

SEQUENCE LISTING

<110> JANSSSEN SCIENCES IRELAND UNLIMITED COMPANY
 ICHOR MEDICAL SYSTEMS, INC.

<120> METHODS AND APPARATUS FOR THE DELIVERY OF HEPATITIS B VIRUS (HBV)
 VACCINES

<130> 688097-405W01

<150> PCT/US2017/067269

<151> 2017-12-19

<150> US 62/607,430

<151> 2017-12-19

<160> 24

<170> PatentIn version 3.5

<210> 1

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> HBV truncated core antigen gene

<400> 1

gacatcgacc cttacaagga gttcggcgcc agcgtggaac tgctgtcttt tctgcccagt	60
gatttctttc cttccattcg agacctgctg gataccgcct ctgctctgta tcgggaagcc	120
ctggagagcc cagaacactg ctccccacac cataccgctc tgcgacaggc aatcctgtgc	180
tgggggggagc tgatgaacct ggccacatgg gtgggatcga atctggagga ccccgcttca	240
cgggaactgg tggtcagcta cgtgaacgctc aatatgggcc tgaaaatccg ccagctgctg	300
tggttccata ttagctgcct gacttttgga cgagagaccg tgctggaata cctggtgtcc	360
ttcggcgtct ggattcgac tccccctgct tatcgaccac ccaacgcacc aattctgtcc	420
accctgcccc agaccacagt ggtc	444

<210> 2

<211> 148

<212> PRT

<213> Artificial Sequence

<220>

<223> HBV truncated core antigen

<400> 2

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

Phe Leu Pro Ser Asp Phe Phe Pro Ser Ile Arg Asp Leu Leu Asp Thr
20 25 30

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

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

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

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

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

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

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

Thr Thr Val Val
145

<210> 3

<211> 2529

<212> DNA

<213> Artificial Sequence

<220>

<223> HBV pol antigen gene

<400> 3

atgcccctgt cttaccagca ctttagaaag cttctgctgc 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 ctttactatc cagagcacct ggtgaaccat	420
tacttccaga ctagacacta tctgcatacc ctgtggaagg ccggaatcct gtacaaacga	480
gaaactaccc ggagtgcctc attttgtggc tccccatatt cttgggaaca ggagctgcag	540
catggcaggc tgggtgtcca gaccagcaca cgccacgggg atgagtcctt ttgccagcag	600
tctagtggca tcctgagcag atccccctg gggccttgct tgcagtctca gctgcggaag	660
agtagactgg gactgcagcc acagcaggga cacctggcac gacggcagca gggaaggctct	720
ggcagtatcc gggctagagt gcatcccaca actagaaggc ctttcggcgt cgagccatca	780
ggaagcggcc acaccacaaa caccgcatca agctcctcta gttgcctgca tcagtcagcc	840
gtgagaaagg ccgcttacag ccacctgtcc acatctaaaa ggcactcaag ctccgggcat	900
gctgtggagc tgcacaacat ccctccaaat tctgcacgca gtcagtcaga aggacccgtg	960
ttcagctgct ggtggctgca gtttcggaac tcaaagcctt gcagcgacta ttgtctgagc	1020
catattgtga atctgctgga ggattggggc cttgtaccg agcacgggga acaccatatc	1080
aggattccac gaacaccagc acgagtgact ggaggggtgt tcctgggtgga caagaacccc	1140
cacaatacta ccgagagccg gctggtggtc gatttcagtc agttttcaag aggcaacaca	1200
agggtgtcat ggcccaaatt cgccgtccct aatctgcaga gtctgactaa cctgctgtct	1260
agtaatctga gctggctgtc cctggacgtg tccgcagcct tttaccacct gcctctgcat	1320
ccagctgcaa tgccccatct gctggtgggg tcaagcggac tgagtcgcta cgtcgcccga	1380

ctgtcctcta actcacgcat cattaatcac cagcatggca ccatgcagaa cctgcacgat	1440
agctgttccc ggaatctgta cgtgtctctg ctgctgctgt ataagacatt cggcagaaaa	1500
ctgcacctgt acagccatcc tatcattctg gggtttagga agatcccaat gggagtggga	1560
ctgagccccct tcctgctggc acagtttacc tccgccattt gctctgtggt ccgccgagcc	1620
ttcccacact gtctggcttt ttcctatatg aacaatgtgg tcctgggcgc caaatccgtg	1680
cagcatctgg agtctctgtt cacagctgtc actaactttc tgctgagcct ggggatccac	1740
ctgaacccaa ataagactaa acgctggggg tacagcctga atttcatggg atatgtgatt	1800
ggatcctggg ggaccctgcc acaggagcac atcgtgcaga agatcaagga atgctttcgg	1860
aagctgcccc tcaacagacc tatcgactgg aaagtgtgcc agcggattgt cggactgctg	1920
ggcttcgccc ctccctttac ccagtgcggg taccagcac tgatgcccct gtatgcctgt	1980
atccagtcta agcaggcttt cacctttagt cctacataca aggcattcct gtgcaaacag	2040
tacctgaacc tgtatccagt ggcaaggcag cgacctggac tgtgccaggt ctttgcaaat	2100
gccactccta cgggctgggg gctggctatc ggacatcagc gaatgcgggg cacattcgtg	2160
gccccctgc ctattcacac tgctcagctg ctggcagcct gctttgctag atctaggagt	2220
ggagcaaagc tgatcggcac cgacaatagt gtggtcctgt caagaaaata cacatccttc	2280
ccatggctgc tgggatgtgc tgcaaactgg attctgaggg gcaccagctt cgtgtacgtc	2340
ccctcagccc tgaatcctgc tgacgatcca tcccgcgggc gactgggact gtaccgacct	2400
ctgctgagac tgcccttcag gcctacaact ggccggacat ctctgtatgc cgattcacca	2460
agcgtgccct cacacctgcc tgacagagtc cactttgctt caccctgca cgtcgcttgg	2520
cggcctcca	2529

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

 <220>
 <223> HBV pol antigen

<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

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 coding sequence

<400> 5
atggctcgac ctctgtgtac cctgctactc ctgatggcta ccctggctgg agctctggcc 60
agc 63

<210> 6
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Cystatin S signal peptide sequence

<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> 586
<212> DNA
<213> Artificial Sequence

<220>

<223> hCMV promoter sequence

<400> 7

tgacattgat tattgactag ttattaatag taatcaatta cggggtcatt agttcatagc	60
ccatatatgg agttccgcgt tacataactt acggtaaatag gcccgcctgg ctgaccgccc	120
aacgaccccc gcccatgac gtcaataatg acgtatgttc ccatagtaac gccaataggg	180
actttccatt gacgtcaatg ggtggactat ttacggtaaa ctgcccactt ggcagtacat	240
caagtgtatc atatgccaag tacgccccct attgacgtca atgacggtaa atggcccgcc	300
tggcattatg cccagtacat gaccttatgg gactttccta cttggcagta catctacgta	360
ttagtcatcg ctattaccat ggtgatgcgg ttttggcagt acatcaatgg gcgtggatag	420
cggtttgact cacgggggatt tccaagtctc caccgccattg acgtcaatgg gagtttgttt	480
tggcaccaaa atcaacggga ctttccaaaa tgtcgtaca actccgcccc attgacgcaa	540
atgggcggtg ggcgtgtacg gtgggaggtc tatataagca gagctc	586

<210> 8

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> triple enhancer regulatory sequence

<400> 8

ggctcgcac tctccttcac gcgcccgcg ccctacctga ggccgccac caccgagggt	60
gagtcgcgt ctgccgctc ccgcctgtgg tgcctcctga actgcgtccg ccgtctaggt	120
aagtttaaag ctcaggctga gaccgggcct ttgtccggcg ctcccttgga gcctacctag	180
actcagccgg ctctccacgc tttgcctgac cctgcttgct caactctagt tctctcgta	240
acttaatgag acagatagaa actggtcttg tagaaacaga gtagtcgcct gcttttctgc	300
cagggtgctga cttctctccc ctgggctttt ttctttttct caggttgaaa agaagaagac	360
gaagaagacg aagaagac	378

<210> 9
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Bla promoter sequence

<400> 9
accctatatt gtttatTTTT ctaaatacat tcaaatatgt atccgctcat gagacaataa 60
ccctgataaa tgcttcaata atattgaaaa aggaagagt 99

<210> 10
<211> 671
<212> DNA
<213> Artificial Sequence

<220>
<223> pUC ori sequence

<400> 10
cccgtagaaa agatcaaagg atcttcttga gatcctTTTT ttctgcgcgt aatctgctgc 60
ttgcaaacaa aaaaaccgct accagcgggtg gtttgtttgc cggatcaaga gctaccaact 120
ctttttccga aggtaactgg cttcagcaga gcgcagatac caaatactgt tcttctagt 180
tagccgtagt taggccacca cttcaagaac tctgtagcac cgcctacata cctcgctctg 240
ctaatcctgt taccagtggc tgctgccagt ggcgataagt cgtgtcttac cgggttggac 300
tcaagacgat agttaccgga taaggcgcag cggtcgggct gaacggggggg ttcgtgcaca 360
cagcccagct tggagcgaac gacctacacc gaactgagat acctacagcg tgagctatga 420
gaaagcgcca cgcttcccga agggagaaaag gcggacaggt atccggtaag cggcagggtc 480
ggaacaggag agcgcacgag ggagcttcca gggggaaacg cctggatatct ttatagtcct 540
gtcgggtttc gccacctctg acttgagcgt cgatttttgt gatgctcgtc aggggggscgg 600
agcctatgga aaaacgccag caacgcggcc tttttacggt tcctggcctt ttgctggcct 660
tttgctcaca t 671

<210> 11
<211> 225

<212> DNA
<213> Artificial Sequence

<220>
<223> bGH polyadenylation signal sequence

<400> 11
ctgtgccttc tagttgccag ccatctgttg tttgcccctc ccccgtcct tccttgaccc 60
tggaagggtgc cactcccact gtcctttcct aataaaatga ggaaattgca tcgcattgtc 120
tgagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag ggggaggatt 180
gggaagacaa tagcaggcat gctggggatg cggtgggctc tatgg 225

<210> 12
<211> 795
<212> DNA
<213> Artificial Sequence

<220>
<223> Kan R gene

<400> 12
atgattgagc aagatgggtct 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
cgctgtcttc acactctcga tccggccacg tgcccccttg 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 cgcttgggtg ttgccgaccg ctatcaagat 660
attgcgctcg caactcgtga catcgctgaa gagctgggcg gagaatgggc tgaccgtttc 720
ctggtactgt atggcattgc agcggccgat tcccaacgca tcgcatttta tcgtctgctg 780

gatgagtttt tctaa

795

<210> 13
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Kan R protein

<400> 13

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> 14

<211> 149

<212> PRT

<213> Artificial Sequence

<220>

<223> HBV truncated core antigen

<400> 14

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> 15
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> HBV truncated core antigen gene

<400> 15
atggacatcg acccttaca ggagttcggc gccagcgtgg aactgctgtc ttttctgccc 60
agtgatttct ttccttccat tcgagacctg ctggataccg cctctgctct gtatcgggaa 120
gccctggaga gcccagaaca ctgctcccca caccataccg ctctgcgaca ggcaatcctg 180
tgctggggggg agctgatgaa cctggccaca tgggtgggat ccaatctgga ggaccccgct 240
tcacgggaac tgggtggtcag ctacgtgaac gtcaatatgg gcctgaaaat ccgccagctg 300

ctgtggttcc atattagctg cctgactttt ggacgagaga ccgtgctgga atacctggtg	360
tccttcggcg tctggatccg cactccccct gcttatcgac caccacacgc accaattctg	420
tccaccctgc ccgagaccac agtggtc	447

<210> 16
 <211> 2529
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HBV pol antigen gene

<400> 16	
atgccccctgt cttaccagca ctttagaaaag ctgctgctgc tggacgatga agccgggcct	60
ctggaggaag agctgccaag gctggcagac gaggggctga accggagagt ggccgaagat	120
ctgaatctgg gaaacctgaa cgtgagcatc ccttggactc ataaagtcgg caacttcacc	180
gggctgtaca gctccacagt gcctgtcttc aatccagagt ggacagacacc atcctttccc	240
aacattcacc tgcaggagga catcattaat agatgcgaac agttcgtggg acctctgaca	300
gtcaacgaaa agaggcgcct gaaactgatc atgcctgccg gggttttacc aaatgtgact	360
aagtatctgc cactggataa gggcatcaag ccttactatc cagagcacct ggtgaaccat	420
tacttccaga ctagacacta tctgcatacc ctgtggaagg ccggaatcct gtacaaacga	480
gaaactaccc ggagtgcctt attttgtggc tccccatatt cttgggaaca ggagctgcag	540
catggcaggc tgggtgtcca gaccagcaca cgccacgggg atgagtcctt ttgccagcag	600
tctagtggca tcctgagcag atccccctg gggccttgct tgcagtctca gctgcggaag	660
agtagactgg gactgcagcc acagcaggga cacctggcac gacggcagca gggaaggtct	720
ggcagtatcc gggctagagt gcatcccaca actagaaggc ctttcggcgt cgagccatca	780
ggaagcggcc acaccacaaa caccgcatca agctcctcta gttgcctgca tcagtcagcc	840
gtgagaaaagg ccgcttacag ccacctgtcc acatctaaaa ggcaactcaag ctccgggcat	900
gctgtggagc tgcacaacat ccctccaaat tctgcacgca gtcagtcaga aggacccgtg	960
ttcagctgct ggtggctgca gtttcggaac tcaaagcctt gcagcgacta ttgtctgagc	1020

catattgtga atctgctgga ggattggggc cttgtaccg agcacgggga acaccatatc	1080
aggattccac gaacaccagc acgagtgact ggaggggtgt tcctggtgga caagaacccc	1140
cacaatacta ccgagagccg gctggtgggc gatttcagtc agttttcaag aggcaacaca	1200
agggtgtcat ggcccaaatt cgccgtccct aatctgcaga gtctgactaa cctgctgtct	1260
agtaatctga gctggctgtc cctggacgtg tccgcagcct ttaccacct gcctctgcat	1320
ccagctgcaa tgcccatct gctgggtggg tcaagcggac tgagtcgcta cgtcgcccga	1380
ctgtcctcta actcacgcat cattaatcac cagcatggca ccatgcagaa cctgcacgat	1440
agctgttccc ggaatctgta cgtgtctctg ctgctgctgt ataagacatt cggcagaaaa	1500
ctgcacctgt acagccatcc tatcattctg gggttagga agatcccaat gggagtggga	1560
ctgagcccct tcctgctggc acagtttacc tccgccattt gctctgtggt ccgccgagcc	1620
ttcccacact gtctggcttt ttcctatatg aacaatgtgg tcctgggcgc caaatccgtg	1680
cagcatctgg agtctctgtt cacagctgtc actaactttc tgctgagcct ggggatccac	1740
ctgaacccaa ataagactaa acgctggggg tacagcctga atttcatggg atatgtgatt	1800
ggatcctggg ggaccctgcc acaggagcac atcgtgcaga agatcaagga atgctttcgg	1860
aagctgcccg tcaacagacc tatcgactgg aaagtgtgcc agcggattgt cggactgtg	1920
ggcttcgccg ctccctttac ccagtgcggg taccagcac tgatgcccct gtatgcctgt	1980
atccagtcta agcaggcttt cacctttagt cctacataca aggcattcct gtgcaaacag	2040
tacctgaacc tgtatccagt ggcaaggcag cgacctggac tgtgccaggt ctttgcaaat	2100
gccactccta ccggctgggg gctggctatc ggacatcagc gaatgcgggg cacattcgtg	2160
gccccctgc ctattcacac tgctcagctg ctggcagcct gctttgctag atctaggagt	2220
ggagcaaagc tgatcggcac cgacaatagt gtggtcctgt caagaaaata cacatccttc	2280
ccatggctgc tgggatgtgc tgcaaactgg attctgaggg gcaccagctt cgtgtacgtc	2340
ccctcagccc tgaatcctgc tgacgatcca tcccgcgggc gactgggact gtaccgacct	2400
ctgctgagac tgcccttcag gcctacaact ggccggacat ctctgtatgc cgattcacca	2460
agcgtgccct cacacctgcc tgacagagtc cactttgctt caccctgca cgtcgcttgg	2520

cggcctcca

2529

<210> 17

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> hCMV promoter sequence

<400> 17

accgccatgt tgacattgat tattgactag ttattaatag taatcaatta cggggtcatt 60

agttcatagc ccatatatgg agttccgcgt tacataactt acggtaaata gcccgcctgg 120

ctgaccgccc aacgaccccc gcccatcgac gtcaataatg acgtatgttc ccatagtaac 180

gccaataggg actttccatt gacgtcaatg ggtggagtat ttacggtaaa ctgcccactt 240

ggcagtacat caagtgtatc atatgccaag tacgccccct attgacgtca atgacggtaa 300

atggccccgcc tggcattatg cccagtacat gaccttatgg gactttccta cttggcagta 360

catctacgta ttagtcatcg ctattaccat ggtgatgcgg ttttggcagt acatcaatgg 420

gcgtggatag cggtttgact cacgggggatt tccaagtctc caccaccattg acgtcaatgg 480

gagtttgttt tggcaccaaa atcaacggga ctttcacaaa tgcgtaaca actccgcccc 540

attgacgcaa atgggacgga ggcgtgtacg gtgggagggtc tatataagca gagctcgttt 600

agtgaaccgt cagatcgctt ggagacgcca tccacgctgt tttgacctcc atagaagaca 660

ccgggaccga tccagcctcc gcgg 684

<210> 18

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> immunoglobulin secretion signal coding sequence

<400> 18

atggagttcg gcctgtcttg ggtctttctg gtggcaatcc tgaaggcggt gcagtgtgaa 60

gtgcagctgc tggagtcttg a 81

<210> 19
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> immunoglobulin secretion signal sequence

<400> 19

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> 20
<211> 996
<212> PRT
<213> Artificial Sequence

<220>
<223> HBV core-pol fusion antigen sequence

<400> 20

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

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

Trp Arg Pro Pro
995

<210> 21

<211> 1023

<212> PRT

<213> Artificial Sequence

<220>

<223> HBV core-pol fusion antigen sequence with Ig signal sequence

<400> 21

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

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> 22

<211> 12

<212> DNA
<213> Artificial Sequence

<220>
<223> linker coding sequence

<400> 22
gccggagctg gc 12

<210> 23
<211> 248
<212> DNA
<213> Artificial Sequence

<220>
<223> ApoAI gene fragment

<400> 23
ttggccgtgc tcttcctgac gggtaggtgt cccctaacct agggagccaa ccatcggggg 60
gccttctccc taaatccccg tggcccaccc tcctgggcag aggcagcagg tttctcactg 120
gccccctctc cccacactcc aagcttggcc tttcggctca gatctcagcc cacagctggc 180
ctgatctggg tctcccctcc caccctcagg gagccaggct cggcatttcg tcgacaagct 240
tagccacc 248

<210> 24
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<223> SV40 polyadenylation signal sequence

<400> 24
aacttgttta ttgcagctta taatgggttac aaataaagca atagcatcac aaatttcaca 60
aataaagcat ttttttcact gcattctagt tgtggtttgt ccaaactcat caatgtatct 120
tatcatgtct 130