SEQUENCE LISTING

<110> TRANSGENE S.A.

<120> Composition for treating HBV infection

<130> TG200

<160> 61

<170> PatentIn version 3.3

<210> 1
<211> 832
<212> PRT
<213> Hepatitis B virus

<400> 1

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Met Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu Leu Asp Asp
1               5                  10                  15

Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
            20                  25                  30

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
        35                  40                  45

Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
    50                  55                  60

Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro Ser Phe Pro
65                  70                  75                  80

Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu Gln Phe Val
                85                  90                  95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu Ile Met Pro
            100                 105                 110

Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
        115                 120                 125

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

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145                 150                 155                 160

Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
                165                 170                 175

Gln Lys Leu Gln His Gly Ala Glu Ser Phe His Gln Gln Ser Ser Gly
            180                 185                 190

Ile Leu Ser Arg Pro Pro Val Gly Ser Ser Leu Gln Ser Lys His Arg
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195 200 205

Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln Gly His Leu Ala Arg Arg
210 215 220

Gln Gln Gly Arg Ser Trp Ser Ile Arg Ala Gly Ile His Pro Thr Ala
225 230 235 240

Arg Arg Ser Phe Gly Val Glu Pro Ser Gly Ser Gly His Ser Thr Asn
245 250 255

Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr Gln Ser Pro Val Arg Lys
260 265 270

Ala Ala Tyr Pro Ala Val Ser Thr Phe Glu Lys His Ser Ser Ser Gly
275 280 285

His Ala Val Glu Leu His Asn Leu Pro Pro Asn Ser Ala Arg Ser Gln
290 295 300

Ser Glu Arg Pro Val Phe Pro Cys Trp Trp Leu Gln Phe Arg Asn Ser
305 310 315 320

Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu
325 330 335

Asp Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile Arg Ile Pro
340 345 350

Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn
355 360 365

Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe
370 375 380

Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn
385 390 395 400

Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser
405 410 415

Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala
420 425 430

Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala
435 440 445

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

Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Leu

```
465                 470                 475                 480

Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro
                485                 490                 495

Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro
            500                 505                 510

Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg
        515                 520                 525

Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met Asp Asp Val Val Leu
    530                 535                 540

Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr
545                 550                 555                 560

Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys
                565                 570                 575

Arg Trp Gly Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly Cys Tyr
            580                 585                 590

Gly Ser Leu Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu Cys Phe
        595                 600                 605

Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg
    610                 615                 620

Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr
625                 630                 635                 640

Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe
                645                 650                 655

Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn
            660                 665                 670

Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala
        675                 680                 685

Asp Ala Thr Pro Thr Gly Trp Gly Leu Val Met Gly His Gln Arg Met
    690                 695                 700

Arg Gly Thr Phe Leu Ala Pro Leu Pro Ile His Thr Ala Glu Leu Leu
705                 710                 715                 720

Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Asn Ile Leu Gly Thr
                725                 730                 735

Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu
```

740 745 750

Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr
755 760 765

Val Pro Ser Ala Leu Asn Pro Thr Asp Asp Pro Ser Arg Gly Arg Leu
770 775 780

Gly Leu Ser Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly
785 790 795 800

Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro
805 810 815

Asp Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
820 825 830

<210> 2
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 2

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

```
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
                165                 170                 175

Gln Ser Arg Glu Ser Gln Cys
            180
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<210> 3
<211> 226
<212> PRT
<213> Hepatitis B virus

<400> 3

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Met Glu Asn Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
1               5                   10                  15

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
            20                  25                  30

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys
        35                  40                  45

Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
    50                  55                  60

Cys Pro Pro Thr Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
65                  70                  75                  80

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
                85                  90                  95

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
            100                 105                 110

Ser Ser Thr Thr Ser Thr Gly Pro Cys Arg Thr Cys Thr Thr Pro Ala
        115                 120                 125

Gln Gly Thr Ser Met Tyr Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
    130                 135                 140

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Gly Lys
145                 150                 155                 160

Phe Leu Trp Glu Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu Leu
                165                 170                 175

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
            180                 185                 190

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile
        195                 200                 205
```

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
210 215 220

Tyr Ile
225

<210> 4
<211> 2499
<212> DNA
<213> Hepatitis B virus

<400> 4
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ctcaatctcg ggaatctcaa tgttagtatt ccttggactc ataaggtggg aaactttacg 180
gggctttatt cttctactgt acctgtcttt aaccctcatt ggaaaacacc ctcttttcct 240
aatatacatt tacaccaaga cattatcaaa aaatgtgaac aatttgtagg cccactcaca 300
gtcaatgaga aaagaagact gcaattgatt atgcctgcta ggttttatcc aaatgttacc 360
aaatatttgc cattggataa gggtattaaa ccttattatc cagaacatct agttaatcat 420
tacttccaaa ccagacatta tttacacact ctatggaagg cgggtatatt atataagaga 480
gaaacaacac atagtgcctc attttgtggg tcaccatatt cttgggaaca aaagctacag 540
catggggcag aatctttcca ccagcaatcc tctgggattc tttcccgacc accagttgga 600
tccagccttc agagcaaaca ccgcaaatcc agattgggac ttcaatccca acaaggacac 660
ctggccagac gccaacaagg taggagctgg agcattcggg ctgggattca ccccaccgca 720
cggaggtctt ttggggtgga gccctcaggc tcagggcatt ctacaaacct tgccagcaaa 780
tccgcctcct gcctctacca atcgccagtc aggaaggcag cctaccccgc tgtctccacc 840
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gcaagatccc agagtgagag gcctgtattt ccctgctggt ggctccagtt caggaacagt 960
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cacgggacca tgcagaacct gcacgactcc tgctcaagga acctctatgt atccctcctg 1440
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tttcggaaaa ttcctatggg agtgggcctc agcccgtttc tcctggctca gtttactagt 1560
gccatttgtt cagtggttcg tagggctttc ccccactgtt tggctttcag ttatatggat 1620

gatgtggtat tgggggccaa gtctgtacag catcttgagt ccctttttac cgctgttacc 1680

aattttcttt tgtctttggg tatacattta aaccctaaca aaacaaaaag atggggttac 1740

tctttacatt tcatgggcta tgtcattgga tgttatgggt cattgccaca agatcacatc 1800

atacaaaaaa tcaaagaatg ttttcgaaaa cttcctgtta acagacctat tgattggaaa 1860

gtctgtcaac gtattgtggg tcttttgggt tttgctgccc cttttacaca atgtggttat 1920

cctgctttaa tgcctttgta tgcatgtatt cagtcgaagc aggcttttac tttctcgcca 1980

acttacaagg cctttctgtg taaacaatac ctgaaccttt accccgttgc ccggcaacgg 2040

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catcagcgca tgcgtggaac ctttctggct cctctgccga tccatactgc ggaactccta 2160

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ttcgcttcac ctctgcacgt cgcatggaga ccaccgtga 2499

<210> 5
<211> 552
<212> DNA
<213> Hepatitis B virus

<400> 5
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tctgacttct ttccttcagt acgtgatctt ctagataccg cctcagctct gtatcgggaa 120

gccttagagt ctcctgagca ttgttcacct caccatactg ctctcaggca agcaattctg 180

tgctgggggg aactaatgac tctagctacc tgggtgggtg gtaatttgga agatccaata 240

tccagggacc tagtagtcag ttatgtcaac actaatatgg gcctaaagtt ccggcaacta 300

ttgtggtttc acatttcttg tctcactttt ggaagagaaa cagttataga atatttggtg 360

tctttcggag tgtggattcg cactcctcca gcttatagac caccaaatgc ccctatctta 420

tcaacacttc cggagactac tgttgttaga cgacgaggca ggtcccctag aagaagaact 480

ccctcgcctc gcagacgaag gtctcaatcg ccgcgtcgca gaagatctca atctcgggaa 540

tctcaatgtt aa 552

<210> 6
<211> 681
<212> DNA
<213> Hepatitis B virus

<400> 6
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ttgttgacaa gaatcctcac aataccgcag agtctagact cgtggtggac ttctctcaat 120

tttctagggg gaactaccgt gtgtcttggc caaaattcgc agtccccaac ctccaatcac 180

tcaccaacct cctgtcctcc aacctgtcct ggttatcgct ggatgtgtct gcggcgtttt 240

atcatcttcc tcttcatcct gctgctatgc ctcatcttct tgttggttct tctggactat 300

caaggtatgt tgcccgtttg tcctctaatt ccaggatctt caactaccag cacgggacca 360

tgcagaacct gcacgactcc tgctcaagga acctctatgt atccctcctg ttgctgtacc 420

aaaccttcgg acggaaattg cacctgtatt cccatcccat catcctgggc tttcggaaaa 480

ttcctatggg agtgggcctc agcccgtttc tcctggctca gtttactagt gccatttgtt 540

cagtggttcg tagggctttc ccccactgtt tggctttcag ttatatggat gatgtggtat 600

tgggggccaa gtctgtacag catcttgagt ccctttttac cgctgttacc aattttcttt 660

tgtctttggg tatacattta a 681

<210> 7
<211> 786
<212> PRT
<213> artificial sequence

<220>
<223> N-terminally truncated HBV polymerase (48-832)

<400> 7

Met Val Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu
1 5 10 15

Tyr Ser Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro Ser
20 25 30

Phe Pro Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu Gln
35 40 45

Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu Ile
50 55 60

Met Pro Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp
65 70 75 80

Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr Phe
85 90 95

Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr
100 105 110

Lys Arg Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser
115 120 125

Trp Glu Gln Lys Leu Gln His Gly Ala Glu Ser Phe His Gln Gln Ser
130 135 140

```
Ser Gly Ile Leu Ser Arg Pro Pro Val Gly Ser Ser Leu Gln Ser Lys
145                 150                 155                 160

His Arg Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln Gly His Leu Ala
                165                 170                 175

Arg Arg Gln Gln Gly Arg Ser Trp Ser Ile Arg Ala Gly Ile His Pro
            180                 185                 190

Thr Ala Arg Arg Ser Phe Gly Val Glu Pro Ser Gly Ser Gly His Ser
        195                 200                 205

Thr Asn Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr Gln Ser Pro Val
    210                 215                 220

Arg Lys Ala Ala Tyr Pro Ala Val Ser Thr Phe Glu Lys His Ser Ser
225                 230                 235                 240

Ser Gly His Ala Val Glu Leu His Asn Leu Pro Pro Asn Ser Ala Arg
                245                 250                 255

Ser Gln Ser Glu Arg Pro Val Phe Pro Cys Trp Trp Leu Gln Phe Arg
            260                 265                 270

Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu
        275                 280                 285

Leu Glu Asp Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile Arg
    290                 295                 300

Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp
305                 310                 315                 320

Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser
                325                 330                 335

Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala Val
            340                 345                 350

Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp
        355                 360                 365

Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro
    370                 375                 380

Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr
385                 390                 395                 400

Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn Tyr Gln His Gly
                405                 410                 415
```

```
Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser
            420                 425                 430

Leu Leu Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser
        435                 440                 445

His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu
    450                 455                 460

Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val
465                 470                 475                 480

Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met Asp Asp Val
                485                 490                 495

Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala
            500                 505                 510

Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys
        515                 520                 525

Thr Lys Arg Trp Gly Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly
    530                 535                 540

Cys Tyr Gly Ser Leu Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu
545                 550                 555                 560

Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys
                565                 570                 575

Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys
            580                 585                 590

Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln
        595                 600                 605

Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr
    610                 615                 620

Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val
625                 630                 635                 640

Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Val Met Gly His Gln
                645                 650                 655

Arg Met Arg Gly Thr Phe Leu Ala Pro Leu Pro Ile His Thr Ala Glu
            660                 665                 670

Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Asn Ile Leu
        675                 680                 685
```

```
Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro
    690                 695                 700

Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe
705                 710                 715                 720

Val Tyr Val Pro Ser Ala Leu Asn Pro Thr Asp Asp Pro Ser Arg Gly
                725                 730                 735

Arg Leu Gly Leu Ser Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr
            740                 745                 750

Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His
        755                 760                 765

Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg
    770                 775                 780

Pro Pro
785
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<210> 8
<211> 832
<212> PRT
<213> artificial sequence

<220>
<223> mutated polymerase deficient in RTase and RNase H activities

<400> 8

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Met Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu Leu Asp Asp
1               5                   10                  15

Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
            20                  25                  30

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
        35                  40                  45

Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
    50                  55                  60

Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro Ser Phe Pro
65                  70                  75                  80

Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu Gln Phe Val
                85                  90                  95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu Ile Met Pro
            100                 105                 110

Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
        115                 120                 125
```

```
Ile Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr Phe Gln Thr
    130                 135                 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145                 150                 155                 160

Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
                165                 170                 175

Gln Lys Leu Gln His Gly Ala Glu Ser Phe His Gln Gln Ser Ser Gly
            180                 185                 190

Ile Leu Ser Arg Pro Pro Val Gly Ser Ser Leu Gln Ser Lys His Arg
        195                 200                 205

Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln Gly His Leu Ala Arg Arg
    210                 215                 220

Gln Gln Gly Arg Ser Trp Ser Ile Arg Ala Gly Ile His Pro Thr Ala
225                 230                 235                 240

Arg Arg Ser Phe Gly Val Glu Pro Ser Gly Ser Gly His Ser Thr Asn
                245                 250                 255

Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr Gln Ser Pro Val Arg Lys
            260                 265                 270

Ala Ala Tyr Pro Ala Val Ser Thr Phe Glu Lys His Ser Ser Ser Gly
        275                 280                 285

His Ala Val Glu Leu His Asn Leu Pro Pro Asn Ser Ala Arg Ser Gln
    290                 295                 300

Ser Glu Arg Pro Val Phe Pro Cys Trp Trp Leu Gln Phe Arg Asn Ser
305                 310                 315                 320

Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu
                325                 330                 335

Asp Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile Arg Ile Pro
            340                 345                 350

Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn
        355                 360                 365

Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe
    370                 375                 380

Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn
385                 390                 395                 400
```

Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser
405 410 415

Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala
420 425 430

Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala
435 440 445

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

Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Leu
465 470 475 480

Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro
485 490 495

Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro
500 505 510

Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg
515 520 525

Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val Leu
530 535 540

Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr
545 550 555 560

Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys
565 570 575

Arg Trp Gly Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly Cys Tyr
580 585 590

Gly Ser Leu Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu Cys Phe
595 600 605

Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg
610 615 620

Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr
625 630 635 640

Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe
645 650 655

Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn
660 665 670

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Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala
        675                 680                 685

Asp Ala Thr Pro Thr Gly Trp Gly Leu Val Met Gly His Gln Arg Met
    690                 695                 700

Arg Gly Thr Phe Leu Ala Pro Leu Pro Ile His Thr Ala His Leu Leu
705                 710                 715                 720

Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Asn Ile Leu Gly Thr
                725                 730                 735

Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu
            740                 745                 750

Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr
        755                 760                 765

Val Pro Ser Ala Leu Asn Pro Thr Asp Asp Pro Ser Arg Gly Arg Leu
    770                 775                 780

Gly Leu Ser Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly
785                 790                 795                 800

Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro
                805                 810                 815

Asp Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
            820                 825                 830
```

<210> 9
<211> 874
<212> PRT
<213> artificial sequence

<220>
<223> truncated and mutated HBV polymerase fused to the transmembrane domain of rabies glycoprotein (TMR)

<400> 9

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Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1               5                   10                  15

Cys Phe Gly Lys Phe Pro Ile Val Ser Ile Pro Trp Thr His Lys Val
            20                  25                  30

Gly Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro
        35                  40                  45

His Trp Lys Thr Pro Ser Phe Pro Asn Ile His Leu His Gln Asp Ile
    50                  55                  60
```

```
Ile Lys Lys Cys Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu Lys
65                  70                  75                  80

Arg Arg Leu Gln Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val Thr
                85                  90                  95

Lys Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His
            100                 105                 110

Leu Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp
        115                 120                 125

Lys Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr His Ser Ala Ser Phe
    130                 135                 140

Cys Gly Ser Pro Tyr Ser Trp Glu Gln Lys Leu Gln His Gly Ala Glu
145                 150                 155                 160

Ser Phe His Gln Gln Ser Ser Gly Ile Leu Ser Arg Pro Pro Val Gly
                165                 170                 175

Ser Ser Leu Gln Ser Lys His Arg Lys Ser Arg Leu Gly Leu Gln Ser
            180                 185                 190

Gln Gln Gly His Leu Ala Arg Arg Gln Gln Gly Arg Ser Trp Ser Ile
        195                 200                 205

Arg Ala Gly Ile His Pro Thr Ala Arg Arg Ser Phe Gly Val Glu Pro
    210                 215                 220

Ser Gly Ser Gly His Ser Thr Asn Leu Ala Ser Lys Ser Ala Ser Cys
225                 230                 235                 240

Leu Tyr Gln Ser Pro Val Arg Lys Ala Ala Tyr Pro Ala Val Ser Thr
                245                 250                 255

Phe Glu Lys His Ser Ser Ser Gly His Ala Val Glu Leu His Asn Leu
            260                 265                 270

Pro Pro Asn Ser Ala Arg Ser Gln Ser Glu Arg Pro Val Phe Pro Cys
        275                 280                 285

Trp Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu
    290                 295                 300

Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu His
305                 310                 315                 320

Gly Glu His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly
                325                 330                 335
```

```
Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg
            340                 345                 350

Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser
        355                 360                 365

Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu
    370                 375                 380

Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr
385                 390                 395                 400

His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser
                405                 410                 415

Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile
            420                 425                 430

Phe Asn Tyr Gln His Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser
        435                 440                 445

Arg Asn Leu Tyr Val Ser Leu Leu Leu Leu Tyr Gln Thr Phe Gly Arg
    450                 455                 460

Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile
465                 470                 475                 480

Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser
                485                 490                 495

Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe
            500                 505                 510

Ser Tyr Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu
        515                 520                 525

Glu Ser Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile
    530                 535                 540

His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu His Phe
545                 550                 555                 560

Met Gly Tyr Val Ile Gly Cys Tyr Gly Ser Leu Pro Gln Asp His Ile
                565                 570                 575

Ile Gln Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro Val Asn Arg Pro
            580                 585                 590

Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala
        595                 600                 605
```

```
Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala
    610                 615                 620

Cys Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala
625                 630                 635                 640

Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg
                645                 650                 655

Pro Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly
            660                 665                 670

Leu Val Met Gly His Gln Arg Met Arg Gly Thr Phe Leu Ala Pro Leu
        675                 680                 685

Pro Ile His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg
    690                 695                 700

Ser Gly Ala Asn Ile Leu Gly Thr Asp Asn Ser Val Val Leu Ser Arg
705                 710                 715                 720

Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile
                725                 730                 735

Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Thr
            740                 745                 750

Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Ser Arg Pro Leu Leu Arg
        755                 760                 765

Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser
    770                 775                 780

Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro
785                 790                 795                 800

Leu His Val Ala Trp Arg Pro Pro Tyr Val Leu Leu Ser Ala Gly Ala
                805                 810                 815

Leu Thr Ala Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg
            820                 825                 830

Val Asn Arg Ser Glu Pro Thr Gln His Asn Leu Arg Gly Thr Gly Arg
        835                 840                 845

Glu Val Ser Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu
    850                 855                 860

Ser His Lys Ser Gly Gly Glu Thr Arg Leu
865                 870
```

<210> 10
<211> 148
<212> PRT
<213> artificial sequence

<220>
<223> truncated core (1-148)

<400> 10

```
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1               5                  10                  15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20                  25                  30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35                  40                  45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65                  70                  75                  80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85                  90                  95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100                 105                 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
        115                 120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130                 135                 140

Glu Thr Thr Val
145
```

<210> 11
<211> 140
<212> PRT
<213> artificial sequence

<220>
<223> truncated and deleted HBV core (1-76 and 85-148)

<400> 11

```
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1               5                  10                  15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20                  25                  30
```

```
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35                  40                  45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Val Val Ser Tyr
65                  70                  75                  80

Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His
                85                  90                  95

Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Ile Glu Tyr Leu Val
            100                 105                 110

Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn
        115                 120                 125

Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val
    130                 135                 140
```

<210> 12
<211> 39
<212> PRT
<213> artificial sequence

<220>
<223> HBV immunogenic domain Env1 (14-51)

<400> 12

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

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
            20                  25                  30

Thr Thr Val Cys Leu Gly Gln
        35
```

<210> 13
<211> 30
<212> PRT
<213> artificial sequence

<220>
<223> HBV immungenic domain Env2 (165-194)

<400> 13

```
Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
1               5                   10                  15

Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
            20                  25                  30
```

<210> 14
<211> 26
<212> PRT
<213> artificial sequence

<220>
<223> HBV immunogenic domain Env 3 (81-106)

<400> 14

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
1 5 10 15

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
20 25

<210> 15
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> HBV immunogenic domain Env 4 (202-226)

<400> 15

Gly Pro Ser Leu Tyr Ser Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro
1 5 10 15

Ile Phe Phe Cys Leu Trp Val Tyr Ile
20 25

<210> 16
<211> 69
<212> PRT
<213> artificial sequence

<220>
<223> fusion of HBV immunogenic domains Env1-Env2

<400> 16

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

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
20 25 30

Thr Thr Val Cys Leu Gly Gln Trp Ala Ser Ala Arg Phe Ser Trp Leu
35 40 45

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
50 55 60

Val Trp Leu Ser Val
65

<210> 17

<211> 94
<212> PRT
<213> artificial sequences

<220>
<223> fusion of HBV immunogenic domains Env1-Env2-Env4

<400> 17

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

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
20 25 30

Thr Thr Val Cys Leu Gly Gln Trp Ala Ser Ala Arg Phe Ser Trp Leu
35 40 45

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
50 55 60

Val Trp Leu Ser Val Gly Pro Ser Leu Tyr Ser Ile Leu Ser Pro Phe
65 70 75 80

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
85 90

<210> 18
<211> 179
<212> PRT
<213> artificial sequence

<220>
<223> fusion of truncated and deleted core (1-76 85-148) with HBV immunogenic domain Env 1

<400> 18

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Val Val Ser Tyr
65 70 75 80

Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His
85 90 95

Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Ile Glu Tyr Leu Val
100 105 110

Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn
115 120 125

Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Met Val Leu Gln
130 135 140

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
145 150 155 160

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys
165 170 175

Leu Gly Gln

<210> 19
<211> 208
<212> PRT
<213> artificial sequence

<220>
<223> fusion of truncated and deleted core (1-76 85-148) with HBV immunogenic domains Env1 and Env2

<400> 19

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Val Val Ser Tyr
65 70 75 80

Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His
85 90 95

Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Ile Glu Tyr Leu Val
100 105 110

Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn
115 120 125

Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val Leu Gln Ala

130 135 140

Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
145 150 155 160

Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys Leu
165 170 175

Gly Gln Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
180 185 190

Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
195 200 205

<210> 20
<211> 276
<212> PRT
<213> artificial sequence

<220>
<223> fusion of core with HBV immunogenic domains Env1, Env2 and Env4

<400> 20

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

```
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
                165                 170                 175

Gln Ser Arg Glu Ser Gln Cys Val Leu Gln Ala Gly Phe Phe Leu Leu
            180                 185                 190

Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser
        195                 200                 205

Leu Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Trp Ala Ser
    210                 215                 220

Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe
225                 230                 235                 240

Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Gly Pro Ser Leu Tyr
                245                 250                 255

Ser Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
            260                 265                 270

Trp Val Tyr Ile
        275
```

<210> 21
<211> 2361
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding HBV truncated polymerase (48-832)

<400> 21

```
atggttagta ttccttggac tcataaggtg ggaaacttta cggggcttta ttcttctact     60

gtacctgtct ttaaccctca ttggaaaaca ccctcttttc ctaatataca tttacaccaa    120

gacattatca aaaaatgtga acaatttgta ggcccactca cagtcaatga gaaaagaaga    180

ctgcaattga ttatgcctgc taggttttat ccaaatgtta ccaaatattt gccattggat    240

aagggtatta aaccttatta tccagaacat ctagttaatc attacttcca aaccagacat    300

tatttacaca ctctatggaa ggcgggtata ttatataaga gagaaacaac acatagtgcc    360

tcattttgtg ggtcaccata ttcttgggaa caaaagctac agcatggggc agaatctttc    420

caccagcaat cctctgggat tctttcccga ccaccagttg gatccagcct tcagagcaaa    480

caccgcaaat ccagattggg acttcaatcc caacaaggac acctggccag acgccaacaa    540

ggtaggagct ggagcattcg ggctgggatt caccccaccg cacggaggtc ttttggggtg    600

gagccctcag gctcagggca ttctacaaac cttgccagca aatccgcctc ctgcctctac    660

caatcgccag tcaggaaggc agcctacccc gctgtctcca cctttgagaa acactcatcc    720

tcaggccatg cagtggaact ccacaacctt ccaccaaact ctgcaagatc ccagagtgag    780
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aggcctgtat ttccctgctg gtggctccag ttcaggaaca gtaaaccctg ttccgactac 840

tgtctctccc atatcgtcaa tcttctcgag gattggggac cctgcgctga acatggagaa 900

catcacatca ggattcctag gacccctgct cgtgttacag gcggggtttt tcttgttgac 960

aagaatcctc acaataccgc agagtctaga ctcgtggtgg acttctctca attttctagg 1020

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ctcctgtcct ccaacctgtc ctggttatcg ctggatgtgt ctgcggcgtt ttatcatctt 1140

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ctgcacgact cctgctcaag gaacctctat gtatccctcc tgttgctgta ccaaaccttc 1320

ggacggaaat tgcacctgta ttcccatccc atcatcctgg gctttcggaa aattcctatg 1380

ggagtgggcc tcagcccgtt tctcctggct cagtttacta gtgccatttg ttcagtggtt 1440

cgtagggctt tcccccactg tttggctttc agttatatgg atgatgtggt attgggggcc 1500

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ggtatacatt taaaccctaa caaaacaaaa agatggggtt actctttaca tttcatgggc 1620

tatgtcattg gatgttatgg gtcattgcca caagatcaca tcatacaaaa aatcaaagaa 1680

tgttttcgaa aacttcctgt taacagacct attgattgga aagtctgtca acgtattgtg 1740

ggtcttttgg gttttgctgc ccctttaca caatgtggtt atcctgcttt aatgcctttg 1800

tatgcatgta ttcagtcgaa gcaggctttt actttctcgc caacttacaa ggcctttctg 1860

tgtaaacaat acctgaacct ttaccccgtt gcccggcaac ggccaggtct gtgccaagtg 1920

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gtttacgtcc cgtcggcgct gaatcccacg gacgaccctt ctcggggtcg cttggggctc 2220

tctcgtcccc ttctccgtct accgtttcga ccgaccacgg ggcgcacctc tctttacgcg 2280

gactccccgt ctgtgccttc tcatctgccg gaccgtgtgc acttcgcttc acctctgcac 2340

gtcgcatgga gaccaccgtg a 2361

<210> 22
<211> 2499
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding a mutated HBV polymerase deficient for RTase and RNase activities

<400> 22
atgcccctat cttatcaaca cttccggaga ctactgttgt tagacgacga ggcaggtccc 60

ctagaagaag aactccctcg cctcgcagac gaaggtctca atcgccgcgt cgcagaagat 120

ctcaatctcg ggaatctcaa tgttagtatt ccttggactc ataaggtggg aaactttacg 180
gggctttatt cttctactgt acctgtcttt aaccctcatt ggaaaacacc ctcttttcct 240
aatatacatt tacaccaaga cattatcaaa aaatgtgaac aatttgtagg cccactcaca 300
gtcaatgaga aaagaagact gcaattgatt atgcctgcta ggttttatcc aaatgttacc 360
aaatatttgc cattggataa gggtattaaa ccttattatc cagaacatct agttaatcat 420
tacttccaaa ccagacatta tttacacact ctatggaagg cgggtatatt atataagaga 480
gaaacaacac atagtgcctc attttgtggg tcaccatatt cttgggaaca aaagctacag 540
catggggcag aatctttcca ccagcaatcc tctgggattc tttcccgacc accagttgga 600
tccagccttc agagcaaaca ccgcaaatcc agattgggac ttcaatccca acaaggacac 660
ctggccagac gccaacaagg taggagctgg agcattcggg ctgggattca ccccaccgca 720
cggaggtctt ttggggtgga gccctcaggc tcagggcatt ctacaaacct tgccagcaaa 780
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tgcgctgaac atggagaaca tcacatcagg attcctagga cccctgctcg tgttacaggc 1080
ggggtttttc ttgttgacaa gaatcctcac aataccgcag agtctagact cgtggtggac 1140
ttctctcaat tttctagggg gaactaccgt gtgtcttggc caaaattcgc agtccccaac 1200
ctccaatcac tcaccaacct cctgtcctcc aacctgtcct ggttatcgct ggatgtgtct 1260
gcggcgtttt atcatcttcc tcttcatcct gctgctatgc ctcatcttct tgttggttct 1320
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cacgggacca tgcagaacct gcacgactcc tgctcaagga acctctatgt atccctcctg 1440
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tttcggaaaa ttcctatggg agtgggcctc agcccgtttc tcctggctca gtttactagt 1560
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gatgtggtat tgggggccaa gtctgtacag catcttgagt ccctttttac cgctgttacc 1680
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atacaaaaaa tcaaagaatg ttttcgaaaa cttcctgtta acagacctat tgattggaaa 1860
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gccgcttgtt ttgctcgcag caggtctgga gcaaacattc tcgggacgga taactctgtt 2220

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ctgcgcggga cgtcctttgt ttacgtcccg tcggcgctga atcccacgga cgacccttct 2340

cggggtcgct tggggctctc tcgtcccctt ctccgtctac cgtttcgacc gaccacgggg 2400

cgcacctctc tttacgcgga ctccccgtct gtgccttctc atctgccgga ccgtgtgcac 2460

ttcgcttcac ctctgcacgt cgcatggaga ccaccgtga 2499

<210> 23
<211> 2628
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding HBV truncated and mutated Pol fused to the transmembrane domain of the rabies glycoprotein (TMR)

<400> 23
atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggaaa 60

ttccctattg ttagtattcc ttggactcat aaggtgggaa actttacggg gctttattct 120

tctactgtac ctgtctttaa ccctcattgg aaaacaccct cttttcctaa tatacattta 180

caccaagaca ttatcaaaaa atgtgaacaa tttgtaggcc cactcacagt caatgagaaa 240

agaagactgc aattgattat gcctgctagg ttttatccaa atgttaccaa atatttgcca 300

ttggataagg gtattaaacc ttattatcca gaacatctag ttaatcatta cttccaaacc 360

agacattatt tacacactct atggaaggcg ggtatattat ataagagaga aacaacacat 420

agtgcctcat tttgtgggtc accatattct tgggaacaaa agctacagca tggggcagaa 480

tctttccacc agcaatcctc tgggattctt tcccgaccac cagttggatc cagccttcag 540

agcaaacacc gcaaatccag attgggactt caatcccaac aaggacacct ggccagacgc 600

caacaaggta ggagctggag cattcgggct gggattcacc ccaccgcacg gaggtctttt 660

ggggtggagc cctcaggctc agggcattct acaaaccttg ccagcaaatc cgcctcctgc 720

ctctaccaat cgccagtcag gaaggcagcc taccccgctg tctccacctt tgagaaacac 780

tcatcctcag gccatgcagt ggaactccac aaccttccac caaactctgc aagatcccag 840

agtgagaggc ctgtatttcc ctgctggtgg ctccagttca ggaacagtaa accctgttcc 900

gactactgtc tctcccatat cgtcaatctt ctcgaggatt ggggaccctg cgctgaacat 960

ggagaacatc acatcaggat tcctaggacc cctgctcgtg ttacaggcgg ggtttttctt 1020

gttgacaaga atcctcacaa taccgcagag tctagactcg tggtggactt ctctcaattt 1080

tctaggggga actaccgtgt gtcttggcca aaattcgcag tccccaacct ccaatcactc 1140

accaacctcc tgtcctccaa cctgtcctgg ttatcgctgg atgtgtctgc ggcgttttat 1200

catcttcctc ttcatcctgc tgctatgcct catcttcttg ttggttcttc tggactatca 1260

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aaagaatgtt ttcgaaaact tcctgttaac agacctattg attggaaagt ctgtcaacgt 1800

attgtgggtc ttttgggttt tgctgcccct tttacacaat gtggttatcc tgctttaatg 1860

cctttgtatg catgtattca gtcgaagcag gcttttactt tctcgccaac ttacaaggcc 1920

tttctgtgta aacaatacct gaacctttac cccgttgccc ggcaacggcc aggtctgtgc 1980

caagtgtttg ctgacgcaac ccccactggc tggggcttgg tcatgggcca tcagcgcatg 2040

cgtggaacct ttctggctcc tctgccgatc catactgcgc atctcctagc cgcttgtttt 2100

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atgttgataa ttttcctgat gacatgttgt agaagagtca atcgatcaga acctacgcaa 2520

cacaatctca gagggacagg gagggaggtg tcagtcactc cccaaagcgg gaagatcata 2580

tcttcatggg aatcacacaa gagtgggggt gagaccagac tgtgatga 2628

<210> 24
<211> 537
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding the HBV truncated and deleted core (1-76 85-148) fused to HBV immunogenic domain Env 1

<400> 24
atggacattg atccttataa agaatttgga gctactgtgg agttactctc ttttttgcct 60

tctgacttct ttccttcagt acgtgatctt ctagataccg cctcagctct gtatcgggaa 120

gccttagagt ctcctgagca ttgttcacct caccatactg ctctcaggca agcaattctg 180

tgctgggggg aactaatgac tctagctacc tgggtgggtg gtaatttgga agtcagttat 240

gtcaacacta atatgggcct aaagttccgg caactattgt ggtttcacat ttcttgtctc 300

acttttggaa gagaaacagt tatagaatat ttggtgtctt tcggagtgtg gattcgcact 360

cctccagctt atagaccacc aaatgcccct atcttatcaa cacttccgga gactactgtt 420

gtcctgcaag caggcttctt cctgctgacc cgtattctga ccattccaca aagcctggat 480

agctggtgga ccagcctgaa cttcctgggt ggcaccacgg tttgcctggg tcagtaa 537

<210> 25
<211> 627
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding the HBV truncated and deleted core (1-76 85-148) fused with HBV immunogenic domains Env1 and Env2

<400> 25
atggacattg atccttataa agaatttgga gctactgtgg agttactctc ttttttgcct 60

tctgacttct ttccttcagt acgtgatctt ctagataccg cctcagctct gtatcgggaa 120

gccttagagt ctcctgagca ttgttcacct caccatactg ctctcaggca agcaattctg 180

tgctgggggg aactaatgac tctagctacc tgggtgggtg gtaatttgga agtcagttat 240

gtcaacacta atatgggcct aaagttccgg caactattgt ggtttcacat ttcttgtctc 300

acttttggaa gagaaacagt tatagaatat ttggtgtctt tcggagtgtg gattcgcact 360

cctccagctt atagaccacc aaatgcccct atcttatcaa cacttccgga gactactgtt 420

gtcctgcaag caggcttctt cctgctgacc cgtattctga ccattccaca aagcctggat 480

agctggtgga ccagcctgaa cttcctgggt ggcaccacgg tttgcctggg tcagtgggca 540

agcgcacgct ttagctggct gagcctgctg gttccgttcg tgcaatggtt tgtgggtctg 600

agcccaaccg tgtggctgag cgtgtaa 627

<210> 26
<211> 828
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence encoding HBV core (1-183) fused to HBV immunogenic domains Env1-Env2 and Env4

<400> 26
atggacattg atccttataa agaatttgga gctactgtgg agttactctc ttttttgcct 60

tctgacttct ttccttcagt acgtgatctt ctagataccg cctcagctct gtatcgggaa 120

gccttagagt ctcctgagca ttgttcacct caccatactg ctctcaggca agcaattctg 180

tgctgggggg aactaatgac tctagctacc tgggtgggtg gtaatttgga agatccaata 240

tccagggacc tagtagtcag ttatgtcaac actaatatgg gcctaaagtt ccggcaacta 300

ttgtggtttc acatttcttg tctcactttt ggaagagaaa cagttataga atatttggtg 360

tctttcggag tgtggattcg cactcctcca gcttatagac caccaaatgc ccctatctta 420

tcaacacttc cggagactac tgttgttaga cgacgaggca ggtcccctag aagaagaact 480

ccctcgcctc gcagacgaag gtctcaatcg ccgcgtcgca gaagatctca atctcgggaa 540

tctcagtgcg tcctgcaagc tggattcttt cttctcacca ggattttgac cattccacaa 600

tctcttgata gctggtggac aagtttgaac ttccttggag gcacaactgt ctgcctcgga 660

cagtgggcaa gtgctcgctt ttcttggttg agcttgctcg ttcccttcgt gcaatggttt 720

gttggactct ctccaacagt ctggttgtcc gtcggaccta gcctttatag tattctcagc 780

ccattcttgc cactcttgcc tatcttcttc tgcttgtggg tttatatc 828

<210> 27
<211> 2499
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence present in the plasmid pGA-15pol

<400> 27
atgcccctat cttatcaaca cttccggaga ctactgttgt tagacgacga ggcaggtccc 60

ctagaagaag aactccctcg cctcgcagac gaaggtctca atcgccgcgt cgcagaagat 120

ctcaatctcg ggaatctcaa tgttagtatt ccttggactc ataaggtggg aaactttacg 180

gggctttatt cttctactgt acctgtcttt aaccctcatt ggaaaacacc ctcttttcct 240

aatatacatt tacaccaaga cattatcaaa aaatgtgaac aatttgtagg cccactcaca 300

gtcaatgaga aaagaagact gcaattgatt atgcctgcta ggttttatcc aaatgttacc 360

aaatatttgc cattggataa gggtattaaa ccttattatc cagaacatct agttaatcat 420

tacttccaaa ccagacatta tttacacact ctatggaagg cgggtatatt atataagaga 480

gaaacaacac atagtgcctc attttgtggg tcaccatatt cttgggaaca aaagctacag 540

catggggcag aatctttcca ccagcaatcc tctgggattc tttcccgacc accagttgga 600

tccagccttc agagcaaaca ccgcaaatcc agattgggac ttcaatccca acaaggacac 660

ctggccagac gccaacaagg taggagctgg agcattcggg ctgggattca ccccaccgca 720

cggaggtctt ttggggtgga gccctcaggc tcagggcatt ctacaaacct tgccagcaaa 780

tccgcctcct gcctctacca atcgccagtc aggaaggcag cctaccccgc tgtctccacc 840

tttgagaaac actcatcctc aggccatgca gtggaactcc acaaccttcc accaaactct 900

gcaagatccc agagtgagag gcctgtattt ccctgctggt ggctccagtt caggaacagt 960

aaaccctgtt ccgactactg tctctcccat atcgtcaatc ttctcgagga ttggggaccc 1020

tgcgctgaac atggagaaca tcacatcagg attcctagga cccctgctcg tgttacaggc 1080

ggggtttttc ttgttgacaa gaatcctcac aataccgcag agtctagact cgtggtggac 1140

ttctctcaat tttctagggg gaactaccgt gtgtcttggc caaaattcgc agtccccaac 1200

ctccaatcac tcaccaacct cctgtcctcc aacctgtcct ggttatcgct ggatgtgtct 1260

gcggcgtttt atcatcttcc tcttcatcct gctgctatgc ctcatcttct tgttggttct 1320

tctggactat caaggtatgt tgcccgtttg tcctctaatt ccaggatctt caactaccag 1380

cacgggacca tgcagaacct gcacgactcc tgctcaagga acctctatgt atccctcctg 1440

ttgctgtacc aaaccttcgg acggaaattg cacctgtatt cccatcccat catcctgggc 1500

tttcggaaaa ttcctatggg agtgggcctc agcccgtttc tcctggctca gtttactagt 1560

gccatttgtt cagtggttcg tagggctttc ccccactgtt tggctttcag ttatatgcat 1620

gatgtggtat tgggggccaa gtctgtacag catcttgagt ccctttttac cgctgttacc 1680

aattttcttt tgtctttggg tatacattta aaccctaaca aaacaaaaag atggggttac 1740

tctttacatt tcatgggcta tgtcattgga tgttatgggt cattgccaca agatcacatc 1800

atacaaaaaa tcaaagaatg ttttcgaaaa cttcctgtta acagacctat tgattggaaa 1860

gtctgtcaac gtattgtggg tcttttgggt tttgctgccc cttttacaca atgtggttat 1920

cctgctttaa tgcctttgta tgcatgtatt cagtcgaagc aggcttttac tttctcgcca 1980

acttacaagg cctttctgtg taaacaatac ctgaaccttt accccgttgc ccggcaacgg 2040

ccaggtctgt gccaagtgtt tgctgacgca acccccactg gctggggctt ggtcatgggc 2100

catcagcgca tgcgtggaac ctttctggct cctctgccga tccatactgc gcatctccta 2160

gccgcttgtt ttgctcgcag caggtctgga gcaaacattc tcgggacgga taactctgtt 2220

gttctctccc gcaaatatac atcgtttcca tggctgctag gctgtgctgc caactggatc 2280

ctgcgcggga cgtcctttgt ttacgtcccg tcggcgctga atcccacgga cgacccttct 2340

cggggtcgct tggggctctc tcgtcccctt ctccgtctac cgtttcgacc gaccacgggg 2400

cgcacctctc tttacgcgga ctccccgtct gtgccttctc atctgccgga ccgtgtgcac 2460

ttcgcttcac ctctgcacgt cgcatggaga ccaccgtga 2499

<210> 28
<211> 37
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 28
gagcgatatc caccatgaat gttagtattc cttggac 37

<210> 29
<211> 31
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 29
gatcgctagc tcacggtggt ctccatgcga c 31

<210> 30
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 30
gagtgatatc caccatggtt cctcaggctc tcctg 35

<210> 31
<211> 46
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 31
gtccaaggaa tactaacatt aatagggaat ttcccaaaac acaatg 46

<210> 32
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 32
gtcgcatgga gaccaccgta tgtattactg agtgcaggg 39

<210> 33
<211> 29
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 33
gagtgctagc tcacagtctg gtctcaccc 29

<210> 34
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 34
gttttgggaa attccctatt aatgttagta ttccttggac tc 42

<210> 35
<211> 41
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 35
ctgcactcag taatacatac ggtggtctcc atgcgacgtg c 41

<210> 36
<211> 552
<212> DNA
<213> artificial sequence

<220>
<223> Core-encoding nucleotide sequence present in pGA4-core plasmide

<400> 36
atggacattg atccttataa agaatttgga gctactgtgg agttactctc ttttttgcct 60

tctgacttct ttccttcagt acgtgatctt ctagataccg cctcagctct gtatcgggaa 120

gccttagagt ctcctgagca ttgttcacct caccatactg ctctcaggca agcaattctg 180

tgctgggggg aactaatgac tctagctacc tgggtgggtg gtaatttgga agatccaata 240

tccagggacc tagtagtcag ttatgtcaac actaatatgg gcctaaagtt ccggcaacta 300

ttgtggtttc acatttcttg tctcactttt ggaagagaaa cagttataga atatttggtg 360

tctttcggag tgtggattcg cactcctcca gcttatagac caccaaatgc ccctatctta 420

tcaacacttc cggagactac tgttgttaga cgacgaggca ggtcccctag aagaagaact 480

ccctcgcctc gcagacgaag gtctcaatcg ccgcgtcgca gaagatctca atctcgggaa 540

tctcagtgct aa 552

<210> 37
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 37
gactgttaac caccatggac attgatcctt ataaagaatt tg 42

<210> 38
<211> 41
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 38
gttgacataa ctgactacca aattaccacc cacccaggta g 41

<210> 39
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 39
gtgggtggta atttggtagt cagttatgtc aacactaata tg 42

<210> 40
<211> 33
<212> DNA
<213> artificial sequence

<220>

<223> primer

<400> 40
gactctcgag ttaaacagta gtctccggaa gtg 33

<210> 41
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 41
gacgggatcc accatggaca ttgatcctta taaagaattt gg 42

<210> 42
<211> 38
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 42
gcctgcttgc aggacaacag tagtctccgg aagtgttg 38

<210> 43
<211> 702
<212> DNA
<213> artificial sequence

<220>
<223> core and env-encoding nucleotide sequence present in pMK-C/E plasmid

<400> 43
atggacattg atccttataa agaatttgga gctactgtgg agttactctc tttcttgcct 60

tctgacttct ttccttcagt acgtgatctt ctagatacag cctcagctct gtatcgggaa 120

gccttagtcc tgcaagcagg cttcttcctg ctgacccgta ttctgaccat tccacaaagc 180

ctggatagct ggtggaccag cctgaacttc ctgggtggca ccacggtttg cctgggtcag 240

gagtctcctg agcattgttc acctcaccat actgctctca ggcaagcaat tctgtgctgg 300

ggagaactaa tgactctagc tacctgggtg ggtggttggg caagcgcacg ctttagctgg 360

ctgagcctgc tggttccgtt cgtgcaatgg tttgtgggtc tgagcccaac cgtgtggctg 420

agcgtgaatt tggtagtcag ttatgtcaac actaatatgg gactaaagtt ccgacaacta 480

ttgtggtttc acatttcttg tctcactttt ggaagagaaa cagttataga atatttggtg 540

tctttcggag tgtggattcg cactcctcca gcttatagac caccaaacgc accgatactg 600

agcaccctgc cagaaaccac cgtgggtccg agcttatatt ctatactgag cccattcctg 660

ccattactgc cgatcttctt ctgcctgtgg gtgtatatct ga 702

<210> 44
<211> 36
<212> DNA

<213> artificial sequence

<220>
<223> primer

<400> 44
ccggagacta ctgttgtcct gcaagcaggc ttcttc 36

<210> 45
<211> 47
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 45
gagtcattct cgacttgcgg ccgcttactg acccaggcaa accgtgg 47

<210> 46
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 46
gcgtgcgctt gcccactgac ccaggcaaac cgtgg 35

<210> 47
<211> 38
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 47
cggtttgcct gggtcagtgg gcaagcgcac gctttagc 38

<210> 48
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 48
gagtcattct cgacttgcgg ccgcttacac gctcagccac acggttgg 48

<210> 49
<211> 50
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 49
gggggctag caagcttcca ccatggacat tgatccttat aaagaatttg 50

<210> 50
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 50
gaaagaatcc agcttgcagg acgcactgag attcccgaga ttgag 45

<210> 51
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 51
ctcaatctcg ggaatctcag tgcgtcctgc aagctggatt ctttc 45

<210> 52
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 52
gagtcattct cgacttgcgg ccgcttagat ataaacccac aagc 44

<210> 53
<211> 52
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 53
gggggggctag caagcttcca ccatgaatgt tagtattcct tggactcata ag 52

<210> 54
<211> 49
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 54
gagtcattct cgacttgcgg ccgctcacgg tggtctccat gcgacgtgc 49

<210> 55
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> peptide

<400> 55

Ser Leu Tyr Ala Asp Ser Pro Ser Val
1 5

<210> 56
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> peptide

<400> 56

Phe Leu Pro Ser Asp Phe Phe Pro Ser Val
1 5 10

<210> 57
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> peptide

<400> 57

Ile Leu Cys Trp Gly Glu Leu Met Thr Leu
1 5 10

<210> 58
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> peptide

<400> 58

Val Leu Gln Ala Gly Phe Phe Leu Leu
1 5

<210> 59
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> peptide

<400> 59

Phe Leu Gly Gly Thr Thr Val Cys Leu
1 5

<210> 60
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> peptide

<400> 60

Gly Leu Ser Pro Thr Val Trp Leu Ser Val
1 5 10

<210> 61
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 61
gactctcgag ttagcactga gattcccgag attg 34