080

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct ggggggtttt 1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 1200

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta 1260

ccttggcacg ctggggcaga caccggaact ccacactgga acaacaaaga agcactggta 1320

gagttcaagg acgcacatgc caaaaggcaa actgtcgtgg ttctagggag tcaagaagga 1380

gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 1440

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 1500

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac 1560

gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1620

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1680

gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1740

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1800

ggcagcacca ttggaaaagc atttgaagcc actgtgagag gtgccaagag aatggcagtc 1860

ttgggagaca cagcctggga ctttggatca gttggaggcg ctctcaactc attgggcaag 1920

ggcatccatc aaatttttgg agcagctttc aaatcattgt ttggaggaat gtcctggttc 1980

tcacaaattc tcattggaac gttgctgatg tggttgggtc tgaacacaaa gaatggatct 2040

atttccctta tgtgcttggc cttaggggga gtgttgatct tcttatccac agccgtctct 2100

gcttga 2106

<210> 106
<211> 2106
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaprME (C1)

<400> 106
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ctgcagacac caacaggcca gatccacgca gaggtgacca ggagaggaag cgcctactat 120

atgtacctgg acaggaatga tgccggcgag gccatctcct tcccaaccac actgggcatg 180

aacaagtgct acatccagat catggacctg ggccacatgt gcgatgccac catgtcctat 240

gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc 300

acatctacat gggtggtgta cggcacctgt caccacaaga agggagaggc ccggcggagc 360

cggcgggccg tgacactgcc ttcccactct accaggaagc tgcagacacg cagccagacc 420

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aatccaggat tcgcactggc agcagcagca atcgcatggc tgctgggaag ctccaccagc 540

cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc 600

atcggcgtga gcaatagaga cttcgtggag ggaatgtccg gaggaacctg ggtggatgtg 660

gtgctggagc acggcggctg cgtgacagtg atggcccagg acaagccaac cgtggatatc 720

gagctggtga ccacaaccgt gtccaacatg gccgaggtga ggtcttactg ctatgaggcc 780

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ggctgtggcc tgtttggcaa gggctctctg gtgacatgcg ccaagttcgc ctgtagcaag 960

aagatgaccg gcaagtccat ccagccagag aacctggagt accggatcat gctgtctgtg 1020

cacggctccc agcactctgg catgatcgtg aacgacacag gccacgagac agatgagaat 1080

cgggccaagg tggagatcac acctaactct ccaagagccg aggccaccct gggaggattt 1140

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gagttcaagg atgcccacgc caagcggcag acagtggtgg tgctgggcag ccaggaggga 1380

gcagtgcaca ccgccctggc aggcgccctg gaggcagaga tggacggagc taagggcaga 1440

ctgtctagcg gccacctgaa gtgcaggctg aagatggata agctgcgcct gaagggcgtg 1500

tcctactctc tgtgcacagc cgccttcacc ttcaccaaga tccctgccga gacactgcac 1560

ggcacagtga ccgtggaggt gcagtatgcc ggcacagacg gaccctgtaa ggtgcctgcc 1620

cagatggccg tggatatgca gacactgaca cctgtgggca ggctgatcac cgccaatcca 1680

gtgatcacag agtctaccga gaacagcaag atgatgctgg agctggaccc accatttggc 1740

gatagctata tcgtgatcgg cgtgggcgag aagaagatca cacaccactg gcaccgcagc 1800

ggctccacaa tcggcaaggc ctttgaggca accgtgcgcg gagcaaagag aatggccgtg 1860

ctgggcgaca ccgcatggga tttcggatct gtgggaggcg ccctgaacag cctgggcaag 1920

ggcatccacc agatcttcgg cgccgccttt aagtccctgt tcggcggcat gagctggttc 1980

tcacagatcc tgatcggcac actgctgatg tggctgggcc tgaacaccaa gaatggctct 2040

atcagcctga tgtgcctggc cctgggaggc gtgctgatct tcctgtccac cgccgtgtct 2100

gcctga 2106

<210> 107
<211> 701
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaprME (C1)

<400> 107

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ala Glu Val
20 25 30

Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
35 40 45

Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
50 55 60

Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65 70 75 80

Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
85 90 95

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Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
            100                 105                 110

Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser
        115                 120                 125

His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
    130                 135                 140

Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145                 150                 155                 160

Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165                 170                 175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180                 185                 190

Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195                 200                 205

Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210                 215                 220

Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile
225                 230                 235                 240

Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr
                245                 250                 255

Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260                 265                 270

Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275                 280                 285
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Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300

Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305                 310                 315                 320

Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325                 330                 335

Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340                 345                 350

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

Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370                 375                 380

Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385                 390                 395                 400

Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405                 410                 415

Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420                 425                 430

Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435                 440                 445

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450                 455                 460

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

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485                 490                 495
```

```
Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500                 505                 510

Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515                 520                 525

Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530                 535                 540

Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545                 550                 555                 560

Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565                 570                 575

Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580                 585                 590

Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe
        595                 600                 605

Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr
    610                 615                 620

Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys
625                 630                 635                 640

Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly
                645                 650                 655

Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu
            660                 665                 670

Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu
        675                 680                 685
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Gly Gly Val Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
690 695 700

<210> 108
<211> 1962
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_Zika_prME_no_anchor (C2)

<400> 108
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ctccaaacac ccaccggtca aatccatgcg gaggtcacta gacgtgggag tgcatactat 120

atgtacttgg acagaaacga tgctggggag gccatatctt ttccaaccac attggggatg 180

aataagtgtt atatacagat catggatctt ggacacatgt gtgatgccac catgagctat 240

gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg 300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct 360

agaagagctg tgacgctccc ctcccattcc actaggaagc tgcaaacgcg gtcgcaaacc 420

tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg 480

aaccctggct tcgcgttagc agcagctgcc atcgcttggc ttttgggaag ctcaacgagc 540

caaaaagtca tatacttggt catgatactg ctgattgccc cggcatacag catcaggtgc 600

ataggagtca gcaataggga ctttgtggaa ggtatgtcag gtgggacttg ggttgatgtt 660

gtcttggaac atggaggttg tgtcaccgta atggcacagg acaaaccgac tgtcgacata 720

gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca 780

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac 840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat 900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag 960

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt 1020

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat 1080

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct ggggggtttt 1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 1200

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta 1260

ccttggcacg ctggggcaga caccggaact ccacactgga acaacaaaga agcactggta 1320

gagttcaagg acgcacatgc caaaaggcaa actgtcgtgg ttctagggag tcaagaagga 1380

gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 1440

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 1500

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac 1560

gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1620

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1680

gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1740

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1800

ggcagcacca ttggaaaagc atttgaagcc actgtgagag gtgccaagag aatggcagtc 1860

ttgggagaca cagcctggga ctttggatca gttggaggcg ctctcaactc attgggcaag 1920

ggcatccatc aaatttttgg agcagctttc aaatcattgt ga 1962

<210> 109
<211> 1962
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_Zika_prME_no_anchor (C2)

<400> 109
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccacgca gaggtgacca ggagaggaag cgcctactat 120

atgtacctgg acaggaatga tgccggcgag gccatctcct tcccaaccac actgggcatg 180

aacaagtgct acatccagat catggacctg ggccacatgt gcgatgccac catgtcctat 240

gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc 300

acatctacat gggtggtgta cggcacctgt caccacaaga agggagaggc ccggcggagc 360

cggcgggccg tgacactgcc ttcccactct accaggaagc tgcagacacg cagccagacc 420

tggctggagt ccagagagta taccaagcac ctgatcaggg tggagaactg gatctttcgc 480

aatccaggat tcgcactggc agcagcagca atcgcatggc tgctgggaag ctccaccagc 540

cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc 600

atcggcgtga gcaatagaga cttcgtggag ggaatgtccg gaggaacctg ggtggatgtg 660

gtgctggagc acggcggctg cgtgacagtg atggcccagg acaagccaac cgtggatatc 720

gagctggtga ccacaaccgt gtccaacatg gccgaggtga ggtcttactg ctatgaggcc 780

agcatctccg acatggcctc tgatagcagg tgtccaaccc agggagaggc atacctggac 840

aagcagtccg atacacagta cgtgtgcaag cggaccctgg tggacagagg ctggggcaat 900

ggctgtggcc tgtttggcaa gggctctctg gtgacatgcg ccaagttcgc ctgtagcaag 960

aagatgaccg gcaagtccat ccagccagag aacctggagt accggatcat gctgtctgtg 1020

cacggctccc agcactctgg catgatcgtg aacgacacag gccacgagac agatgagaat 1080

cgggccaagg tggagatcac acctaactct ccaagagccg aggccaccct gggaggattt 1140

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ctgaccatga acaataagca ctggctggtg cacaaggagt ggtttcacga catcccactg 1260

ccatggcacg caggagcaga tacaggaaca ccacactgga acaataagga ggccctggtg 1320

gagttcaagg atgcccacgc caagcggcag acagtggtgg tgctgggcag ccaggaggga 1380

gcagtgcaca ccgccctggc aggcgccctg gaggcagaga tggacggagc taagggcaga 1440

ctgtctagcg gccacctgaa gtgcaggctg aagatggata agctgcgcct gaagggcgtg 1500

tcctactctc tgtgcacagc cgccttcacc ttcaccaaga tccctgccga gacactgcac 1560

ggcacagtga ccgtggaggt gcagtatgcc ggcacagacg gaccctgtaa ggtgcctgcc 1620

cagatggccg tggatatgca gacactgaca cctgtgggca ggctgatcac cgccaatcca 1680

gtgatcacag agtctaccga gaacagcaag atgatgctgg agctggaccc accatttggc 1740

gatagctata tcgtgatcgg cgtgggcgag aagaagatca cacaccactg gcaccgcagc 1800

ggctccacaa tcggcaaggc ctttgaggca accgtgcgcg gagcaaagag aatggccgtg 1860

ctgggcgaca ccgcatggga tttcggatct gtgggaggcg ccctgaacag cctgggcaag 1920

ggcatccacc agatcttcgg cgccgccttt aagtccctgt ga 1962

<210> 110
<211> 653
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_Zika_prME_no_anchor (C2)

<400> 110

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ala Glu Val
20 25 30

Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
35 40 45

Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
50 55 60

Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65 70 75 80

Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
85 90 95

Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
100 105 110

Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser
115 120 125

His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
130 135 140

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Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145                 150                 155                 160

Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165                 170                 175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180                 185                 190

Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195                 200                 205

Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210                 215                 220

Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile
225                 230                 235                 240

Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr
                245                 250                 255

Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260                 265                 270

Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275                 280                 285

Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300

Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305                 310                 315                 320

Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325                 330                 335
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Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340                 345                 350

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

Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370                 375                 380

Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385                 390                 395                 400

Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405                 410                 415

Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420                 425                 430

Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435                 440                 445

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450                 455                 460

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

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485                 490                 495

Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500                 505                 510

Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515                 520                 525

Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530                 535                 540
```

```
Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545                 550                 555                 560

Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565                 570                 575

Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580                 585                 590

Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe
        595                 600                 605

Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr
    610                 615                 620

Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys
625                 630                 635                 640

Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
                645                 650
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<210> 111
<211> 1932
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_Zika_prME411 (C3)

<400> 111

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atgtacttgg acagaaacga tgctggggag gccatatctt ttccaaccac attggggatg      180

aataagtgtt atatacagat catggatctt ggacacatgt gtgatgccac catgagctat      240

gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg      300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct      360
```

agaagagctg tgacgctccc ctcccattcc actaggaagc tgcaaacgcg gtcgcaaacc 420

tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg 480

aaccctggct tcgcgttagc agcagctgcc atcgcttggc ttttgggaag ctcaacgagc 540

caaaaagtca tatacttggt catgatactg ctgattgccc cggcatacag catcaggtgc 600

ataggagtca gcaataggga ctttgtggaa ggtatgtcag gtgggacttg ggttgatgtt 660

gtcttggaac atggaggttg tgtcaccgta atggcacagg acaaaccgac tgtcgacata 720

gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca 780

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac 840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat 900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag 960

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt 1020

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat 1080

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct ggggggtttt 1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 1200

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta 1260

ccttggcacg ctggggcaga caccggaact ccacactgga acaacaaaga agcactggta 1320

gagttcaagg acgcacatgc caaaaggcaa actgtcgtgg ttctagggag tcaagaagga 1380

gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 1440

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 1500

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac 1560

gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1620

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1680

gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1740

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1800

ggcagcacca ttggaaaagc atttgaagcc actgtgagag gtgccaagag aatggcagtc 1860

ttgggagaca cagcctggga ctttggatca gttggaggcg ctctcaactc attgggcaag 1920

ggcatctgat ga 1932

<210> 112
<211> 1932
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_Zika_prME411 (C3)

<400> 112
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ctgcagacac caacaggcca gatccacgca gaggtgacca ggagaggaag cgcctactat 120

atgtacctgg acaggaatga tgccggcgag gccatctcct tcccaaccac actgggcatg 180

aacaagtgct acatccagat catggacctg ggccacatgt gcgatgccac catgtcctat 240

gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc 300

acatctacat gggtggtgta cggcacctgt caccacaaga agggagaggc ccggcggagc 360

cggcgggccg tgacactgcc ttcccactct accaggaagc tgcagacacg cagccagacc 420

tggctggagt ccagagagta taccaagcac ctgatcaggg tggagaactg gatctttcgc 480

aatccaggat tcgcactggc agcagcagca atcgcatggc tgctgggaag ctccaccagc 540

cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc 600

atcggcgtga gcaatagaga cttcgtggag ggaatgtccg gaggaacctg ggtggatgtg 660

gtgctggagc acggcggctg cgtgacagtg atggcccagg acaagccaac cgtggatatc 720

gagctggtga ccacaaccgt gtccaacatg gccgaggtga ggtcttactg ctatgaggcc 780

agcatctccg acatggcctc tgatagcagg tgtccaaccc agggagaggc atacctggac 840

aagcagtccg atacacagta cgtgtgcaag cggaccctgg tggacagagg ctggggcaat 900

ggctgtggcc tgtttggcaa gggctctctg gtgacatgcg ccaagttcgc ctgtagcaag 960

aagatgaccg gcaagtccat ccagccagag aacctggagt accggatcat gctgtctgtg 1020

cacggctccc agcactctgg catgatcgtg aacgacacag gccacgagac agatgagaat 1080

cgggccaagg tggagatcac acctaactct ccaagagccg aggccaccct gggaggattt 1140

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gcagtgcaca ccgccctggc aggcgccctg gaggcagaga tggacggagc taagggcaga 1440

ctgtctagcg gccacctgaa gtgcaggctg aagatggata agctgcgcct gaagggcgtg 1500

tcctactctc tgtgcacagc cgccttcacc ttcaccaaga tccctgccga gacactgcac 1560

ggcacagtga ccgtggaggt gcagtatgcc ggcacagacg gaccctgtaa ggtgcctgcc 1620

cagatggccg tggatatgca gacactgaca cctgtgggca ggctgatcac cgccaatcca 1680

gtgatcacag agtctaccga gaacagcaag atgatgctgg agctggaccc accatttggc 1740

gatagctata tcgtgatcgg cgtgggcgag aagaagatca cacaccactg gcaccgcagc 1800

ggctccacaa tcggcaaggc ctttgaggca accgtgcgcg gagcaaagag aatggccgtg 1860

ctgggcgaca ccgcatggga tttcggatct gtgggaggcg ccctgaacag cctgggcaag 1920

ggcatctgat ga 1932

<210> 113
<211> 642
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_Zika_prME411 (C3)

<400> 113

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ala Glu Val
20 25 30

```
Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
        35                  40                  45

Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
    50                  55                  60

Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65                  70                  75                  80

Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
                85                  90                  95

Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
            100                 105                 110

Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser
        115                 120                 125

His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
    130                 135                 140

Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145                 150                 155                 160

Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165                 170                 175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180                 185                 190

Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195                 200                 205

Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210                 215                 220

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

Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260                 265                 270

Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275                 280                 285

Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300

Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305                 310                 315                 320

Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325                 330                 335

Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340                 345                 350

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

Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370                 375                 380

Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385                 390                 395                 400

Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405                 410                 415

Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420                 425                 430
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Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435                 440                 445

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450                 455                 460

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

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485                 490                 495

Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500                 505                 510

Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515                 520                 525

Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530                 535                 540

Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545                 550                 555                 560

Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565                 570                 575

Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580                 585                 590

Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe
        595                 600                 605

Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr
    610                 615                 620

Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys
625                 630                 635                 640
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Gly Ile

<210> 114
<211> 1806
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_Zika_prME395 (C4)

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atgtacttgg acagaaacga tgctggggag gccatatctt ttccaaccac attggggatg 180

aataagtgtt atatacagat catggatctt ggacacatgt gtgatgccac catgagctat 240

gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg 300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct 360

agaagagctg tgacgctccc ctcccattcc actaggaagc tgcaaacgcg gtcgcaaacc 420

tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg 480

aaccctggct tcgcgttagc agcagctgcc atcgcttggc ttttgggaag ctcaacgagc 540

caaaaagtca tatacttggt catgatactg ctgattgccc cggcatacag catcaggtgc 600

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gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca 780

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac 840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat 900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag 960

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt 1020

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat 1080

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct ggggggtttt 1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 1200

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta 1260

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gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 1440

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 1500

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac 1560

gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1620

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1680

gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1740

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1800

ggctga 1806

<210> 115
<211> 1806
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_Zika_prME395 (C4)

<400> 115
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aacaagtgct acatccagat catggacctg ggccacatgt gcgatgccac catgtcctat 240

gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc 300

acatctacat gggtggtgta cggcacctgt caccacaaga agggagaggc ccggcggagc 360

cggcgggccg tgacactgcc ttcccactct accaggaagc tgcagacacg cagccagacc 420

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aatccaggat tcgcactggc agcagcagca atcgcatggc tgctgggaag ctccaccagc 540

cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc 600

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ggctgtggcc tgtttggcaa gggctctctg gtgacatgcg ccaagttcgc ctgtagcaag 960

aagatgaccg gcaagtccat ccagccagag aacctggagt accggatcat gctgtctgtg 1020

cacggctccc agcactctgg catgatcgtg aacgacacag gccacgagac agatgagaat 1080

cgggccaagg tggagatcac acctaactct ccaagagccg aggccaccct gggaggattt 1140

ggctctctgg gcctggactg cgagcctaga acaggcctgg acttctccga tctgtactat 1200

ctgaccatga acaataagca ctggctggtg cacaaggagt ggtttcacga catcccactg 1260

ccatggcacg caggagcaga tacaggaaca ccacactgga acaataagga ggccctggtg 1320

gagttcaagg atgcccacgc caagcggcag acagtggtgg tgctgggcag ccaggaggga 1380

gcagtgcaca ccgccctggc aggcgccctg gaggcagaga tggacggagc taagggcaga 1440

ctgtctagcg gccacctgaa gtgcaggctg aagatggata agctgcgcct gaagggcgtg 1500

tcctactctc tgtgcacagc cgccttcacc ttcaccaaga tccctgccga gacactgcac 1560

ggcacagtga ccgtggaggt gcagtatgcc ggcacagacg gaccctgtaa ggtgcctgcc 1620

cagatggccg tggatatgca gacactgaca cctgtgggca ggctgatcac cgccaatcca 1680

gtgatcacag agtctaccga gaacagcaag atgatgctgg agctggaccc accatttggc 1740

gatagctata tcgtgatcgg cgtgggcgag aagaagatca cacaccactg gcaccgcagc 1800

ggctga 1806

<210> 116
<211> 601
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_Zika_prME395 (C4)

<400> 116

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Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1               5                  10                  15


Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ala Glu Val
            20                  25                  30


Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
        35                  40                  45


Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
    50                  55                  60


Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65                  70                  75                  80


Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
                85                  90                  95


Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
            100                 105                 110


Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser
        115                 120                 125


His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
    130                 135                 140


Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145                 150                 155                 160
```

```
Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165                 170                 175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180                 185                 190

Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195                 200                 205

Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210                 215                 220

Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile
225                 230                 235                 240

Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr
                245                 250                 255

Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260                 265                 270

Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275                 280                 285

Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300

Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305                 310                 315                 320

Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325                 330                 335

Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340                 345                 350

Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro
        355                 360                 365
```

```
Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370                 375                 380

Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385                 390                 395                 400

Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405                 410                 415

Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420                 425                 430

Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435                 440                 445

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450                 455                 460

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

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485                 490                 495

Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500                 505                 510

Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515                 520                 525

Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530                 535                 540

Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545                 550                 555                 560
```

```
Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565                 570                 575


Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580                 585                 590


Ile Thr His His Trp His Arg Ser Gly
        595                 600


<210>  117
<211>  1602
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of MVsp_ZikaE (C5)

<400>  117
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact       60

ctccaaacac ccaccggtca aatccatatc aggtgcatag gagtcagcaa tagggacttt      120

gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc      180

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc      240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac      300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc      360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg      420

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag      480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg      540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc      600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa      660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg      720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc      780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa      840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga      900
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gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt 960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg 1020

ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag 1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact 1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac 1200

tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc 1260

ggggagaaga agatcaccca ccactggcac aggagtggca gcaccattgg aaaagcattt 1320

gaagccactg tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt 1380

ggatcagttg gaggcgctct caactcattg ggcaagggca tccatcaaat ttttggagca 1440

gctttcaaat cattgtttgg aggaatgtcc tggttctcac aaattctcat tggaacgttg 1500

ctgatgtggt tgggtctgaa cacaaagaat ggatctattt cccttatgtg cttggcctta 1560

gggggagtgt tgatcttctt atccacagcc gtctctgctt ga 1602

<210> 118
<211> 1602
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaE (C5)

<400> 118
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccacatc cggtgcatcg gcgtgagcaa tagagacttc 120

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg 360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc 420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag 480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg 540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct 600

aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag 660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg 720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca 780

ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag 840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc 900

gccctggagg cagagatgga cggagctaag ggcagactgt ctagcggcca cctgaagtgc 960

aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc 1020

ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag 1080

tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca 1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac 1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg 1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ccacaatcgg caaggccttt 1320

gaggcaaccg tgcgcggagc aaagagaatg gccgtgctgg gcgacaccgc atgggatttc 1380

ggatctgtgg gaggcgccct gaacagcctg ggcaagggca tccaccagat cttcggcgcc 1440

gcctttaagt ccctgttcgg cggcatgagc tggttctcac agatcctgat cggcacactg 1500

ctgatgtggc tgggcctgaa caccaagaat ggctctatca gcctgatgtg cctggccctg 1560

ggaggcgtgc tgatcttcct gtccaccgcc gtgtctgcct ga 1602

<210> 119
<211> 533
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaE (C5)

<400> 119

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Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1               5                  10                  15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
            20                  25                  30

Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
        35                  40                  45

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

Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser
65                  70                  75                  80

Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
                85                  90                  95

Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
            100                 105                 110

Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
        115                 120                 125

Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
    130                 135                 140

Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145                 150                 155                 160

Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165                 170                 175

His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180                 185                 190

Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195                 200                 205
```

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Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210                 215                 220

Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225                 230                 235                 240

Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245                 250                 255

Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260                 265                 270

Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275                 280                 285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290                 295                 300

Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305                 310                 315                 320

Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325                 330                 335

Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340                 345                 350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355                 360                 365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370                 375                 380

Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385                 390                 395                 400
```

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
405 410 415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
420 425 430

Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys
435 440 445

Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
450 455 460

Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala
465 470 475 480

Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu
485 490 495

Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser
500 505 510

Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser
515 520 525

Thr Ala Val Ser Ala
530

<210> 120
<211> 1458
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_ZikaE_no_anchor (C6)

<400> 120
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact 60

ctccaaacac ccaccggtca aatccatatc aggtgcatag gagtcagcaa tagggacttt 120

gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc 180

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc 240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac 300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc 360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg 420

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag 480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg 540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc 600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa 660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg 720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc 780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa 840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga 900

gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt 960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg 1020

ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag 1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact 1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac 1200

tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc 1260

ggggagaaga agatcaccca ccactggcac aggagtggca gcaccattgg aaaagcattt 1320

gaagccactg tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt 1380

ggatcagttg gaggcgctct caactcattg ggcaagggca tccatcaaat ttttggagca 1440

gctttcaaat cattgtga 1458

<210> 121
<211> 1458
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaE_no_anchor (C6)

<400> 121
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccacatc cggtgcatcg gcgtgagcaa tagagacttc 120

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg 360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc 420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag 480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg 540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct 600

aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag 660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg 720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca 780

ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag 840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc 900

gccctggagg cagagatgga cggagctaag ggcagactgt ctagcggcca cctgaagtgc 960

aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc 1020

ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag 1080

tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca 1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac 1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg 1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ccacaatcgg caaggccttt 1320

gaggcaaccg tgcgcggagc aaagagaatg gccgtgctgg gcgacaccgc atgggatttc 1380

ggatctgtgg gaggcgccct gaacagcctg ggcaagggca tccaccagat cttcggcgcc 1440

gcctttaagt ccctgtga 1458

<210> 122
<211> 485
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaE_no_anchor (C6)

<400> 122

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
20 25 30

Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
35 40 45

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

Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser
65 70 75 80

Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
85 90 95

Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
100 105 110

Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
115 120 125

Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
130 135 140

```
Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145                 150                 155                 160

Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165                 170                 175

His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180                 185                 190

Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195                 200                 205

Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210                 215                 220

Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225                 230                 235                 240

Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245                 250                 255

Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260                 265                 270

Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275                 280                 285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290                 295                 300

Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305                 310                 315                 320

Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325                 330                 335
```

```
Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340                 345                 350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355                 360                 365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370                 375                 380

Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385                 390                 395                 400

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
                405                 410                 415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
            420                 425                 430

Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys
        435                 440                 445

Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
    450                 455                 460

Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala
465                 470                 475                 480

Ala Phe Lys Ser Leu
                485
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<210> 123
<211> 1428
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_ZikaE411 (C7)

<400> 123
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ctccaaacac ccaccggtca aatccatatc aggtgcatag gagtcagcaa tagggacttt 120

gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc 180

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc 240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac 300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc 360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg 420

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag 480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg 540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc 600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa 660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg 720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc 780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa 840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga 900

gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt 960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg 1020

ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag 1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact 1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac 1200

tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc 1260

ggggagaaga agatcaccca ccactggcac aggagtggca gcaccattgg aaaagcattt 1320

gaagccactg tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt 1380

ggatcagttg gaggcgctct caactcattg ggcaagggca tctgatga 1428

<210> 124
<211> 1428

<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaE411 (C7)

<400> 124
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccacatc cggtgcatcg gcgtgagcaa tagagacttc 120

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg 360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc 420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag 480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg 540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct 600

aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag 660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg 720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca 780

ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag 840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc 900

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aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc 1020

ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag 1080

tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca 1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac 1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg 1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ccacaatcgg caaggccttt 1320

gaggcaaccg tgcgcggagc aaagagaatg gccgtgctgg gcgacaccgc atgggatttc 1380

ggatctgtgg gaggcgccct gaacagcctg ggcaagggca tctgatga 1428

<210> 125
<211> 474
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaE411 (C7)

<400> 125

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
20 25 30

Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
35 40 45

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

Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser
65 70 75 80

Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
85 90 95

Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
100 105 110

Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
115 120 125

Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
130 135 140

```
Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145                 150                 155                 160

Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165                 170                 175

His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180                 185                 190

Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195                 200                 205

Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210                 215                 220

Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225                 230                 235                 240

Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245                 250                 255

Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260                 265                 270

Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275                 280                 285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290                 295                 300

Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305                 310                 315                 320

Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325                 330                 335
```

```
Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340                 345                 350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355                 360                 365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370                 375                 380

Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385                 390                 395                 400

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
                405                 410                 415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
            420                 425                 430

Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys
        435                 440                 445

Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
    450                 455                 460

Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
465                 470
```

<210> 126
<211> 1302
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_ZikaE395 (C8)

<400> 126

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atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact       60

ctccaaacac ccaccggtca aatccatatc aggtgcatag gagtcagcaa tagggacttt      120

gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc      180
```

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc 240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac 300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc 360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg 420

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag 480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg 540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc 600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa 660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg 720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc 780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa 840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga 900

gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt 960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg 1020

ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag 1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact 1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac 1200

tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc 1260

ggggagaaga agatcaccca ccactggcac aggagtggct ga 1302

<210> 127
<211> 1302
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaE395 (C8)

<400> 127
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ctgcagacac caacaggcca gatccacatc cggtgcatcg gcgtgagcaa tagagacttc 120

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg 360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc 420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag 480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg 540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct 600

aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag 660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg 720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca 780

ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag 840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc 900

gccctggagg cagagatgga cggagctaag ggcagactgt ctagcggcca cctgaagtgc 960

aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc 1020

ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag 1080

tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca 1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac 1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg 1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ga 1302

<210> 128
<211> 433
<212> PRT
<213> Artificial sequence

<220>

<223> MVsp_ZikaE395 (C8)

<400> 128

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Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1               5                   10                  15


Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
            20                  25                  30


Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
        35                  40                  45


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


Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser
65                  70                  75                  80


Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
                85                  90                  95


Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
            100                 105                 110


Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
        115                 120                 125


Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
    130                 135                 140


Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145                 150                 155                 160


Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165                 170                 175


His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180                 185                 190
```

```
Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195                 200                 205

Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210                 215                 220

Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225                 230                 235                 240

Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245                 250                 255

Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260                 265                 270

Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275                 280                 285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290                 295                 300

Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305                 310                 315                 320

Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325                 330                 335

Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340                 345                 350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355                 360                 365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370                 375                 380
```

```
Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385                 390                 395                 400

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
                405                 410                 415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
            420                 425                 430

Gly
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<210> 129
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_ZikaprME_MVTMintracyto (C9)

<400> 129

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atgtacttgg acagaaacga tgctggggag gccatatctt ttccaaccac attggggatg      180

aataagtgtt atatacagat catggatctt ggacacatgt gtgatgccac catgagctat      240

gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg      300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct      360

agaagagctg tgacgctccc ctcccattcc actaggaagc tgcaaacgcg gtcgcaaacc      420

tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg      480

aaccctggct tcgcgttagc agcagctgcc atcgcttggc ttttgggaag ctcaacgagc      540

caaaaagtca tatacttggt catgatactg ctgattgccc cggcatacag catcaggtgc      600

ataggagtca gcaataggga ctttgtggaa ggtatgtcag gtgggacttg ggttgatgtt      660

gtcttggaac atggaggttg tgtcaccgta atggcacagg acaaaccgac tgtcgacata      720

gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca      780
```

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac 840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat 900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag 960

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt 1020

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat 1080

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct gggggggtttt 1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 1200

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta 1260

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gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 1440

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 1500

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac 1560

gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1620

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1680

gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1740

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1800

ggcagcacca ttggaaaagc atttgaagcc actgtgagag gtgccaagag aatggcagtc 1860

ttgggagaca cagcctggga ctttggatca gttggaggcg ctctcaactc attgggcaag 1920

ggcatccatc aaatttttgg agcagctttc aaatcattgt ttggaggaat gtcctggttc 1980

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gggttgatag ggatccccgc tttaatatgt tgctgcaggg ggcgttgtaa caaaaaggga 2100

gaacaagttg gtatgtcaag accaggccta aagcctgatc ttacgggaac atcaaaatcc 2160

tatgtaaggt cgctctga 2178

<210> 130
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaprME_MVTMintracyto (C9)

<400> 130
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ctgcagacac caacaggcca gatccacgca gaggtgacca ggagaggaag cgcctactat 120

atgtacctgg acaggaatga tgccggcgag gccatctcct tcccaaccac actgggcatg 180

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gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc 300

acatctacat gggtggtgta cggcacctgt caccacaaga agggagaggc ccggcggagc 360

cggcgggccg tgacactgcc ttcccactct accaggaagc tgcagacacg cagccagacc 420

tggctggagt ccagagagta taccaagcac ctgatcaggg tggagaactg gatctttcgc 480

aatccaggat tcgcactggc agcagcagca atcgcatggc tgctgggaag ctccaccagc 540

cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc 600

atcggcgtga gcaatagaga cttcgtggag ggaatgtccg gaggaacctg ggtggatgtg 660

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cacggctccc agcactctgg catgatcgtg aacgacacag gccacgagac agatgagaat 1080

cgggccaagg tggagatcac acctaactct ccaagagccg aggccaccct gggaggattt 1140

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gcagtgcaca ccgccctggc aggcgccctg gaggcagaga tggacggagc taagggcaga 1440

ctgtctagcg gccacctgaa gtgcaggctg aagatggata agctgcgcct gaagggcgtg 1500

tcctactctc tgtgcacagc cgccttcacc ttcaccaaga tccctgccga gacactgcac 1560

ggcacagtga ccgtggaggt gcagtatgcc ggcacagacg gaccctgtaa ggtgcctgcc 1620

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gatagctata tcgtgatcgg cgtgggcgag aagaagatca cacaccactg gcaccgcagc 1800

ggctccacaa tcggcaaggc ctttgaggca accgtgcgcg gagcaaagag aatggccgtg 1860

ctgggcgaca ccgcatggga tttcggatct gtgggaggcg ccctgaacag cctgggcaag 1920

ggcatccacc agatcttcgg cgccgccttt aagtccctgt tcggcggcat gagctggttc 1980

tcaatgaagg gcctgtcctc tacctctatc gtgtacatcc tgatcgccgt gtgcctggga 2040

ggcctgatcg gaatcccagc cctgatctgc tgttgcagag gccgctgcaa caagaaggga 2100

gagcaagtgg gaatgtctcg gccaggcctg aagccagacc tgacaggcac ctccaagtct 2160

tatgtgagaa gcctgtga 2178

<210> 131
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaprME_MVTMintracyto (C9)

<400> 131

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ala Glu Val
20 25 30

```
Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
        35                  40                  45

Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
    50                  55                  60

Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65                  70                  75                  80

Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
                85                  90                  95

Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
            100                 105                 110

Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser
        115                 120                 125

His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
    130                 135                 140

Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145                 150                 155                 160

Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165                 170                 175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180                 185                 190

Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195                 200                 205

Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210                 215                 220
```

```
Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile
225                 230                 235                 240


Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr
                245                 250                 255


Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260                 265                 270


Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275                 280                 285


Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300


Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305                 310                 315                 320


Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325                 330                 335


Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340                 345                 350


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


Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370                 375                 380


Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385                 390                 395                 400


Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405                 410                 415


Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420                 425                 430
```

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Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435                 440                 445

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450                 455                 460

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

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485                 490                 495

Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500                 505                 510

Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515                 520                 525

Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530                 535                 540

Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545                 550                 555                 560

Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565                 570                 575

Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580                 585                 590

Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe
        595                 600                 605

Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr
    610                 615                 620
```

```
Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys
625                 630                 635                 640


Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly
                645                 650                 655


Met Ser Trp Phe Ser Met Lys Gly Leu Ser Ser Thr Ser Ile Val Tyr
            660                 665                 670


Ile Leu Ile Ala Val Cys Leu Gly Gly Leu Ile Gly Ile Pro Ala Leu
        675                 680                 685


Ile Cys Cys Cys Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Val Gly
    690                 695                 700


Met Ser Arg Pro Gly Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys Ser
705                 710                 715                 720


Tyr Val Arg Ser Leu
                725
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<210> 132
<211> 1674
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_Zika_MVTMintracytoE (C10)

<400> 132

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gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc      180

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc      240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac      300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc      360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg      420
```

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag 480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg 540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc 600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa 660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg 720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc 780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa 840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga 900

gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt 960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg 1020

ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag 1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact 1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac 1200

tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc 1260

ggggagaaga agatcaccca ccactggcac aggagtggca gcaccattgg aaaagcattt 1320

gaagccactg tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt 1380

ggatcagttg gaggcgctct caactcattg ggcaagggca tccatcaaat ttttggagca 1440

gctttcaaat cattgtttgg aggaatgtcc tggttctcaa tgaaaggttt atcgagcact 1500

agcatagtct acatcctgat tgcagtgtgt cttggagggt tgatagggat ccccgcttta 1560

atatgttgct gcagggggcg ttgtaacaaa aagggagaac aagttggtat gtcaagacca 1620

ggcctaaagc ctgatcttac gggaacatca aaatcctatg taaggtcgct ctga 1674

<210> 133
<211> 1674
<212> DNA
<213> Artificial sequence

<220>

<223> Codon-optimized nucleotide sequence of MVsp_Zika_MVTMintracytoE (C10)

<400> 133

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ctgcagacac caacaggcca gatccacatc cggtgcatcg gcgtgagcaa tagagacttc 120

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg 360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc 420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag 480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg 540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct 600

aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag 660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg 720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca 780

ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag 840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc 900

gccctggagg cagagatgga cggagctaag ggcagactgt ctagcggcca cctgaagtgc 960

aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc 1020

ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag 1080

tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca 1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac 1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg 1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ccacaatcgg caaggccttt 1320

gaggcaaccg tgcgcggagc aaagagaatg gccgtgctgg gcgacaccgc atgggatttc 1380

ggatctgtgg gaggcgccct gaacagcctg ggcaagggca tccaccagat cttcggcgcc 1440

gcctttaagt ccctgttcgg cggcatgagc tggttctcaa tgaagggcct gtcctctacc 1500

tctatcgtgt acatcctgat cgccgtgtgc ctgggaggcc tgatcggaat cccagccctg 1560

atctgctgtt gcagaggccg ctgcaacaag aagggagagc aagtgggaat gtctcggcca 1620

ggcctgaagc cagacctgac aggcacctcc aagtcttatg tgagaagcct gtga 1674

<210> 134
<211> 557
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_Zika_MVTMintracytoE (C10)

<400> 134

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
20 25 30

Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
35 40 45

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

Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser
65 70 75 80

Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
85 90 95

Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
100 105 110

Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
115 120 125

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Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
    130                 135                 140

Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145                 150                 155                 160

Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165                 170                 175

His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180                 185                 190

Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195                 200                 205

Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210                 215                 220

Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225                 230                 235                 240

Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245                 250                 255

Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260                 265                 270

Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275                 280                 285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290                 295                 300

Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305                 310                 315                 320
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Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325                 330                 335

Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340                 345                 350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355                 360                 365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370                 375                 380

Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385                 390                 395                 400

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
                405                 410                 415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
            420                 425                 430

Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys
        435                 440                 445

Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
    450                 455                 460

Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala
465                 470                 475                 480

Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Met Lys Gly
                485                 490                 495

Leu Ser Ser Thr Ser Ile Val Tyr Ile Leu Ile Ala Val Cys Leu Gly
            500                 505                 510

Gly Leu Ile Gly Ile Pro Ala Leu Ile Cys Cys Cys Arg Gly Arg Cys
        515                 520                 525
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Asn Lys Lys Gly Glu Gln Val Gly Met Ser Arg Pro Gly Leu Lys Pro
530 535 540

Asp Leu Thr Gly Thr Ser Lys Ser Tyr Val Arg Ser Leu
545 550 555

<210> 135
<211> 2100
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_ZikaprME (D1)

<400> 135
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ctccaaacac ccaccggtca agcggaggtc actagacgtg ggagtgcata ctatatgtac 120

ttggacagaa acgatgctgg ggaggccata tcttttccaa ccacattggg gatgaataag 180

tgttatatac agatcatgga tcttggacac atgtgtgatg ccaccatgag ctatgaatgc 240

cctatgctgg atgaggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca 300

acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga 360

gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg 420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct 480

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540

gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600

gtcagcaata gggactttgt ggaaggtatg tcaggtggga cttgggttga tgttgtcttg 660

gaacatggag gttgtgtcac cgtaatggca caggacaaac cgactgtcga catagagctg 720

gttacaacaa cagtcagcaa catggcggag gtaagatcct actgctatga ggcatcaata 780

tcagacatgg cttcggacag ccgctgccca acacaaggtg aagcctacct tgacaagcaa 840

tcagacactc aatatgtctg caaaagaacg ttagtggaca gaggctgggg aaatggatgt 900

ggacttttg gcaaagggag cctggtgaca tgcgctaagt ttgcatgctc caagaaaatg 960

accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020

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aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140

ctaggacttg attgtgaacc gaggacaggc cttgactttt cagatttgta ttacttgact 1200

atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260

cacgctgggg cagacaccgg aactccacac tggaacaaca aagaagcact ggtagagttc 1320

aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380

cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440

tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500

tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560

gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620

gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680

actgaaagca ctgagaactc taagatgatg ctggaacttg atccaccatt tggggactct 1740

tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggcagc 1800

accattggaa aagcatttga agccactgtg agaggtgcca agagaatggc agtcttggga 1860

gacacagcct gggactttgg atcagttgga ggcgctctca actcattggg caagggcatc 1920

catcaaattt ttggagcagc tttcaaatca ttgtttggag gaatgtcctg gttctcacaa 1980

attctcattg gaacgttgct gatgtggttg ggtctgaaca caaagaatgg atctatttcc 2040

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<210> 136
<211> 2100
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaprME (D1)

<400> 136
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ctggacagga atgatgccgg cgaggccatc tccttcccaa ccacactggg catgaacaag 180

tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt 240

ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct 300

acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg 360

gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg 420

gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca 480

ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa 540

gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc 600

gtgagcaata gagacttcgt ggagggaatg tccggaggaa cctgggtgga tgtggtgctg 660

gagcacggcg gctgcgtgac agtgatggcc caggacaagc caaccgtgga tatcgagctg 720

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ggcctgtttg gcaagggctc tctggtgaca tgcgccaagt tcgcctgtag caagaagatg 960

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ctgggcctgg actgcgagcc tagaacaggc ctggacttct ccgatctgta ctatctgacc 1200

atgaacaata agcactggct ggtgcacaag gagtggtttc acgacatccc actgccatgg 1260

cacgcaggag cagatacagg aacaccacac tggaacaata aggaggccct ggtggagttc 1320

aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380

cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440

agcggccacc tgaagtgcag gctgaagatg gataagctgc gcctgaaggg cgtgtcctac 1500

tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560

gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620

gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680

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gacaccgcat gggatttcgg atctgtggga ggcgccctga acagcctggg caagggcatc 1920

caccagatct tcggcgccgc ctttaagtcc ctgttcggcg gcatgagctg gttctcacag 1980

atcctgatcg gcacactgct gatgtggctg ggcctgaaca ccaagaatgg ctctatcagc 2040

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<210> 137
<211> 699
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_ZikaprME (D1)

<400> 137

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ala Glu Val Thr Arg
20 25 30

Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
35 40 45

Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
50 55 60

Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65 70 75 80

```
Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
                85                  90                  95

Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
            100                 105                 110

Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser
        115                 120                 125

Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130                 135                 140

Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145                 150                 155                 160

Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
                165                 170                 175

Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180                 185                 190

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195                 200                 205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210                 215                 220

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225                 230                 235                 240

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245                 250                 255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
            260                 265                 270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275                 280                 285
```

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Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290                 295                 300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305                 310                 315                 320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325                 330                 335

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
            340                 345                 350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
    370                 375                 380

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385                 390                 395                 400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
                405                 410                 415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
            420                 425                 430

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
        435                 440                 445

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
    450                 455                 460

Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser
465                 470                 475                 480
```

```
Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
                485                 490                 495

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
            500                 505                 510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
        515                 520                 525

Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
    530                 535                 540

Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545                 550                 555                 560

Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565                 570                 575

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
            580                 585                 590

His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala
        595                 600                 605

Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp
    610                 615                 620

Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625                 630                 635                 640

His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser
                645                 650                 655

Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu
            660                 665                 670

Asn Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly
        675                 680                 685
```

Val Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
690 695

<210> 138
<211> 1956
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_Zika_prME_no_anchor (D2)

<400> 138
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ctccaaacac ccaccggtca agcggaggtc actagacgtg ggagtgcata ctatatgtac 120

ttggacagaa acgatgctgg ggaggccata tcttttccaa ccacattggg gatgaataag 180

tgttatatac agatcatgga tcttggacac atgtgtgatg ccaccatgag ctatgaatgc 240

cctatgctgg atgagggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca 300

acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga 360

gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg 420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct 480

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540

gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600

gtcagcaata gggactttgt ggaaggtatg tcaggtggga cttgggttga tgttgtcttg 660

gaacatggag gttgtgtcac cgtaatggca caggacaaac cgactgtcga catagagctg 720

gttacaacaa cagtcagcaa catggcggag gtaagatcct actgctatga ggcatcaata 780

tcagacatgg cttcggacag ccgctgccca acacaaggtg aagcctacct tgacaagcaa 840

tcagacactc aatatgtctg caaaagaacg ttagtggaca gaggctgggg aaatggatgt 900

ggacttttg gcaaagggag cctggtgaca tgcgctaagt ttgcatgctc caagaaaatg 960

accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020

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aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140

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atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260

cacgctgggg cagacaccgg aactccacac tggaacaaca aagaagcact ggtagagttc 1320

aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380

cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440

tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500

tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560

gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620

gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680

actgaaagca ctgagaactc taagatgatg ctggaacttg atccaccatt tggggactct 1740

tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggcagc 1800

accattggaa aagcatttga agccactgtg agaggtgcca agagaatggc agtcttggga 1860

gacacagcct gggactttgg atcagttgga ggcgctctca actcattggg caagggcatc 1920

catcaaattt ttggagcagc tttcaaatca ttgtga 1956

<210> 139
<211> 1956
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_Zika_prME_no_anchor (D2)

<400> 139
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ctggacagga atgatgccgg cgaggccatc tccttcccaa ccacactggg catgaacaag 180

tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt 240

ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct 300

acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg 360

gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg 420

gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca 480

ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa 540

gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc 600

gtgagcaata gagacttcgt ggagggaatg tccggaggaa cctgggtgga tgtggtgctg 660

gagcacggcg gctgcgtgac agtgatggcc caggacaagc caaccgtgga tatcgagctg 720

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tccgacatgg cctctgatag caggtgtcca acccagggag aggcatacct ggacaagcag 840

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accggcaagt ccatccagcc agagaacctg gagtaccgga tcatgctgtc tgtgcacggc 1020

tcccagcact ctggcatgat cgtgaacgac acaggccacg agacagatga gaatcgggcc 1080

aaggtggaga tcacacctaa ctctccaaga gccgaggcca ccctgggagg atttggctct 1140

ctgggcctgg actgcgagcc tagaacaggc ctggacttct ccgatctgta ctatctgacc 1200

atgaacaata agcactggct ggtgcacaag gagtggtttc acgacatccc actgccatgg 1260

cacgcaggag cagatacagg aacaccacac tggaacaata aggaggccct ggtggagttc 1320

aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380

cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440

agcggccacc tgaagtgcag gctgaagatg gataagctgc gcctgaaggg cgtgtcctac 1500

tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560

gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620

gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680

acagagtcta ccgagaacag caagatgatg ctggagctgg acccaccatt tggcgatagc 1740

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acaatcggca aggcctttga ggcaaccgtg cgcggagcaa agagaatggc cgtgctgggc 1860

gacaccgcat gggatttcgg atctgtggga ggcgccctga acagcctggg caagggcatc 1920

caccagatct tcggcgccgc ctttaagtcc ctgtga 1956

<210> 140
<211> 651
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_Zika_prME_no_anchor (D2)

<400> 140

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ala Glu Val Thr Arg
20 25 30

Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
35 40 45

Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
50 55 60

Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65 70 75 80

Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
85 90 95

Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
100 105 110

Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser
115 120 125

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Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130                 135                 140

Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145                 150                 155                 160

Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
                165                 170                 175

Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180                 185                 190

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195                 200                 205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210                 215                 220

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225                 230                 235                 240

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245                 250                 255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
            260                 265                 270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275                 280                 285

Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290                 295                 300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305                 310                 315                 320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325                 330                 335
```

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Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
            340                 345                 350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
    370                 375                 380

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385                 390                 395                 400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
                405                 410                 415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
            420                 425                 430

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
        435                 440                 445

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
    450                 455                 460

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

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
                485                 490                 495

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
            500                 505                 510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
        515                 520                 525
```

```
Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
    530                 535                 540

Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545                 550                 555                 560

Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565                 570                 575

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
            580                 585                 590

His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala
        595                 600                 605

Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp
    610                 615                 620

Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625                 630                 635                 640

His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
                645                 650
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<210> 141
<211> 1926
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp’_Zika_prME411 (D3)

<400> 141

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tgttatatac agatcatgga tcttggacac atgtgtgatg ccaccatgag ctatgaatgc      240

cctatgctgg atgagggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca      300
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acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga 360

gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg 420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct 480

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540

gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600

gtcagcaata gggactttgt ggaaggtatg tcaggtggga cttgggttga tgttgtcttg 660

gaacatggag gttgtgtcac cgtaatggca caggacaaac cgactgtcga catagagctg 720

gttacaacaa cagtcagcaa catggcggag gtaagatcct actgctatga ggcatcaata 780

tcagacatgg cttcggacag ccgctgccca acacaaggtg aagcctacct tgacaagcaa 840

tcagacactc aatatgtctg caaaagaacg ttagtggaca gaggctgggg aaatggatgt 900

ggacttttg gcaaagggag cctggtgaca tgcgctaagt ttgcatgctc caagaaaatg 960

accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020

tcccagcaca gtgggatgat cgttaatgac acaggacatg aaactgatga gaatagagcg 1080

aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140

ctaggacttg attgtgaacc gaggacaggc cttgactttt cagatttgta ttacttgact 1200

atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260

cacgctgggg cagacaccgg aactccacac tggaacaaca aagaagcact ggtagagttc 1320

aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380

cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440

tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500

tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560

gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620

gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680

actgaaagca ctgagaactc taagatgatg ctggaacttg atccaccatt tggggactct 1740

tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggcagc 1800

accattggaa aagcatttga agccactgtg agaggtgcca agagaatggc agtcttggga 1860

gacacagcct gggactttgg atcagttgga ggcgctctca actcattggg caagggcatc 1920

tgatga 1926

<210> 142
<211> 1926
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp'_Zika_prME411 (D3)

<400> 142
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ctggacagga atgatgccgg cgaggccatc tccttcccaa ccacactggg catgaacaag 180

tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt 240

ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct 300

acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg 360

gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg 420

gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca 480

ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa 540

gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc 600

gtgagcaata gagacttcgt ggagggaatg tccggaggaa cctgggtgga tgtggtgctg 660

gagcacggcg gctgcgtgac agtgatggcc caggacaagc caaccgtgga tatcgagctg 720

gtgaccacaa ccgtgtccaa catggccgag gtgaggtctt actgctatga ggccagcatc 780

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atgaacaata agcactggct ggtgcacaag gagtggtttc acgacatccc actgccatgg 1260

cacgcaggag cagatacagg aacaccacac tggaacaata aggaggccct ggtggagttc 1320

aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380

cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440

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tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560

gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620

gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680

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acaatcggca aggcctttga ggcaaccgtg cgcggagcaa agagaatggc cgtgctgggc 1860

gacaccgcat gggatttcgg atctgtggga ggcgccctga acagcctggg caagggcatc 1920

tgatga 1926

<210> 143
<211> 640
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp’_Zika_prME411 (D3)

<400> 143

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ala Glu Val Thr Arg
20 25 30

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Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
        35                  40                  45

Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
    50                  55                  60

Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65                  70                  75                  80

Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
                85                  90                  95

Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
            100                 105                 110

Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser
        115                 120                 125

Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130                 135                 140

Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145                 150                 155                 160

Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
                165                 170                 175

Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180                 185                 190

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195                 200                 205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210                 215                 220
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Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225                 230                 235                 240

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245                 250                 255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
            260                 265                 270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275                 280                 285

Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290                 295                 300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305                 310                 315                 320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325                 330                 335

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
            340                 345                 350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
    370                 375                 380

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385                 390                 395                 400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
                405                 410                 415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
            420                 425                 430
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Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
        435                 440                 445

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
    450                 455                 460

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

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
                485                 490                 495

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
            500                 505                 510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
        515                 520                 525

Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
    530                 535                 540

Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545                 550                 555                 560

Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565                 570                 575

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
            580                 585                 590

His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala
        595                 600                 605

Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp
    610                 615                 620
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Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625 630 635 640

<210> 144
<211> 1800
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_Zika_prME395 (D4)

<400> 144
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tgttatatac agatcatgga tcttggacac atgtgtgatg ccaccatgag ctatgaatgc 240

cctatgctgg atgagggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca 300

acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga 360

gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg 420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct 480

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540

gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600

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tcagacatgg cttcggacag ccgctgccca acacaaggtg aagcctacct tgacaagcaa 840

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ggacttttg gcaaagggag cctggtgaca tgcgctaagt ttgcatgctc caagaaaatg 960

accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020

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aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140

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atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260

cacgctgggg cagacaccgg aactccacac tggaacaaca aagaagcact ggtagagttc 1320

aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380

cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440

tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500

tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560

gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620

gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680

actgaaagca ctgagaactc taagatgatg ctggaacttg atccaccatt tggggactct 1740

tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggctga 1800

<210> 145
<211> 1800
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_Zika_prME395 (D4)

<400> 145
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca ggcagaggtg accaggagag gaagcgccta ctatatgtac 120

ctggacagga atgatgccgg cgaggccatc tccttcccaa ccacactggg catgaacaag 180

tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt 240

ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct 300

acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg 360

gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg 420

gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca 480

ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa 540

gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc 600

gtgagcaata gagacttcgt ggagggaatg tccggaggaa cctgggtgga tgtggtgctg 660

gagcacggcg gctgcgtgac agtgatggcc caggacaagc caaccgtgga tatcgagctg 720

gtgaccacaa ccgtgtccaa catggccgag gtgaggtctt actgctatga ggccagcatc 780

tccgacatgg cctctgatag caggtgtcca acccagggag aggcatacct ggacaagcag 840

tccgatacac agtacgtgtg caagcggacc ctggtggaca gaggctgggg caatggctgt 900

ggcctgtttg gcaagggctc tctggtgaca tgcgccaagt tcgcctgtag caagaagatg 960

accggcaagt ccatccagcc agagaacctg gagtaccgga tcatgctgtc tgtgcacggc 1020

tcccagcact ctggcatgat cgtgaacgac acaggccacg agacagatga gaatcgggcc 1080

aaggtggaga tcacacctaa ctctccaaga gccgaggcca ccctgggagg atttggctct 1140

ctgggcctgg actgcgagcc tagaacaggc ctggacttct ccgatctgta ctatctgacc 1200

atgaacaata agcactggct ggtgcacaag gagtggtttc acgacatccc actgccatgg 1260

cacgcaggag cagatacagg aacaccacac tggaacaata aggaggccct ggtggagttc 1320

aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380

cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440

agcggccacc tgaagtgcag gctgaagatg gataagctgc gcctgaaggg cgtgtcctac 1500

tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560

gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620

gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680

acagagtcta ccgagaacag caagatgatg ctggagctgg acccaccatt tggcgatagc 1740

tatatcgtga tcggcgtggg cgagaagaag atcacacacc actggcaccg cagcggctga 1800

<210> 146
<211> 599
<212> PRT
<213> Artificial sequence

<220>

<223> MVsp'_Zika_prME395 (D4)

<400> 146

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Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1               5                   10                  15


Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ala Glu Val Thr Arg
            20                  25                  30


Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
        35                  40                  45


Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
    50                  55                  60


Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65                  70                  75                  80


Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
                85                  90                  95


Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
            100                 105                 110


Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser
        115                 120                 125


Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130                 135                 140


Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145                 150                 155                 160


Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
                165                 170                 175


Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180                 185                 190
```

```
Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195                 200                 205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210                 215                 220

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225                 230                 235                 240

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245                 250                 255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
            260                 265                 270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275                 280                 285

Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290                 295                 300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305                 310                 315                 320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325                 330                 335

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
            340                 345                 350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
    370                 375                 380
```

```
Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385                 390                 395                 400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
                405                 410                 415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
            420                 425                 430

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
        435                 440                 445

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
    450                 455                 460

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

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
                485                 490                 495

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
            500                 505                 510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
        515                 520                 525

Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
    530                 535                 540

Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545                 550                 555                 560

Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565                 570                 575

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
            580                 585                 590
```

His His Trp His Arg Ser Gly
595

<210> 147
<211> 1596
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_ZikaE (D5)

<400> 147
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact 60

ctccaaacac ccaccggtca aatcaggtgc ataggagtca gcaataggga ctttgtggaa 120

ggtatgtcag gtgggacttg ggttgatgtt gtcttggaac atggaggttg tgtcaccgta 180

atggcacagg acaaaccgac tgtcgacata gagctggtta caacaacagt cagcaacatg 240

gcggaggtaa gatcctactg ctatgaggca tcaatatcag acatggcttc ggacagccgc 300

tgcccaacac aaggtgaagc ctaccttgac aagcaatcag acactcaata tgtctgcaaa 360

agaacgttag tggacagagg ctggggaaat ggatgtggac tttttggcaa agggagcctg 420

gtgacatgcg ctaagtttgc atgctccaag aaaatgaccg ggaagagcat ccagccagag 480

aatctggagt accggataat gctgtcagtt catggctccc agcacagtgg gatgatcgtt 540

aatgacacag gacatgaaac tgatgagaat agagcgaagg ttgagataac gcccaattca 600

ccaagagccg aagccaccct ggggggtttt ggaagcctag gacttgattg tgaaccgagg 660

acaggccttg acttttcaga tttgtattac ttgactatga ataacaagca ctggttggtt 720

cacaaggagt ggttccacga cattccatta ccttggcacg ctggggcaga caccggaact 780

ccacactgga acaacaaaga agcactggta gagttcaagg acgcacatgc caaaaggcaa 840

actgtcgtgg ttctagggag tcaagaagga gcagttcaca cggcccttgc tggagctctg 900

gaggctgaga tggatggtgc aaagggaagg ctgtcctctg gccacttgaa atgtcgcctg 960

aaaatggata aacttagatt gaagggcgtg tcatactcct tgtgtaccgc agcgttcaca 1020

ttcaccaaga tcccggctga aacactgcac gggacagtca cagtggaggt acagtacgca 1080

gggacagatg gaccttgcaa ggttccagct cagatggcgg tggacatgca aactctgacc 1140

ccagttggga ggttgataac cgctaacccc gtaatcactg aaagcactga gaactctaag 1200

atgatgctgg aacttgatcc accatttggg gactcttaca ttgtcatagg agtcggggag 1260

aagaagatca cccaccactg gcacaggagt ggcagcacca ttggaaaagc atttgaagcc 1320

actgtgagag gtgccaagag aatggcagtc ttgggagaca cagcctggga ctttggatca 1380

gttggaggcg ctctcaactc attgggcaag ggcatccatc aaatttttgg agcagctttc 1440

aaatcattgt ttggaggaat gtcctggttc tcacaaattc tcattggaac gttgctgatg 1500

tggttgggtc tgaacacaaa gaatggatct atttccctta tgtgcttggc cttaggggga 1560

gtgttgatct tcttatccac agccgtctct gcttga 1596

<210> 148
<211> 1596
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaE (D5)

<400> 148
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccggtgc atcggcgtga gcaatagaga cttcgtggag 120

ggaatgtccg gaggaacctg ggtggatgtg gtgctggagc acggcggctg cgtgacagtg 180

atggcccagg acaagccaac cgtggatatc gagctggtga ccacaaccgt gtccaacatg 240

gccgaggtga ggtcttactg ctatgaggcc agcatctccg acatggcctc tgatagcagg 300

tgtccaaccc agggagaggc atacctggac aagcagtccg atacacagta cgtgtgcaag 360

cggaccctgg tggacagagg ctggggcaat ggctgtggcc tgtttggcaa gggctctctg 420

gtgacatgcg ccaagttcgc ctgtagcaag aagatgaccg gcaagtccat ccagccagag 480

aacctggagt accggatcat gctgtctgtg cacggctccc agcactctgg catgatcgtg 540

aacgacacag gccacgagac agatgagaat cgggccaagg tggagatcac acctaactct 600

ccaagagccg aggccaccct gggaggattt ggctctctgg gcctggactg cgagcctaga 660

acaggcctgg acttctccga tctgtactat ctgaccatga acaataagca ctggctggtg 720

cacaaggagt ggtttcacga catcccactg ccatggcacg caggagcaga tacaggaaca 780

ccacactgga acaataagga ggccctggtg gagttcaagg atgcccacgc caagcggcag 840

acagtggtgg tgctgggcag ccaggaggga gcagtgcaca ccgccctggc aggcgccctg 900

gaggcagaga tggacggagc taagggcaga ctgtctagcg gccacctgaa gtgcaggctg 960

aagatggata agctgcgcct gaagggcgtg tcctactctc tgtgcacagc cgccttcacc 1020

ttcaccaaga tccctgccga gacactgcac ggcacagtga ccgtggaggt gcagtatgcc 1080

ggcacagacg gaccctgtaa ggtgcctgcc cagatggccg tggatatgca gacactgaca 1140

cctgtgggca ggctgatcac cgccaatcca gtgatcacag agtctaccga gaacagcaag 1200

atgatgctgg agctggaccc accatttggc gatagctata tcgtgatcgg cgtgggcgag 1260

aagaagatca cacaccactg gcaccgcagc ggctccacaa tcggcaaggc ctttgaggca 1320

accgtgcgcg gagcaaagag aatggccgtg ctgggcgaca ccgcatggga tttcggatct 1380

gtgggaggcg ccctgaacag cctgggcaag ggcatccacc agatcttcgg cgccgccttt 1440

aagtccctgt tcggcggcat gagctggttc tcacagatcc tgatcggcac actgctgatg 1500

tggctgggcc tgaacaccaa gaatggctct atcagcctga tgtgcctggc cctgggaggc 1560

gtgctgatct tcctgtccac cgccgtgtct gcctga 1596

<210> 149
<211> 531
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp’_ZikaE (D5)

<400> 149

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile Arg Cys Ile Gly
20 25 30

```
Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val
        35                  40                  45

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

Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
65                  70                  75                  80

Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
                85                  90                  95

Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
            100                 105                 110

Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
        115                 120                 125

Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
    130                 135                 140

Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
145                 150                 155                 160

Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
                165                 170                 175

Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
            180                 185                 190

Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
        195                 200                 205

Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
    210                 215                 220
```

```
Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
225                 230                 235                 240

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

Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
            260                 265                 270

Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
        275                 280                 285

Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
    290                 295                 300

Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
305                 310                 315                 320

Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr
                325                 330                 335

Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr
            340                 345                 350

Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
        355                 360                 365

Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
    370                 375                 380

Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
385                 390                 395                 400

Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
                405                 410                 415

Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser
            420                 425                 430
```

```
Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met
        435                 440                 445

Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala
    450                 455                 460

Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe
465                 470                 475                 480

Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly
                485                 490                 495

Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser
            500                 505                 510

Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser Thr Ala
        515                 520                 525

Val Ser Ala
    530
```

<210> 150
<211> 1452
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp’_ZikaE_no_anchor (D6)

<400> 150

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ctccaaacac ccaccggtca aatcaggtgc ataggagtca gcaataggga ctttgtggaa      120

ggtatgtcag gtgggacttg ggttgatgtt gtcttggaac atggaggttg tgtcaccgta      180

atggcacagg acaaaccgac tgtcgacata gagctggtta caacaacagt cagcaacatg      240

gcggaggtaa gatcctactg ctatgaggca tcaatatcag acatggcttc ggacagccgc      300

tgcccaacac aaggtgaagc ctaccttgac aagcaatcag acactcaata tgtctgcaaa      360
```

agaacgttag tggacagagg ctggggaaat ggatgtggac tttttggcaa agggagcctg 420

gtgacatgcg ctaagtttgc atgctccaag aaaatgaccg ggaagagcat ccagccagag 480

aatctggagt accggataat gctgtcagtt catggctccc agcacagtgg gatgatcgtt 540

aatgacacag gacatgaaac tgatgagaat agagcgaagg ttgagataac gcccaattca 600

ccaagagccg aagccaccct ggggggtttt ggaagcctag gacttgattg tgaaccgagg 660

acaggccttg acttttcaga tttgtattac ttgactatga ataacaagca ctggttggtt 720

cacaaggagt ggttccacga cattccatta ccttggcacg ctggggcaga caccggaact 780

ccacactgga acaacaaaga agcactggta gagttcaagg acgcacatgc caaaaggcaa 840

actgtcgtgg ttctagggag tcaagaagga gcagttcaca cggcccttgc tggagctctg 900

gaggctgaga tggatggtgc aaagggaagg ctgtcctctg gccacttgaa atgtcgcctg 960

aaaatggata aacttagatt gaagggcgtg tcatactcct tgtgtaccgc agcgttcaca 1020

ttcaccaaga tcccggctga aacactgcac gggacagtca cagtggaggt acagtacgca 1080

gggacagatg gaccttgcaa ggttccagct cagatggcgg tggacatgca aactctgacc 1140

ccagttggga ggttgataac cgctaacccc gtaatcactg aaagcactga gaactctaag 1200

atgatgctgg aacttgatcc accatttggg gactcttaca ttgtcatagg agtcggggag 1260

aagaagatca cccaccactg gcacaggagt ggcagcacca ttggaaaagc atttgaagcc 1320

actgtgagag gtgccaagag aatggcagtc ttgggagaca cagcctggga ctttggatca 1380

gttggaggcg ctctcaactc attgggcaag ggcatccatc aaatttttgg agcagctttc 1440

aaatcattgt ga 1452

<210> 151
<211> 1452
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaE_no_anchor (D6)

<400> 151
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccggtgc atcggcgtga gcaatagaga cttcgtggag 120

ggaatgtccg gaggaacctg ggtggatgtg gtgctggagc acggcggctg cgtgacagtg 180

atggcccagg acaagccaac cgtggatatc gagctggtga ccacaaccgt gtccaacatg 240

gccgaggtga ggtcttactg ctatgaggcc agcatctccg acatggcctc tgatagcagg 300

tgtccaaccc agggagaggc atacctggac aagcagtccg atacacagta cgtgtgcaag 360

cggaccctgg tggacagagg ctggggcaat ggctgtggcc tgtttggcaa gggctctctg 420

gtgacatgcg ccaagttcgc ctgtagcaag aagatgaccg gcaagtccat ccagccagag 480

aacctggagt accggatcat gctgtctgtg cacggctccc agcactctgg catgatcgtg 540

aacgacacag gccacgagac agatgagaat cgggccaagg tggagatcac acctaactct 600

ccaagagccg aggccaccct gggaggattt ggctctctgg gcctggactg cgagcctaga 660

acaggcctgg acttctccga tctgtactat ctgaccatga acaataagca ctggctggtg 720

cacaaggagt ggtttcacga catcccactg ccatggcacg caggagcaga tacaggaaca 780

ccacactgga acaataagga ggccctggtg gagttcaagg atgcccacgc caagcggcag 840

acagtggtgg tgctgggcag ccaggaggga gcagtgcaca ccgccctggc aggcgccctg 900

gaggcagaga tggacggagc taagggcaga ctgtctagcg gccacctgaa gtgcaggctg 960

aagatggata agctgcgcct gaagggcgtg tcctactctc tgtgcacagc cgccttcacc 1020

ttcaccaaga tccctgccga gacactgcac ggcacagtga ccgtggaggt gcagtatgcc 1080

ggcacagacg gaccctgtaa ggtgcctgcc cagatggccg tggatatgca gacactgaca 1140

cctgtgggca ggctgatcac cgccaatcca gtgatcacag agtctaccga gaacagcaag 1200

atgatgctgg agctggaccc accatttggc gatagctata tcgtgatcgg cgtgggcgag 1260

aagaagatca cacaccactg gcaccgcagc ggctccacaa tcggcaaggc ctttgaggca 1320

accgtgcgcg gagcaaagag aatggccgtg ctgggcgaca ccgcatggga tttcggatct 1380

gtgggaggcg ccctgaacag cctgggcaag ggcatccacc agatcttcgg cgccgccttt 1440

aagtccctgt ga 1452

<210> 152
<211> 483
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_ZikaE_no_anchor (D6)

<400> 152

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Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1               5                   10                  15


Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile Arg Cys Ile Gly
            20                  25                  30


Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val
        35                  40                  45


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


Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
65                  70                  75                  80


Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
                85                  90                  95


Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
            100                 105                 110


Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
        115                 120                 125


Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
    130                 135                 140


Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
145                 150                 155                 160
```

```
Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
                165                 170                 175

Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
            180                 185                 190

Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
        195                 200                 205

Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
    210                 215                 220

Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
225                 230                 235                 240

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

Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
            260                 265                 270

Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
        275                 280                 285

Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
    290                 295                 300

Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
305                 310                 315                 320

Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr
                325                 330                 335

Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr
            340                 345                 350

Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
        355                 360                 365
```

```
Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
    370                 375                 380

Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
385                 390                 395                 400

Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
                405                 410                 415

Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser
            420                 425                 430

Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met
        435                 440                 445

Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala
    450                 455                 460

Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe
465                 470                 475                 480

Lys Ser Leu
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<210> 153
<211> 1422
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp’_ZikaE411 (D7)

<400> 153

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ctccaaacac ccaccggtca aatcaggtgc ataggagtca gcaataggga ctttgtggaa      120

ggtatgtcag gtgggacttg ggttgatgtt gtcttggaac atggaggttg tgtcaccgta      180

atggcacagg acaaaccgac tgtcgacata gagctggtta caacaacagt cagcaacatg      240
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gcggaggtaa gatcctactg ctatgaggca tcaatatcag acatggcttc ggacagccgc 300

tgcccaacac aaggtgaagc ctaccttgac aagcaatcag acactcaata tgtctgcaaa 360

agaacgttag tggacagagg ctggggaaat ggatgtggac tttttggcaa agggagcctg 420

gtgacatgcg ctaagtttgc atgctccaag aaaatgaccg ggaagagcat ccagccagag 480

aatctggagt accggataat gctgtcagtt catggctccc agcacagtgg gatgatcgtt 540

aatgacacag gacatgaaac tgatgagaat agagcgaagg ttgagataac gcccaattca 600

ccaagagccg aagccaccct ggggggtttt ggaagcctag gacttgattg tgaaccgagg 660

acaggccttg acttttcaga tttgtattac ttgactatga ataacaagca ctggttggtt 720

cacaaggagt ggttccacga cattccatta ccttggcacg ctggggcaga caccggaact 780

ccacactgga acaacaaaga agcactggta gagttcaagg acgcacatgc caaaaggcaa 840

actgtcgtgg ttctagggag tcaagaagga gcagttcaca cggcccttgc tggagctctg 900

gaggctgaga tggatggtgc aaagggaagg ctgtcctctg gccacttgaa atgtcgcctg 960

aaaatggata aacttagatt gaagggcgtg tcatactcct tgtgtaccgc agcgttcaca 1020

ttcaccaaga tcccggctga aacactgcac gggacagtca cagtggaggt acagtacgca 1080

gggacagatg gaccttgcaa ggttccagct cagatggcgg tggacatgca aactctgacc 1140

ccagttggga ggttgataac cgctaacccc gtaatcactg aaagcactga gaactctaag 1200

atgatgctgg aacttgatcc accatttggg gactcttaca ttgtcatagg agtcggggag 1260

aagaagatca cccaccactg gcacaggagt ggcagcacca ttggaaaagc atttgaagcc 1320

actgtgagag gtgccaagag aatggcagtc ttgggagaca cagcctggga ctttggatca 1380

gttggaggcg ctctcaactc attgggcaag ggcatctgat ga 1422

<210> 154
<211> 1422
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaE411 (D7)

<400> 154
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ggaatgtccg gaggaacctg ggtggatgtg gtgctggagc acggcggctg cgtgacagtg 180

atggcccagg acaagccaac cgtggatatc gagctggtga ccacaaccgt gtccaacatg 240

gccgaggtga ggtcttactg ctatgaggcc agcatctccg acatggcctc tgatagcagg 300

tgtccaaccc agggagaggc atacctggac aagcagtccg atacacagta cgtgtgcaag 360

cggaccctgg tggacagagg ctggggcaat ggctgtggcc tgtttggcaa gggctctctg 420

gtgacatgcg ccaagttcgc ctgtagcaag aagatgaccg gcaagtccat ccagccagag 480

aacctggagt accggatcat gctgtctgtg cacggctccc agcactctgg catgatcgtg 540

aacgacacag gccacgagac agatgagaat cgggccaagg tggagatcac acctaactct 600

ccaagagccg aggccaccct gggaggattt ggctctctgg gcctggactg cgagcctaga 660

acaggcctgg acttctccga tctgtactat ctgaccatga acaataagca ctggctggtg 720

cacaaggagt ggtttcacga catcccactg ccatggcacg caggagcaga tacaggaaca 780

ccacactgga acaataagga ggccctggtg gagttcaagg atgcccacgc caagcggcag 840

acagtggtgg tgctgggcag ccaggaggga gcagtgcaca ccgccctggc aggcgccctg 900

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atgatgctgg agctggaccc accatttggc gatagctata tcgtgatcgg cgtgggcgag 1260

aagaagatca cacaccactg gcaccgcagc ggctccacaa tcggcaaggc ctttgaggca 1320

accgtgcgcg gagcaaagag aatggccgtg ctgggcgaca ccgcatggga tttcggatct 1380

gtgggaggcg ccctgaacag cctgggcaag ggcatctgat ga 1422

<210> 155
<211> 472
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp’_ZikaE411 (D7)

<400> 155

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Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1               5                   10                  15


Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile Arg Cys Ile Gly
            20                  25                  30


Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val
        35                  40                  45


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


Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
65                  70                  75                  80


Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
                85                  90                  95


Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
            100                 105                 110


Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
        115                 120                 125


Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
    130                 135                 140


Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
145                 150                 155                 160
```

```
Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
                165                 170                 175

Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
            180                 185                 190

Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
        195                 200                 205

Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
    210                 215                 220

Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
225                 230                 235                 240

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

Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
            260                 265                 270

Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
        275                 280                 285

Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
    290                 295                 300

Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
305                 310                 315                 320

Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr
                325                 330                 335

Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr
            340                 345                 350

Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
        355                 360                 365
```

```
Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
    370                 375                 380

Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
385                 390                 395                 400

Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
                405                 410                 415

Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser
            420                 425                 430

Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met
        435                 440                 445

Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala
    450                 455                 460

Leu Asn Ser Leu Gly Lys Gly Ile
465                 470
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<210> 156
<211> 1296
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp’_ZikaE395 (D8)

<400> 156

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ggtatgtcag gtgggacttg ggttgatgtt gtcttggaac atggaggttg tgtcaccgta      180

atggcacagg acaaaccgac tgtcgacata gagctggtta caacaacagt cagcaacatg      240

gcggaggtaa gatcctactg ctatgaggca tcaatatcag acatggcttc ggacagccgc      300

tgcccaacac aaggtgaagc ctaccttgac aagcaatcag acactcaata tgtctgcaaa      360
```

agaacgttag tggacagagg ctggggaaat ggatgtggac tttttggcaa agggagcctg 420

gtgacatgcg ctaagtttgc atgctccaag aaaatgaccg ggaagagcat ccagccagag 480

aatctggagt accggataat gctgtcagtt catggctccc agcacagtgg gatgatcgtt 540

aatgacacag gacatgaaac tgatgagaat agagcgaagg ttgagataac gcccaattca 600

ccaagagccg aagccaccct ggggggtttt ggaagcctag gacttgattg tgaaccgagg 660

acaggccttg acttttcaga tttgtattac ttgactatga ataacaagca ctggttggtt 720

cacaaggagt ggttccacga cattccatta ccttggcacg ctggggcaga caccggaact 780

ccacactgga acaacaaaga agcactggta gagttcaagg acgcacatgc caaaaggcaa 840

actgtcgtgg ttctagggag tcaagaagga gcagttcaca cggcccttgc tggagctctg 900

gaggctgaga tggatggtgc aaagggaagg ctgtcctctg gccacttgaa atgtcgcctg 960

aaaatggata aacttagatt gaagggcgtg tcatactcct tgtgtaccgc agcgttcaca 1020

ttcaccaaga tcccggctga aacactgcac gggacagtca cagtggaggt acagtacgca 1080

gggacagatg gaccttgcaa ggttccagct cagatggcgg tggacatgca aactctgacc 1140

ccagttggga ggttgataac cgctaacccc gtaatcactg aaagcactga gaactctaag 1200

atgatgctgg aacttgatcc accatttggg gactcttaca ttgtcatagg agtcggggag 1260

aagaagatca cccaccactg gcacaggagt ggctga 1296

<210> 157
<211> 1296
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaE395 (D8)

<400> 157
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ggaatgtccg gaggaacctg ggtggatgtg gtgctggagc acggcggctg cgtgacagtg 180

atggcccagg acaagccaac cgtggatatc gagctggtga ccacaaccgt gtccaacatg 240

gccgaggtga ggtcttactg ctatgaggcc agcatctccg acatggcctc tgatagcagg 300

tgtccaaccc agggagaggc atacctggac aagcagtccg atacacagta cgtgtgcaag 360

cggaccctgg tggacagagg ctggggcaat ggctgtggcc tgtttggcaa gggctctctg 420

gtgacatgcg ccaagttcgc ctgtagcaag aagatgaccg gcaagtccat ccagccagag 480

aacctggagt accggatcat gctgtctgtg cacggctccc agcactctgg catgatcgtg 540

aacgacacag gccacgagac agatgagaat cgggccaagg tggagatcac acctaactct 600

ccaagagccg aggccaccct gggaggattt ggctctctgg gcctggactg cgagcctaga 660

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ccacactgga acaataagga ggccctggtg gagttcaagg atgcccacgc caagcggcag 840

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gaggcagaga tggacggagc taagggcaga ctgtctagcg gccacctgaa gtgcaggctg 960

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aagaagatca cacaccactg gcaccgcagc ggctga 1296

<210> 158
<211> 431
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp’_ZikaE395 (D8)

<400> 158

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala

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1               5                   10                  15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile Arg Cys Ile Gly
            20                  25                  30

Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val
        35                  40                  45

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

Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
65                  70                  75                  80

Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
                85                  90                  95

Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
            100                 105                 110

Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
        115                 120                 125

Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
    130                 135                 140

Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
145                 150                 155                 160

Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
                165                 170                 175

Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
            180                 185                 190

Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
        195                 200                 205
```

```
Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
    210                 215                 220

Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
225                 230                 235                 240

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

Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
            260                 265                 270

Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
        275                 280                 285

Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
    290                 295                 300

Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
305                 310                 315                 320

Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr
                325                 330                 335

Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr
            340                 345                 350

Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
        355                 360                 365

Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
    370                 375                 380

Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
385                 390                 395                 400

Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
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405 410 415

Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly
420 425 430

<210> 159
<211> 2172
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_ZikaprME_MVTMintracyto (D9)

<400> 159
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tgttatatac agatcatgga tcttggacac atgtgtgatg ccaccatgag ctatgaatgc 240

cctatgctgg atgagggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca 300

acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga 360

gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg 420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct 480

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540

gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600

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tcagacatgg cttcggacag ccgctgccca acacaaggtg aagcctacct tgacaagcaa 840

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ggacttttg gcaaagggag cctggtgaca tgcgctaagt ttgcatgctc caagaaaatg 960

accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020

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aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140

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atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260

cacgctgggg cagacaccgg aactccacac tggaacaaca aagaagcact ggtagagttc 1320

aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380

cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440

tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500

tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560

gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620

gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680

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tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggcagc 1800

accattggaa aagcatttga agccactgtg agaggtgcca agagaatggc agtcttggga 1860

gacacagcct gggactttgg atcagttgga ggcgctctca actcattggg caagggcatc 1920

catcaaattt ttggagcagc tttcaaatca ttgtttggag gaatgtcctg gttctcaatg 1980

aaaggtttat cgagcactag catagtctac atcctgattg cagtgtgtct tggagggttg 2040

atagggatcc ccgctttaat atgttgctgc agggggcgtt gtaacaaaaa gggagaacaa 2100

gttggtatgt caagaccagg cctaaagcct gatcttacgg gaacatcaaa atcctatgta 2160

aggtcgctct ga 2172

<210> 160
<211> 2172
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaprME_MVTMintracyto (D9)

<400> 160

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ctggacagga atgatgccgg cgaggccatc tccttcccaa ccacactggg catgaacaag 180

tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt 240

ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct 300

acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg 360

gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg 420

gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca 480

ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa 540

gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc 600

gtgagcaata gagacttcgt ggagggaatg tccggaggaa cctgggtgga tgtggtgctg 660

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tccgatacac agtacgtgtg caagcggacc ctggtggaca gaggctgggg caatggctgt 900

ggcctgtttg gcaagggctc tctggtgaca tgcgccaagt tcgcctgtag caagaagatg 960

accggcaagt ccatccagcc agagaacctg gagtaccgga tcatgctgtc tgtgcacggc 1020

tcccagcact ctggcatgat cgtgaacgac acaggccacg agacagatga gaatcgggcc 1080

aaggtggaga tcacacctaa ctctccaaga gccgaggcca ccctgggagg atttggctct 1140

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atgaacaata agcactggct ggtgcacaag gagtggtttc acgacatccc actgccatgg 1260

cacgcaggag cagatacagg aacaccacac tggaacaata aggaggccct ggtggagttc 1320

aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380

cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440

agcggccacc tgaagtgcag gctgaagatg gataagctgc gcctgaaggg cgtgtcctac 1500

tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560

gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620

gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680

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caccagatct tcggcgccgc ctttaagtcc ctgttcggcg gcatgagctg gttctcaatg 1980

aagggcctgt cctctacctc tatcgtgtac atcctgatcg ccgtgtgcct gggaggcctg 2040

atcggaatcc cagccctgat ctgctgttgc agaggccgct gcaacaagaa gggagagcaa 2100

gtgggaatgt ctcggccagg cctgaagcca gacctgacag gcacctccaa gtcttatgtg 2160

agaagcctgt ga 2172

<210> 161
<211> 723
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_ZikaprME_MVTMintracyto (D9)

<400> 161

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ala Glu Val Thr Arg
20 25 30

Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
35 40 45

Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
50 55 60

```
Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65                  70                  75                  80

Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
                85                  90                  95

Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
            100                 105                 110

Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser
        115                 120                 125

Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130                 135                 140

Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145                 150                 155                 160

Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
                165                 170                 175

Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180                 185                 190

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195                 200                 205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210                 215                 220

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225                 230                 235                 240

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245                 250                 255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
```

```
            260                 265                 270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275                 280                 285

Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290                 295                 300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305                 310                 315                 320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325                 330                 335

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
            340                 345                 350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
    370                 375                 380

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385                 390                 395                 400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
                405                 410                 415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
            420                 425                 430

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
        435                 440                 445

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
    450                 455                 460
```

```
Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser
465                 470                 475                 480

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
                485                 490                 495

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
            500                 505                 510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
        515                 520                 525

Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
    530                 535                 540

Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545                 550                 555                 560

Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565                 570                 575

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
            580                 585                 590

His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala
        595                 600                 605

Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp
    610                 615                 620

Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625                 630                 635                 640

His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser
                645                 650                 655

Trp Phe Ser Met Lys Gly Leu Ser Ser Thr Ser Ile Val Tyr Ile Leu
```

660 665 670

Ile Ala Val Cys Leu Gly Gly Leu Ile Gly Ile Pro Ala Leu Ile Cys
675 680 685

Cys Cys Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Val Gly Met Ser
690 695 700

Arg Pro Gly Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys Ser Tyr Val
705 710 715 720

Arg Ser Leu

<210> 162
<211> 1668
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_Zika_MVTMintracytoE (D10)

<400> 162
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ctccaaacac ccaccggtca aatcaggtgc ataggagtca gcaataggga ctttgtggaa 120

ggtatgtcag gtgggacttg ggttgatgtt gtcttggaac atggaggttg tgtcaccgta 180

atggcacagg acaaaccgac tgtcgacata gagctggtta caacaacagt cagcaacatg 240

gcggaggtaa gatcctactg ctatgaggca tcaatatcag acatggcttc ggacagccgc 300

tgcccaacac aaggtgaagc ctaccttgac aagcaatcag acactcaata tgtctgcaaa 360

agaacgttag tggacagagg ctggggaaat ggatgtggac tttttggcaa agggagcctg 420

gtgacatgcg ctaagtttgc atgctccaag aaaatgaccg ggaagagcat ccagccagag 480

aatctggagt accggataat gctgtcagtt catggctccc agcacagtgg gatgatcgtt 540

aatgacacag gacatgaaac tgatgagaat agagcgaagg ttgagataac gcccaattca 600

ccaagagccg aagccaccct ggggggtttt ggaagcctag gacttgattg tgaaccgagg 660

acaggccttg acttttcaga tttgtattac ttgactatga ataacaagca ctggttggtt 720

cacaaggagt ggttccacga cattccatta ccttggcacg ctggggcaga caccggaact 780

ccacactgga acaacaaaga agcactggta gagttcaagg acgcacatgc caaaaggcaa 840

actgtcgtgg ttctagggag tcaagaagga gcagttcaca cggcccttgc tggagctctg 900

gaggctgaga tggatggtgc aaagggaagg ctgtcctctg gccacttgaa atgtcgcctg 960

aaaatggata aacttagatt gaagggcgtg tcatactcct tgtgtaccgc agcgttcaca 1020

ttcaccaaga tcccggctga aacactgcac gggacagtca cagtggaggt acagtacgca 1080

gggacagatg gaccttgcaa ggttccagct cagatggcgg tggacatgca aactctgacc 1140

ccagttggga ggttgataac cgctaacccc gtaatcactg aaagcactga gaactctaag 1200

atgatgctgg aacttgatcc accatttggg gactcttaca ttgtcatagg agtcggggag 1260

aagaagatca cccaccactg gcacaggagt ggcagcacca ttggaaaagc atttgaagcc 1320

actgtgagag gtgccaagag aatggcagtc ttgggagaca cagcctggga ctttggatca 1380

gttggaggcg ctctcaactc attgggcaag ggcatccatc aaatttttgg agcagctttc 1440

aaatcattgt ttggaggaat gtcctggttc tcaatgaaag gtttatcgag cactagcata 1500

gtctacatcc tgattgcagt gtgtcttgga gggttgatag ggatccccgc tttaatatgt 1560

tgctgcaggg ggcgttgtaa caaaaaggga gaacaagttg gtatgtcaag accaggccta 1620

aagcctgatc ttacgggaac atcaaaatcc tatgtaaggt cgctctga 1668

<210> 163
<211> 1668
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_Zika_MVTMintracytoE (D10)

<400> 163
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccggtgc atcggcgtga gcaatagaga cttcgtggag 120

ggaatgtccg gaggaacctg ggtggatgtg gtgctggagc acggcggctg cgtgacagtg 180

atggcccagg acaagccaac cgtggatatc gagctggtga ccacaaccgt gtccaacatg 240

gccgaggtga ggtcttactg ctatgaggcc agcatctccg acatggcctc tgatagcagg 300

tgtccaaccc agggagaggc atacctggac aagcagtccg atacacagta cgtgtgcaag 360

cggaccctgg tggacagagg ctggggcaat ggctgtggcc tgtttggcaa gggctctctg 420

gtgacatgcg ccaagttcgc ctgtagcaag aagatgaccg gcaagtccat ccagccagag 480

aacctggagt accggatcat gctgtctgtg cacggctccc agcactctgg catgatcgtg 540

aacgacacag gccacgagac agatgagaat cgggccaagg tggagatcac acctaactct 600

ccaagagccg aggccaccct gggaggattt ggctctctgg gcctggactg cgagcctaga 660

acaggcctgg acttctccga tctgtactat ctgaccatga acaataagca ctggctggtg 720

cacaaggagt ggtttcacga catcccactg ccatggcacg caggagcaga tacaggaaca 780

ccacactgga acaataagga ggccctggtg gagttcaagg atgcccacgc caagcggcag 840

acagtggtgg tgctgggcag ccaggaggga gcagtgcaca ccgccctggc aggcgccctg 900

gaggcagaga tggacggagc taagggcaga ctgtctagcg gccacctgaa gtgcaggctg 960

aagatggata agctgcgcct gaagggcgtg tcctactctc tgtgcacagc cgccttcacc 1020

ttcaccaaga tccctgccga gacactgcac ggcacagtga ccgtggaggt gcagtatgcc 1080

ggcacagacg gaccctgtaa ggtgcctgcc cagatggccg tggatatgca gacactgaca 1140

cctgtgggca ggctgatcac cgccaatcca gtgatcacag agtctaccga gaacagcaag 1200

atgatgctgg agctggaccc accatttggc gatagctata tcgtgatcgg cgtgggcgag 1260

aagaagatca cacaccactg gcaccgcagc ggctccacaa tcggcaaggc ctttgaggca 1320

accgtgcgcg gagcaaagag aatggccgtg ctgggcgaca ccgcatggga tttcggatct 1380

gtgggaggcg ccctgaacag cctgggcaag ggcatccacc agatcttcgg cgccgccttt 1440

aagtccctgt tcggcggcat gagctggttc tcaatgaagg gcctgtcctc tacctctatc 1500

gtgtacatcc tgatcgccgt gtgcctggga ggcctgatcg gaatcccagc cctgatctgc 1560

tgttgcagag gccgctgcaa caagaaggga gagcaagtgg gaatgtctcg gccaggcctg 1620

aagccagacc tgacaggcac ctccaagtct tatgtgagaa gcctgtga 1668

<210> 164
<211> 555
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp’_Zika_MVTMintracytoE (D10)

<400> 164

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Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1               5                   10                  15


Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile Arg Cys Ile Gly
            20                  25                  30


Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val
        35                  40                  45


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


Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
65                  70                  75                  80


Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
                85                  90                  95


Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
            100                 105                 110


Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
        115                 120                 125


Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
    130                 135                 140


Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
145                 150                 155                 160
```

```
Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
                165                 170                 175

Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
            180                 185                 190

Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
        195                 200                 205

Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
    210                 215                 220

Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
225                 230                 235                 240

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

Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
            260                 265                 270

Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
        275                 280                 285

Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
    290                 295                 300

Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
305                 310                 315                 320

Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr
                325                 330                 335

Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr
            340                 345                 350

Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
```

```
        355                 360                 365

Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
    370                 375                 380

Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
385                 390                 395                 400

Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
                405                 410                 415

Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser
            420                 425                 430

Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met
        435                 440                 445

Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala
    450                 455                 460

Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe
465                 470                 475                 480

Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Met Lys Gly Leu Ser
                485                 490                 495

Ser Thr Ser Ile Val Tyr Ile Leu Ile Ala Val Cys Leu Gly Gly Leu
            500                 505                 510

Ile Gly Ile Pro Ala Leu Ile Cys Cys Cys Arg Gly Arg Cys Asn Lys
        515                 520                 525

Lys Gly Glu Gln Val Gly Met Ser Arg Pro Gly Leu Lys Pro Asp Leu
    530                 535                 540

Thr Gly Thr Ser Lys Ser Tyr Val Arg Ser Leu
545                 550                 555
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<210> 165
<211> 21169
<212> DNA
<213> Artificial sequence

<220>
<223> pTM2-MVSchw_A1_Zikasp_ZikaprME

<220>
<221> misc_feature
<222> (9)..(28)
<223> T7 promoter

<220>
<221> misc_feature
<222> (83)..(189)
<223> MV Leader and N promoter

<220>
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<222> (190)..(1767)
<223> MV N ORF

<220>
<221> misc_feature
<222> (1889)..(3414)
<223> MV P ORF

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<222> (3532)..(5625)
<223> A1. Zikasp_ZikaprME

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<222> (5722)..(6729)
<223> MV M ORF

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<222> (9555)..(11408)
<223> MV H ORF

<220>

<221> misc_feature
<222> (11518)..(18069)
<223> MV L ORF

<220>
<221> misc_feature
<222> (18179)..(18262)
<223> HDV ribozyme

<220>
<221> misc_feature
<222> (18263)..(18404)
<223> T7 terminator

<220>
<221> misc_feature
<222> (18438)..(18457)
<223> T3

<220>
<221> misc_feature
<222> (18475)..(18495)
<223> M13-rev

<220>
<221> misc_feature
<222> (18863)..(19491)
<223> ColE1 origin

<220>
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<222> (20642)..(21082)
<223> F1 ori

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<222> (20632)..(21087)
<223> M13 origin

<220>
<221> misc_feature
<222> (21089)..(21157)
<223> LacZ alpha

<220>
<221> misc_feature
<222> (18501)..(18523)
<223> LacO

<220>

<221> misc_feature
<222> (19643)..(20302)
<223> AmpR

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<221> misc_feature
<222> (20542)..(20570)
<223> Amp prom

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acgaaacccg gagtcccggg tcaccaaaca aagttgggta aggatagttc aatcaatgat 120

catcttctag tgcacttagg attcaagatc ctattatcag ggacaagagc aggattaggg 180

atatccgaga tggccacact tttaaggagc ttagcattgt tcaaaagaaa caaggacaaa 240

ccacccatta catcaggatc cggtggagcc atcagaggaa tcaaacacat tattatagta 300

ccaatccctg gagattcctc aattaccact cgatccagac ttctggaccg gttggtgagg 360

ttaattggaa acccggatgt gagcgggccc aaactaacag gggcactaat aggtatatta 420

tccttatttg tggagtctcc aggtcaattg attcagagga tcaccgatga ccctgacgtt 480

agcataaggc tgttagaggt tgtccagagt gaccagtcac aatctggcct taccttcgca 540

tcaagaggta ccaacatgga ggatgaggcg gaccaatact tttcacatga tgatccaatt 600

agtagtgatc aatccaggtt cggatggttc gggaacaagg aaatctcaga tattgaagtg 660

caagaccctg agggattcaa catgattctg ggtaccatcc tagcccaaat ttgggtcttg 720

ctcgcaaagg cggttacggc cccagacacg gcagctgatt cggagctaag aaggtggata 780

aagtacaccc aacaaagaag ggtagttggt gaatttagat tggagagaaa atggttggat 840

gtggtgagga acaggattgc cgaggacctc tccttacgcc gattcatggt cgctctaatc 900

ctggatatca agagaacacc cggaaacaaa cccaggattg ctgaaatgat atgtgacatt 960

gatacatata tcgtagaggc aggattagcc agttttatcc tgactattaa gtttgggata 1020

gaaactatgt atcctgctct tggactgcat gaatttgctg gtgagttatc cacacttgag 1080

tccttgatga acctttacca gcaaatgggg gaaactgcac cctacatggt aatcctggag 1140

aactcaattc agaacaagtt cagtgcagga tcataccctc tgctctggag ctatgccatg 1200

ggagtaggag tggaacttga aaactccatg ggaggtttga actttggccg atcttacttt 1260

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gcaatgcata ctactgagga caagatcagt agagcggttg gacccagaca agcccaagta 1440

tcatttctac acggtgatca aagtgagaat gagctaccga gattgggggg caaggaagat 1500

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tacaatgaca gaaatcttct agactaggtg cgagaggccg agggccagaa caacatccgc 1800

ctaccatcca tcattgttat aaaaaactta ggaaccaggt ccacacagcc gccagcccat 1860

caaccatcca ctcccacgat tggagccaat ggcagaagag caggcacgcc atgtcaaaaa 1920

cggactggaa tgcatccggg ctctcaaggc cgagcccatc ggctcactgg ccatcgagga 1980

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aactttggga atccccccaa gaaatctcca ggcatcaagc actgggttac agtgttatta 2220

cgtttatgat cacagcggtg aagcggttaa gggaatccaa gatgctgact ctatcatggt 2280

tcaatcaggc cttgatggtg atagcaccct ctcaggagga gacaatgaat ctgaaaacag 2340

cgatgtggat attggcgaac ctgataccga gggatatgct atcactgacc ggggatctgc 2400

tcccatctct atggggttca gggcttctga tgttgaaact gcagaaggag gggagatcca 2460

cgagctcctg agactccaat ccagaggcaa caactttccg aagcttggga aaactctcaa 2520

tgttcctccg cccccggacc ccggtagggc cagcacttcc gggacaccca ttaaaaaggg 2580

cacagacgcg agattagcct catttggaac ggagatcgcg tctttattga caggtggtgc 2640

aacccaatgt gctcgaaagt caccctcgga accatcaggg ccaggtgcac ctgcggggaa 2700

tgtccccgag tgtgtgagca atgccgcact gatacaggag tggacacccg aatctggtac 2760

cacaatctcc ccgagatccc agaataatga agaaggggga gactattatg atgatgagct 2820

gttctctgat gtccaagata ttaaaacagc cttggccaaa atacacgagg ataatcagaa 2880

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gcagatcaac aggcaaaata tcagcatatc caccctggaa ggacacctct caagcatcat 3000

gatcgccatt cctggacttg ggaaggatcc caacgacccc actgcagatg tcgaaatcaa 3060

tcccgacttg aaacccatca taggcagaga ttcaggccga gcactggccg aagttctcaa 3120

gaaacccgtt gccagccgac aactccaagg aatgacaaat ggacggacca gttccagagg 3180

acagctgctg aaggaatttc agctaaagcc gatcgggaaa aagatgagct cagccgtcgg 3240

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ccggctagag gaggatcgga agcgttacct gatgactctc cttgatgata tcaaaggagc 3360

caatgatctt gccaagttcc accagatgct gatgaagata ataatgaagt agctacagct 3420

caacttacct gccaacccca tgccagtcga cccaactagc ctaccctcca tcattgttat 3480

aaaaaactta ggaaccaggt ccacacagcc gccagcccat caacgcgtac gatggagaag 3540

aagcggagag gagcagacac aagcgtggga atcgtgggcc tgctgctgac cacagcaatg 3600

gcagcagagg tgaccaggag aggaagcgcc tactatatgt acctggacag gaatgatgcc 3660

ggcgaggcca tctccttccc aaccacactg ggcatgaaca agtgctacat ccagatcatg 3720

gacctgggcc acatgtgcga tgccaccatg tcctatgagt gtccaatgct ggacgagggc 3780

gtggagcccg acgatgtgga ttgctggtgt aataccacat ctacatgggt ggtgtacggc 3840

acctgtcacc acaagaaggg agaggcccgg cggagccggc gggccgtgac actgccttcc 3900

cactctacca ggaagctgca gacacgcagc cagacctggc tggagtccag agagtatacc 3960

aagcacctga tcagggtgga gaactggatc tttcgcaatc caggattcgc actggcagca 4020

gcagcaatcg catggctgct gggaagctcc accagccaga aagtgatcta cctggtcatg 4080

atcctgctga tcgctcctgc ctattctatc cggtgcatcg gcgtgagcaa tagagacttc 4140

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 4200

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 4260

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 4320

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cacctatctc agcgatctgt ctatttcgtt catccatagt tgcctgactg cccgtcgtgt 19020

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ggcgagttac atgatccccc atgttgtgaa aaaaagcggt tagctccttc ggtcctccga 19380

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cacccaactg atcttcagca tcttttactt tcaccagcgt ttctgggtga gcaaaaacag 19740

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<211> 1764
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of insert 4

<400> 168
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gatgccacca tgagctatga atgccctatg ctggatgagg gggtggaacc agatgacgtc 240

gattgttggt gcaacacgac gtcaacttgg gttgtgtacg gaacctgcca tcacaaaaaa 300

ggtgaagcac ggagatctag aagagctgtg acgctcccct cccattccac taggaagctg 360

caaacgcggt cgcaaacctg gttggaatca agagaataca caaagcactt gattagagtc 420

gaaaattgga tattcaggaa ccctggcttc gcgttagcag cagctgccat cgcttggctt 480

ttgggaagct caacgagcca aaaagtcata tacttggtca tgatactgct gattgccccg 540

gcatacagca tcaggtgcat aggagtcagc aatagggact ttgtggaagg tatgtcaggt 600

gggacttggg ttgatgttgt cttggaacat ggaggttgtg tcaccgtaat ggcacaggac 660

aaaccgactg tcgacataga gctggttaca acaacagtca gcaacatggc ggaggtaaga 720

tcctactgct atgaggcatc aatatcggac atggcttcgg acagccgctg cccaacacaa 780

ggtgaagcct accttgacaa gcaatcagac actcaatatg tctgcaaaag aacgttagtg 840

gacagaggct ggggaaatgg atgtggactt tttggcaaag ggagcctggt gacatgcgct 900

aagtttgcat gctccaagaa aatgaccggg aagagcatcc agccagagaa tctggagtac 960

cggataatgc tgtcagttca tggctcccag cacagtggga tgatcgttaa tgacacagga 1020

catgaaactg atgagaatag agcgaaggtt gagataacgc ccaattcacc aagagccgaa 1080

gccaccctgg ggggttttgg aagcctagga cttgattgtg aaccgaggac aggccttgac 1140

ttttcagatt tgtattactt gactatgaat aacaagcact ggttggttca caaggagtgg 1200

ttccacgaca ttccattacc ttggcacgct ggggcagaca ccggaactcc acactggaac 1260

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ctagggagtc aagaaggagc agttcacacg gcccttgctg gagctctgga ggctgagatg 1380

gatggtgcaa agggaaggct gtcctctggc cacttgaaat gtcgcctgaa aatggataaa 1440

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ccggctgaaa cactgcacgg gacagtcaca gtggaggtac agtacgcagg gacagatgga 1560

ccttgcaagg ttccagctca gatggcggtg gacatgcaaa ctctgacccc agttgggagg 1620

ttgataaccg ctaaccccgt aatcactgaa agcactgaga actctaagat gatgctggaa 1680

cttgatccac catttgggga ctcttacatt gtcataggag tcggggagaa gaagatcacc 1740

caccactggc acaggagtgg ctaa 1764

<210> 169
<211> 587
<212> PRT
<213> Artificial sequence

<220>
<223> Insert 4

<400> 169

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Glu Val Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn
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Asp Ala Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys
        35                  40                  45

Cys Tyr Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met
    50                  55                  60

Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val
65                  70                  75                  80

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

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

Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu
        115                 120                 125

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

Phe Arg Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu
145                 150                 155                 160

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

Leu Ile Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg
            180                 185                 190

Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu
        195                 200                 205

Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val
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    210                 215                 220

Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg
225                 230                 235                 240

Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg
                245                 250                 255

Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln
            260                 265                 270

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

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

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

Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val
                325                 330                 335

Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile
            340                 345                 350

Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser
        355                 360                 365

Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu
    370                 375                 380

Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp
385                 390                 395                 400

Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr
                405                 410                 415
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Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His
            420                 425                 430

Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val
        435                 440                 445

His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys
    450                 455                 460

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

Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr
                485                 490                 495

Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu
            500                 505                 510

Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met
        515                 520                 525

Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala
    530                 535                 540

Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu
545                 550                 555                 560

Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu
                565                 570                 575

Lys Lys Ile Thr His His Trp His Arg Ser Gly
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<210> 170
<211> 1392
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of insert 5

<400> 170
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gtcttggaac atggaggttg tgtcaccgta atggcacagg acaaaccgac tgtcgacata 180

gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca 240

tcaatatcgg acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac 300

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat 360

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag 420

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt 480

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat 540

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct ggggggtttt 600

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 660

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta 720

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gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 900

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 960

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac 1020

gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1080

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1140

gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1200

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1260

ggcagcacca ttggaaaagc atttgaagcc actgtgagag gtgccaagag aatggcagtc 1320

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ggcatctaat aa 1392

<210> 171
<211> 462
<212> PRT
<213> Artificial sequence

<220>
<223> Insert 5

<400> 171

Met Glu Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr
1 5 10 15

Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met
20 25 30

Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val
35 40 45

Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr
50 55 60

Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala
65 70 75 80

Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu
85 90 95

Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr
100 105 110

Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly
115 120 125

Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly
130 135 140

Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val

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145                 150                 155                 160

His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu
                165                 170                 175

Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg
            180                 185                 190

Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu
        195                 200                 205

Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn
    210                 215                 220

Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu
225                 230                 235                 240

Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys
                245                 250                 255

Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val
            260                 265                 270

Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly
        275                 280                 285

Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly
    290                 295                 300

His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val
305                 310                 315                 320

Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala
                325                 330                 335

Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr
            340                 345                 350
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Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr
        355                 360                 365

Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu
    370                 375                 380

Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly
385                 390                 395                 400

Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His
                405                 410                 415

Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val
            420                 425                 430

Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe
        435                 440                 445

Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
    450                 455                 460
```