SEQUENCE LISTING

<110> Janssen Sciences Ireland Unlimited Company
Bavarian Nordic A/S

<120> Methods and Compositions for Inducing an Immune Response Against Hepatitis B Virus (HBV)

<130> 688097-413WO1

<150> PCT/IB2017/058148
<151> 2017-12-19

<150> US 62/607,439
<151> 2017-12-19

<160> 28

<170> PatentIn version 3.5

<210> 1
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> HBV core

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agcgacttct tcccttccat cagagacctg ctggacactg ccagcgcact gtacagagag 120

gctctggaaa gccctgagca ctgcagccct caccacaccg ctctgagaca ggccatcctg 180

tgctggggag agctgatgaa cctggccacc tgggtcggaa gcaacctgga agatccagcc 240

agtcgcgagc tggtggtgtc ctacgtgaac gtgaacatgg gcttgaagat ccggcagctc 300

ctgtggttcc acatcagctg cctgaccttc ggacgggaaa ccgtgctgga atacctggtg 360

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agcaccctgc ctgagacaac cgtggtg 447

<210> 2
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> HBV core

<400> 2

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

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

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

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

Glu Thr Val Leu 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
145

<210> 3
<211> 2529
<212> DNA
<213> Artificial Sequence

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<223> HBV pol

<400> 3
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ctgaacctgg gcaacctgaa cgtgtccatc ccttggaccc acaaggtcgg aaacttcacc 180

ggtctgtaca gcagcaccgt gcctgtgttc aaccctgagt ggcagacacc cagctttccc 240

aacatccatc tgcaggaaga tatcatcaac cgctgcgagc agttcgtggg acctctgacc 300

gtgaacgaga agcggagact gaagctgatc atgccagcca gattctaccc taacgtgacc 360

aagtacctgc ctctggacaa gggcatcaag ccctactacc ctgagcacct ggtcaaccac 420

tacttccaga ccagacacta cctgcacacc ctgtggaagg ccggcatcct gtacaagaga 480

gagacaacca gaagcgccag cttctgcggc agcccttaca gctgggagca ggaactccag 540

cacggacgcc tggtgttcca gaccagcacc agacacggcg acgagagctt ttgccagcag 600

agcagcggca tcctgagcag atctcctgtg ggtccttgcc tgcagagcca gctgaggaag 660

tccagactgg gcctgcagcc tcagcaggga catctggcta gacggcagca gggcagaagc 720

ggcagcatca gagccagagt gcaccctacc accagacggc ctttcggcgt ggaacctagc 780

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gctgtcgagc tgcacaacat ccctcccaac agcgccagaa gccagagcga gggtcctgtg 960

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cggatcccta gaacaccagc cagagtgaca ggaggcgtgt tcctcgtgga caagaaccct 1140

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aagcttcccg tgaacagacc catcgactgg aaagtgtgcc agcggatcgt tggactgctg 1920

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atccagagca agcaggcctt caccttcagc cctacctaca aggccttcct gtgcaagcag 2040

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gctcctctgc ccatccacac agcccagctg ctggctgcct gcttcgccag aagcagatcc 2220

ggagccaagc tgatcggcac cgacaactcc gtggtgctga gccggaagta caccagcttc 2280

ccttggctgc tgggctgcgc tgccaactgg atcctgcgag gcaccagctt cgtgtacgtg 2340

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ctgcttagac tgcccttcag acccaccacc ggacggacca gcctgtacgc cgatagccct 2460

agcgtgccca gccatctgcc cgacagagtg cacttcgcca gccctctgca tgtggcctgg 2520

agacctcca 2529

<210> 4
<211> 843
<212> PRT
<213> Artificial Sequence

<220>
<223> HBV pol

<400> 4

Met Pro Leu Ser Tyr Gln His Phe Arg Lys 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 Glu Trp Gln Thr Pro Ser Phe Pro
65                  70                  75                  80

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

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys 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 Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
                165                 170                 175

Gln Glu Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Thr Arg His
            180                 185                 190

Gly Asp Glu Ser Phe Cys Gln Gln Ser Ser Gly Ile Leu Ser Arg Ser
        195                 200                 205

Pro Val Gly Pro Cys Leu Gln Ser Gln Leu Arg Lys Ser Arg Leu Gly
    210                 215                 220

Leu Gln Pro Gln Gln Gly His Leu Ala Arg Arg Gln Gln Gly Arg Ser
225                 230                 235                 240

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

Val Glu Pro Ser Gly Ser Gly His Thr Thr Asn Thr Ala Ser Ser Ser
            260                 265                 270
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Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Ala Ala Tyr Ser His
        275                 280                 285

Leu Ser Thr Ser Lys Arg His Ser Ser Ser Gly His Ala Val Glu Leu
    290                 295                 300

His Asn Ile Pro Pro Asn Ser Ala Arg Ser Gln Ser Glu Gly Pro Val
305                 310                 315                 320

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

Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys
            340                 345                 350

Thr Glu His Gly Glu His His Ile Arg Ile Pro Arg Thr Pro Ala Arg
        355                 360                 365

Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Thr
    370                 375                 380

Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Thr
385                 390                 395                 400

Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr
                405                 410                 415

Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala
            420                 425                 430

Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu
        435                 440                 445

Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn
    450                 455                 460

Ser Arg Ile Ile Asn His Gln His Gly Thr Met Gln Asn Leu His Asp
465                 470                 475                 480

Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Leu Leu Leu Tyr Lys Thr
                485                 490                 495
```

```
Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe
            500                 505                 510

Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln
        515                 520                 525

Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys
    530                 535                 540

Leu Ala Phe Ser Tyr Met Asn Asn Val Val Leu Gly Ala Lys Ser Val
545                 550                 555                 560

Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser
                565                 570                 575

Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser
            580                 585                 590

Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln
        595                 600                 605

Glu His Ile Val Gln Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro Val
    610                 615                 620

Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu
625                 630                 635                 640

Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro
                645                 650                 655

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

Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala
        675                 680                 685

Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asn Ala Thr Pro Thr
    690                 695                 700
```

```
Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg Gly Thr Phe Val
705                 710                 715                 720


Ala Pro Leu Pro Ile His Thr Ala Gln Leu Leu Ala Ala Cys Phe Ala
                725                 730                 735


Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val
            740                 745                 750


Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala
        755                 760                 765


Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu
    770                 775                 780


Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro
785                 790                 795                 800


Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr
                805                 810                 815


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


Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
        835                 840


<210>  5
<211>  63
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Cystatin S signal peptide

<400>  5
atggctcgac ctctgtgtac cctgctactc ctgatggcta ccctggctgg agctctggcc       60

agc                                                                     63


<210>  6
<211>  21
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> Cystatin S signal peptide

<400> 6

Met Ala Arg Pro Leu Cys Thr Leu Leu Leu Leu Met Ala Thr Leu Ala
1 5 10 15

Gly Ala Leu Ala Ser
20

<210> 7
<211> 684
<212> DNA
<213> Artificial Sequence

<220>
<223> hCMV promoter

<400> 7
accgccatgt tgacattgat tattgactag ttattaatag taatcaatta cggggtcatt 60

agttcatagc ccatatatgg agttccgcgt tacataactt acggtaaatg gcccgcctgg 120

ctgaccgccc aacgaccccc gcccattgac gtcaataatg acgtatgttc ccatagtaac 180

gccaataggg actttccatt gacgtcaatg ggtggagtat ttacggtaaa ctgcccactt 240

ggcagtacat caagtgtatc atatgccaag tacgcccccc attgacgtca atgacggtaa 300

atggcccgcc tggcattatg cccagtacat gaccttatgg gactttccta cttggcagta 360

catctacgta ttagtcatcg ctattaccat ggtgatgcgg ttttggcagt acatcaatgg 420

gcgtggatag cggtttgact cacggggatt tccaagtctc caccccattg acgtcaatgg 480

gagtttgttt tggcaccaaa atcaacggga ctttccaaaa tgtcgtaaca actccgcccc 540

attgacgcaa atgggcggta ggcgtgtacg gtgggaggtc tatataagca gagctcgttt 600

agtgaaccgt cagatcgcct ggagacgcca tccacgctgt tttgacctcc atagaagaca 660

ccgggaccga tccagcctcc gcgg 684

<210> 8
<211> 378
<212> DNA
<213> Artificial Sequence

<220>

<223> triple enhancer

<400> 8
ggctcgcatc tctccttcac gcgcccgccg ccctacctga ggccgccatc cacgccggtt 60

gagtcgcgtt ctgccgcctc ccgcctgtgg tgcctcctga actgcgtccg ccgtctaggt 120

aagtttaaag ctcaggtcga gaccgggcct ttgtccggcg ctcccttgga gcctacctag 180

actcagccgg ctctccacgc tttgcctgac cctgcttgct caactctagt tctctcgtta 240

acttaatgag acagatagaa actggtcttg tagaaacaga gtagtcgcct gcttttctgc 300

caggtgctga cttctctccc ctgggctttt ttctttttct caggttgaaa agaagaagac 360

gaagaagacg aagaagac 378

<210> 9
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> BGH poly A

<400> 9
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tggaaggtgc cactcccact gtcctttcct aataaaatga ggaaattgca tcgcattgtc 120

tgagtaggtg tcattctatt ctgggggggtg gggtggggca ggacagcaag ggggaggatt 180

gggaagacaa tagcaggcat gctggggatg cggtgggctc tatgg 225

<210> 10
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Immunoglobulin secretion signal

<400> 10
atggagttcg gcctgtcttg ggtctttctg gtggcaatcc tgaagggcgt gcagtgtgaa 60

gtgcagctgc tggagtctgg a 81

<210> 11
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Immunoglobulin secretion signal

<400> 11

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

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly
            20   25

<210> 12
<211> 996
<212> PRT
<213> Artificial Sequence

<220>
<223> Core-Pol fusion

<400> 12

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

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

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

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

Glu Thr Val Leu 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 Ala Gly Ala Gly Met Pro Leu Ser Tyr Gln His
145                 150                 155                 160

Phe Arg Lys Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu
                165                 170                 175

Glu Leu Pro Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu
            180                 185                 190

Asp Leu Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys
        195                 200                 205

Val Gly Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn
    210                 215                 220

Pro Glu Trp Gln Thr Pro Ser Phe Pro Asn Ile His Leu Gln Glu Asp
225                 230                 235                 240

Ile Ile Asn Arg Cys Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu
                245                 250                 255

Lys Arg Arg Leu Lys Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val
            260                 265                 270

Thr Lys Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu
        275                 280                 285

His Leu Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu
    290                 295                 300

Trp Lys Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr Arg Ser Ala Ser
305                 310                 315                 320

Phe Cys Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu Gln His Gly Arg
                325                 330                 335
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Leu Val Phe Gln Thr Ser Thr Arg His Gly Asp Glu Ser Phe Cys Gln
            340                 345                 350

Gln Ser Ser Gly Ile Leu Ser Arg Ser Pro Val Gly Pro Cys Leu Gln
        355                 360                 365

Ser Gln Leu Arg Lys Ser Arg Leu Gly Leu Gln Pro Gln Gln Gly His
    370                 375                 380

Leu Ala Arg Arg Gln Gln Gly Arg Ser Gly Ser Ile Arg Ala Arg Val
385                 390                 395                 400

His Pro Thr Thr Arg Arg Pro Phe Gly Val Glu Pro Ser Gly Ser Gly
                405                 410                 415

His Thr Thr Asn Thr Ala Ser Ser Ser Ser Ser Cys Leu His Gln Ser
            420                 425                 430

Ala Val Arg Lys Ala Ala Tyr Ser His Leu Ser Thr Ser Lys Arg His
        435                 440                 445

Ser Ser Ser Gly His Ala Val Glu Leu His Asn Ile Pro Pro Asn Ser
    450                 455                 460

Ala Arg Ser Gln Ser Glu Gly Pro Val Phe Ser Cys Trp Trp Leu Gln
465                 470                 475                 480

Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val
                485                 490                 495

Asn Leu Leu Glu Asp Trp Gly Pro Cys Thr Glu His Gly Glu His His
            500                 505                 510

Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu
        515                 520                 525

Val Asp Lys Asn Pro His Asn Thr Thr Glu Ser Arg Leu Val Val Asp
    530                 535                 540

Phe Ser Gln Phe Ser Arg Gly Asn Thr Arg Val Ser Trp Pro Lys Phe
545                 550                 555                 560
```

```
Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu
                565                 570                 575

Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu
            580                 585                 590

His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser
        595                 600                 605

Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Ile Asn His Gln
    610                 615                 620

His Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr
625                 630                 635                 640

Val Ser Leu Leu Leu Leu Tyr Lys Thr Phe Gly Arg Lys Leu His Leu
                645                 650                 655

Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val
            660                 665                 670

Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser
        675                 680                 685

Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met Asn
    690                 695                 700

Asn Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe
705                 710                 715                 720

Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro
                725                 730                 735

Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val
            740                 745                 750

Ile Gly Ser Trp Gly Thr Leu Pro Gln Glu His Ile Val Gln Lys Ile
        755                 760                 765
```

```
Lys Glu Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys
    770                 775                 780

Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr
785                 790                 795                 800

Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser
                805                 810                 815

Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys
            820                 825                 830

Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys
        835                 840                 845

Gln Val Phe Ala Asn Ala Thr Pro Thr Gly Trp Gly Leu Ala Ile Gly
    850                 855                 860

His Gln Arg Met Arg Gly Thr Phe Val Ala Pro Leu Pro Ile His Thr
865                 870                 875                 880

Ala Gln Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Lys
                885                 890                 895

Leu Ile Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser
            900                 905                 910

Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr
        915                 920                 925

Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser
    930                 935                 940

Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro Phe Arg
945                 950                 955                 960

Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro
                965                 970                 975

Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu His Val Ala
            980                 985                 990
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Trp Arg Pro Pro
995

<210> 13
<211> 1023
<212> PRT
<213> Artificial Sequence

<220>
<223> Core-Pol fusion

<400> 13

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

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Met Asp Ile Asp Pro
20 25 30

Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu Ser Phe Leu Pro Ser
35 40 45

Asp Phe Phe Pro Ser Ile Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu
50 55 60

Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr
65 70 75 80

Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Asn Leu Ala
85 90 95

Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala Ser Arg Glu Leu Val
100 105 110

Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys Ile Arg Gln Leu Leu
115 120 125

Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu Glu
130 135 140

Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg
145 150 155 160

```
Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val
               165                 170                 175

Ala Gly Ala Gly Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu
            180                 185                 190

Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu
        195                 200                 205

Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly
    210                 215                 220

Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr
225                 230                 235                 240

Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Thr
               245                 250                 255

Pro Ser Phe Pro Asn Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys
            260                 265                 270

Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys
        275                 280                 285

Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro
    290                 295                 300

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

Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile
               325                 330                 335

Leu Tyr Lys Arg Glu Thr Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro
            340                 345                 350

Tyr Ser Trp Glu Gln Glu Leu Gln His Gly Arg Leu Val Phe Gln Thr
        355                 360                 365
```

```
Ser Thr Arg His Gly Asp Glu Ser Phe Cys Gln Gln Ser Ser Gly Ile
    370                 375                 380

Leu Ser Arg Ser Pro Val Gly Pro Cys Leu Gln Ser Gln Leu Arg Lys
385                 390                 395                 400

Ser Arg Leu Gly Leu Gln Pro Gln Gln Gly His Leu Ala Arg Arg Gln
                405                 410                 415

Gln Gly Arg Ser Gly Ser Ile Arg Ala Arg Val His Pro Thr Thr Arg
            420                 425                 430

Arg Pro Phe Gly Val Glu Pro Ser Gly Ser Gly His Thr Thr Asn Thr
        435                 440                 445

Ala Ser Ser Ser Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Ala
    450                 455                 460

Ala Tyr Ser His Leu Ser Thr Ser Lys Arg His Ser Ser Ser Gly His
465                 470                 475                 480

Ala Val Glu Leu His Asn Ile Pro Pro Asn Ser Ala Arg Ser Gln Ser
                485                 490                 495

Glu Gly Pro Val Phe Ser Cys Trp Trp Leu Gln Phe Arg Asn Ser Lys
            500                 505                 510

Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu Asp
        515                 520                 525

Trp Gly Pro Cys Thr Glu His Gly Glu His His Ile Arg Ile Pro Arg
    530                 535                 540

Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro
545                 550                 555                 560

His Asn Thr Thr Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser
                565                 570                 575

Arg Gly Asn Thr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu
            580                 585                 590
```

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Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu
        595                 600                 605

Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met
    610                 615                 620

Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg
625                 630                 635                 640

Leu Ser Ser Asn Ser Arg Ile Ile Asn His Gln His Gly Thr Met Gln
                645                 650                 655

Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Leu Leu
            660                 665                 670

Leu Tyr Lys Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile
        675                 680                 685

Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe
    690                 695                 700

Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala
705                 710                 715                 720

Phe Pro His Cys Leu Ala Phe Ser Tyr Met Asn Asn Val Val Leu Gly
                725                 730                 735

Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn
            740                 745                 750

Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg
        755                 760                 765

Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly
    770                 775                 780

Thr Leu Pro Gln Glu His Ile Val Gln Lys Ile Lys Glu Cys Phe Arg
785                 790                 795                 800
```

```
Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile
                805                 810                 815

Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro
            820                 825                 830

Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr
        835                 840                 845

Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu
    850                 855                 860

Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asn
865                 870                 875                 880

Ala Thr Pro Thr Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg
                885                 890                 895

Gly Thr Phe Val Ala Pro Leu Pro Ile His Thr Ala Gln Leu Leu Ala
            900                 905                 910

Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp
        915                 920                 925

Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu
    930                 935                 940

Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val
945                 950                 955                 960

Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly
                965                 970                 975

Leu Tyr Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg
            980                 985                 990

Thr Ser Leu Tyr Ala Asp Ser Pro  Ser Val Pro Ser His  Leu Pro Asp
        995                 1000                1005

Arg Val  His Phe Ala Ser Pro  Leu His Val Ala Trp  Arg Pro Pro
    1010                1015                1020
```

<210> 14
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Linker coding sequence

<400> 14
gccggagctg gc 12

<210> 15
<211> 248
<212> DNA
<213> Artificial Sequence

<220>
<223> ApoA1 gene fragment

<400> 15
ttggccgtgc tcttcctgac gggtaggtgt cccctaacct agggagccaa ccatcggggg 60

gccttctccc taaatccccg tggcccaccc tcctgggcag aggcagcagg tttctcactg 120

gccccctctc ccccacctcc aagcttggcc tttcggctca gatctcagcc cacagctggc 180

ctgatctggg tctcccctcc caccctcagg gagccaggct cggcatttcg tcgacaagct 240

tagccacc 248

<210> 16
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<223> SV40 polyadenylation signal

<400> 16
aacttgttta ttgcagctta taatggttac aaataaagca atagcatcac aaatttcaca 60

aataaagcat ttttttcact gcattctagt tgtggtttgt ccaaactcat caatgtatct 120

tatcatgtct 130

<210> 17
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> HBV core

<400> 17
atggacatcg acccttacaa ggagttcggc gccagcgtgg aactgctgtc ttttctgccc 60

agtgatttct ttccttccat tcgagacctg ctggataccg cctctgctct gtatcgggaa 120

gccctggaga gcccagaaca ctgctcccca caccataccg ctctgcgaca ggcaatcctg 180

tgctgggggg agctgatgaa cctggccaca tgggtgggat ccaatctgga ggaccccgct 240

tcacgggaac tggtggtcag ctacgtgaac gtcaatatgg gcctgaaaat ccgccagctg 300

ctgtggttcc atattagctg cctgactttt ggacgagaga ccgtgctgga atacctggtg 360

tccttcggcg tctggatccg cactcccccc gcttatcgac cacccaacgc accaattctg 420

tccaccctgc ccgagaccac agtggtc 447

<210> 18
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> HBV core

<400> 18
atggacatcg acccttacaa ggagttcggc gccagcgtgg aactgctgtc ttttctgccc 60

agtgatttct ttccttccat tcgagacctg ctggataccg cctctgctct gtatcgggaa 120

gccctggaga gcccagaaca ctgctcccca caccataccg ctctgcgaca ggcaatcctg 180

tgctgggggg agctgatgaa cctggccaca tgggtgggat cgaatctgga ggaccccgct 240

tcacgggaac tggtggtcag ctacgtgaac gtcaatatgg gcctgaaaat ccgccagctg 300

ctgtggttcc atattagctg cctgactttt ggacgagaga ccgtgctgga atacctggtg 360

tccttcggcg tctggattcg cactcccccc gcttatcgac cacccaacgc accaattctg 420

tccaccctgc ccgagaccac agtggtc 447

<210> 19
<211> 2529
<212> DNA
<213> Artificial Sequence

<220>

<223> HBV pol

<400> 19

atgcccctgt cttaccagca ctttagaaag ctgctgctgc tggacgatga agccgggcct 60

ctggaggaag agctgccaag gctggcagac gaggggctga accggagagt ggccgaagat 120

ctgaatctgg gaaacctgaa cgtgagcatc ccttggactc ataaagtcgg caacttcacc 180

gggctgtaca gctccacagt gcctgtcttc aatccagagt ggcagacacc atcctttccc 240

aacattcacc tgcaggagga catcattaat agatgcgaac agttcgtggg acctctgaca 300

gtcaacgaaa agaggcgcct gaaactgatc atgcctgcca ggttttaccc aaatgtgact 360

aagtatctgc cactggataa gggcatcaag ccttactatc cagagcacct ggtgaaccat 420

tacttccaga ctagacacta tctgcatacc ctgtggaagg ccggaatcct gtacaaacga 480

gaaactaccc ggagtgcttc attttgtggc tccccatatt cttgggaaca ggagctgcag 540

catggcaggc tggtgttcca gaccagcaca cgccacgggg atgagtcctt ttgccagcag 600

tctagtggca tcctgagcag atcccccgtg gggccttgtc tgcagtctca gctgcggaag 660

agtagactgg gactgcagcc acagcaggga cacctggcac gacggcagca gggaaggtct 720

ggcagtatcc gggctagagt gcatcccaca actagaaggc ctttcggcgt cgagccatca 780

ggaagcggcc acaccacaaa caccgcatca agctcctcta gttgcctgca tcagtcagcc 840

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ggatcctggg ggaccctgcc acaggagcac atcgtgcaga agatcaagga atgctttcgg 1860

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gccactccta ccggctgggg gctggctatc ggacatcagc gaatgcgggg cacattcgtg 2160

gccccctgc ctattcacac tgctcagctg ctggcagcct gctttgctag atctaggagt 2220

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ctgctgagac tgcccttcag gcctacaact ggccggacat ctctgtatgc cgattcacca 2460

agcgtgccct cacacctgcc tgacagagtc cactttgctt cacccctgca cgtcgcttgg 2520

cggcctcca 2529

<210> 20
<211> 2529
<212> DNA
<213> Artificial Sequence

<220>
<223> HBV pol

<400> 20
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ctggaggaag agctgccaag gctggcagac gaggggctga accggagagt ggccgaagat 120

ctgaatctgg gaaacctgaa cgtgagcatc ccttggactc ataaagtcgg caacttcacc 180

gggctgtaca gctccacagt gcctgtcttc aatccagagt ggcagacacc atcctttccc 240

aacattcacc tgcaggagga catcattaat agatgcgaac agttcgtggg acctctgaca 300

gtcaacgaaa agaggcgcct gaaactgatc atgcctgcca ggttttaccc aaatgtgact 360

aagtatctgc cactggataa gggcatcaag ccttactatc cagagcacct ggtgaaccat 420

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gaaactaccc ggagtgcttc attttgtggc tccccatatt cttgggaaca ggagctgcag 540

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agtagactgg gactgcagcc acagcaggga cacctggcac gacggcagca gggaaggtct 720

ggcagtatcc gggctagagt gcatcccaca actagaaggc ctttcggcgt cgagccatca 780

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aggattccac gaacaccagc acgagtgact ggaggggtgt tcctggtgga caagaacccc 1140

cacaatacta ccgagagccg gctggtggtc gatttcagtc agttttcaag aggcaacaca 1200

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agtaatctga gctggctgtc cctggacgtg tccgcagcct tttaccacct gcctctgcat 1320

ccagctgcaa tgccccatct gctggtgggg tcaagcggac tgagtcgcta cgtcgcccga 1380

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ctgaacccaa ataagactaa acgctggggg tacagcctga atttcatggg atatgtgatt 1800

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aagctgcccg tcaacagacc tatcgactgg aaagtgtgcc agcggattgt cggactgctg 1920

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atccagtcta agcaggcttt cacctttagt cctacataca aggcattcct gtgcaaacag 2040

tacctgaacc tgtatccagt ggcaaggcag cgacctggac tgtgccaggt ctttgcaaat 2100

gccactccta ccggctgggg gctggctatc ggacatcagc gaatgcgggg cacattcgtg 2160

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ctgctgagac tgcccttcag gcctacaact ggccggacat ctctgtatgc cgattcacca 2460

agcgtgccct cacacctgcc tgacagagtc cactttgctt cacccctgca cgtcgcttgg 2520

cggcctcca 2529

<210> 21
<211> 671
<212> DNA
<213> Artificial Sequence

<220>
<223> pUC Ori

<400> 21
cccgtagaaa agatcaaagg atcttcttga gatccttttt ttctgcgcgt aatctgctgc 60

ttgcaaacaa aaaaaccgct accagcggtg gtttgtttgc cggatcaaga gctaccaact 120

ctttttccga aggtaactgg cttcagcaga gcgcagatac caaatactgt tcttctagtg 180

tagccgtagt taggccacca cttcaagaac tctgtagcac cgcctacata cctcgctctg 240

ctaatcctgt taccagtggc tgctgccagt ggcgataagt cgtgtcttac cgggttggac 300

tcaagacgat agttaccgga taaggcgcag cggtcgggct gaacgggggg ttcgtgcaca 360

cagcccagct tggagcgaac gacctacacc gaactgagat acctacagcg tgagctatga 420

gaaagcgcca cgcttcccga agggagaaag gcggacaggt atccggtaag cggcagggtc 480

ggaacaggag agcgcacgag ggagcttcca gggggaaacg cctggtatct ttatagtcct 540

gtcgggtttc gccacctctg acttgagcgt cgatttttgt gatgctcgtc agggggggcgg 600

agcctatgga aaaacgccag caacgcggcc tttttacggt tcctggcctt ttgctggcct 660

tttgctcaca t 671

<210> 22
<211> 795
<212> DNA
<213> Artificial Sequence

<220>
<223> Kan resistance

<400> 22
atgattgagc aagatggtct tcacgctggc tcgccagctg cgtgggtgga acgcctgttt 60

ggttatgatt gggcgcagca gactattgga tgttccgacg cggctgtatt tcggctgtct 120

gctcagggtc gccccgtgct gtttgtgaag acggatttgt ctggcgcatt aaatgagtta 180

caggacgagg cggctcgtct gagttggttg gccaccaccg gcgtgccctg cgccgcagtg 240

ctggatgtcg tgacagaagc aggccgcgat tggctccttc tcggcgaagt gccgggccag 300

gacctgctca gcagccactt ggcaccggca gaaaaagttt ctatcatggc cgacgccatg 360

cgtcgtcttc acactctcga tccggccacg tgccccttg accaccaggc caagcatcgt 420

attgaacgtg cgcgtactcg gatggaagca ggtttagtag accaggacga tttggatgag 480

gaacatcaag gcctggcccc ggctgaactg tttgcgcgct taaaagcgtc gatgccagat 540

ggcgaagatt tggtagtcac ccatggagat gcgtgtttgc caaacatcat ggttgaaaat 600

ggccgcttct caggctttat tgactgtggg cgcctgggtg ttgccgaccg ctatcaagat 660

attgcgctcg caactcgtga catcgctgaa gagctgggcg gagaatgggc tgaccgtttc 720

ctggtactgt atggcattgc agcgcccgat tcccaacgca tcgcatttta tcgtctgctg 780

gatgagtttt tctaa 795

<210> 23
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Kan resistance

<400> 23

Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1 5 10 15

```
Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
            20                  25                  30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
        35                  40                  45

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
    50                  55                  60

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65                  70                  75                  80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
                85                  90                  95

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

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
        115                 120                 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
    130                 135                 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145                 150                 155                 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
                165                 170                 175

Ser Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
            180                 185                 190

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

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
    210                 215                 220
```

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225 230 235 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
245 250 255

Tyr Arg Leu Leu Asp Glu Phe Phe
260

<210> 24
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> bla promoter

<400> 24
acccctattt gtttattttt ctaaatacat tcaaatatgt atccgctcat gagacaataa 60

ccctgataaa tgcttcaata tattgaaaa aggaagagt 99

<210> 25
<211> 124
<212> DNA
<213> Artificial Sequence

<220>
<223> PrMVA13.5 Long Promoter

<400> 25
taaaaataga aactataatc atataatagt gtaggttggt agtattgctc ttgtgactag 60

agactttagt taaggtactg taaaaataga aactataatc atataatagt gtaggttggt 120

agta 124

<210> 26
<211> 227
<212> DNA
<213> Artificial Sequence

<220>
<223> PrHyb Promoter

<400> 26
gttttgaaaa ttttttata ataaatatcc ggtaaaaatt gaaaaactat tctaatttat 60

tgcacggtcc ggtaaaaatt gaaaaactat tctaatttat tgcacggtcc ggtaaaaatt 120

gaaaaactat tctaatttat tgcacggtcc ggtaaaaatt gaaaaactat tctaatttat 180

tgcacggtcc ggtaaaaatt gaaaaactat tctaatttat tgcacgg 227

<210> 27
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Immunoglobulin Secretion Tag

<400> 27
atggaattcg gcctgagctg ggtgttcctg gtggccatcc tgaagggagt gcagtgcgag 60

gtgcagctgc tggaaagcgg t 81

<210> 28
<211> 7
<212> DNA
<213> Artificial Sequence

<220>
<223> Transcription Termination Sequence

<220>
<221> n
<222> (6)..(6)
<223> n, wherein n can be any nucleotide

<400> 28
tttttnt 7