SEQUENCE LISTING

<110> APSE, LLC
Arhancet, Juan P. H.
Arhancet, Juan P.
Delaney, Kimberly
Hall, Kathleen B.
Summers, Neena
Oates, Edward

<120> Compositions and Methods Using Capsids Resistant to Hydrolases

<130> PCT APSE

<150> US 61/836,833
<151> 2013-06-19

<150> US 61/838,736
<151> 2013-06-24

<150> US 61/857,965
<151> 2013-07-24

<160> 20

<170> PatentIn version 3.5

<210> 1
<211> 3569
<212> RNA
<213> Bacteriophage MS2

<400> 1
gggugggacc ccuuucgggg uccugcucaa cuuccugucg agcuaaugcc auuuuuaaug 60

ucuuuagcga gacgcuacca uggcuaucgc uguagguagc cggaauucca uuccuaggag 120

guuugaccug ugcgagcuuu uaguacccuu gauagggaga acgagaccuu cguccccucc 180

guucgcguuu acgcggacgg ugagacugaa gauaacucau ucucuuuaaa auaucguucg 240

aacuggacuc ccggucguuu uaacucgacu ggggccaaaa cgaaacagug gcacuacccc 300

ucuccguauu cacggggggc guuaaguguc acaucgauag aucaaggugc cuacaagcga 360

agugggucau cgugggucg cccguacgag gagaaagccg guuucggcuu cucccucgac 420

gcacgcuccu gcuacagccu cuucccugua agccaaaacu ugacuuacau cgaagugccg 480

cagaacguug cgaaccgggc gucgaccgaa guccugcaaa aggucaccca ggguaauuuu 540

aaccuuggug uugcuuuagc agaggccagg ucgacagccu cacaacucgc gacgcaaacc 600

auugcgcucg ugaaggcgua cacugccgcu cgucgcggua auuggcgcca ggcgcuccgc 660

uaccuugccc uaaacgaaga ucgaaaguuu cgaucaaaac acguggccgg caggugguug 720

gaguugcagu ucgguugguu accacuaaug agugauaucc agggugcaua ugagaugcuu 780

acgaagguuc accuucaaga guuucuuccu augagagccg uacgucaggu cgguacuaac 840

aucaaguuag auggccgucu gucguaucca gcugcaaacu uccagacaac gugcaacaua 900

ucgcgacgua ucgugauaug guuuuacaua aacgaugcac guuuggcaug guugucgucu 960

cuagguaucu ugaacccacu agguauagug ugggaaaagg ugccuuucuc auucguuguc 1020

gacuggcucc uaccuguagg uaacaugcuc gagggccuua cggccccgu gggaugcucc 1080

uacaugucag gaacaguuac ugacguaaua acgggugagu ccaucauaag cguugacgcu 1140

cccuacgggu ggacugugga gagacagggc acugcuaagg cccaaaucuc agccaugcau 1200

cgagggguac aauccguaug gccaacaacu ggcgcguacg uaaagucucc uuucucgaug 1260

guccauaccu uagaugcguu agcauuaauc aggcaacggc ucucuagaua gagcccucaa 1320

ccggaguuug aagcauggcu ucuaacuuua cucaguucgu ucucgucgac aauggcggaa 1380

cuggcgacgu gacugucgcc ccaagcaacu ucgcuaacgg ggucgcugaa uggaucagcu 1440

cuaacucgcg uucacaggcu uacaaaguaa ccuguagcgu ucgucagagc ucugcgcaga 1500

aucgcaaaua caccaucaaa gucgaggugc cuaaaguggc aacccagacu guugguggug 1560

uagagcuucc uguagccgca uggcguucgu acuuaaauau ggaacuaacc auuccaauuu 1620

ucgcuacgaa uuccgacugc gagcuuauug uuaaggcaau gcaaggucuc cuaaaagaug 1680

gaaacccgau ucccucagca aucgcagcaa acuccggcau cuacuaauag acgccggcca 1740

uucaaacaug aggauuaccc augucgaaga caacaaagaa guucaacucu uuauguauug 1800

aucuuccucg cgaucuuucu cucgaaauuu accaaucaau ugcuucuguc gcuacuggaa 1860

gcggugaucc gcacagugac gacuuuacag caauugcuua cuuaagggac gaauugcuca 1920

caaagcaucc gaccuuaggu ucugguaaug acgaggcgac ccgucguacc uuagcuaucg 1980

cuaagcuacg ggaggcgaau ggugaucgcg gucagauaaa uagagaaggu uucuuacaug 2040

acaaauccuu gucaugggau ccggauguuu uacaaaccag cauccguagc cuuauuggca 2100

accuccucuc uggcuaccga ucgucguugu uugggcaaug cacguucucc aacggugcuc 2160

cuauggggca caaguugcag gaugcagcgc cuuacaagaa guucgcugaa caagcaaccg 2220

uuaccccccg cgcucugaga gcggcucuau ugguccgaga ccaaugugcg ccguggauca 2280

gacacgcggu ccgcuauaac gagucauaug aauuuaggcu cguuguaggg aacggagugu 2340

uuacaguucc gaagaauaau aaaauagauc gggcugccug uaaggagccu gauaugaaua 2400

uguaccucca gaaagggguc ggugcuuuca ucagacgccg gcucaaaucc guugguauag 2460

accugaauga ucaaucgauc aaccagcguc uggcucagca gggcagcgua gaugguucgc 2520

uugcgacgau agacuuaucg ucugcauccg auuccaucuc cgaucgccug guguggaguu 2580

uucucccacc agagcuauau ucauaucucg aucguauccg cucacacuac ggaaucguag 2640

auggcgagac gauacgaugg gaacuauuuu ccacaauggg aaauggguuc acauuugagc 2700

uagaguccau gauauucugg gcaauaguca aagcgaccca aauccauuuu gguaacgccg 2760

gaaccauagg caucuacggg gacgauauua uaugucccag ugagauugca ccccgugugc 2820

uagaggcacu ugccuacuac gguuuuaaac cgaaucuucg uaaaacguuc guguccgggc 2880

ucuuucgcga gagcugcggc gcgcacuuuu accguggugu cgaugucaaa ccguuuuaca 2940

ucaagaaacc uguugacaau cucuucgccc ugaugcugau auuaaaucgg cuacgggguu 3000

ggggaguugu cggagguaug ucagauccac gccucuauaa ggugugggua cggcucuccu 3060

cccaggugcc uucgauguuc uucgguggga cggaccucgc ugccgacuac uacguaguca 3120

gcccgccuac ggcagucucg guauacacca agacuccgua cgggcggcug cucgcggaua 3180

cccguaccuc ggguuuccgu cuugcucgua ucgcucgaga acgcaaguuc uucagcgaaa 3240

agcacgacag uggucgcuac auagcguggu uccauacugg aggugaaauc accgacagca 3300

ugaaguccgc cggcgugcgc guuauacgca cuucggagug gcuaacgccg guucccacau 3360

ucccucagga gugugggcca gcgagcucuc cucgguagcu gaccgaggga cccccguaaa 3420

cgggggugggu gugcucgaaa gagcacgggu gcgaaagcgg uccggcucca ccgaaaggug 3480

ggcgggcuuc ggcccaggga ccucccccua aagagaggac ccgggauucu cccgauuugg 3540

uaacuagcug cuuggcuagu uaccaccca 3569

<210> 2
<211> 398
<212> DNA
<213> Bacteriophage MS2

<400> 2
artcaatggc ttctaacttt actcagttcg ttctcgtcga caatggcgga actggcgacg 60

tgactgtcgc cccaagcaac ttcgctaacg gggtcgctga atggatcagc tctaactcgc 120

gttcacaggc ttacaaagta acctgtagcg ttcgtcagag ctctgcgcag aatcgcaaat 180

acaccatcaa agtcgaggtg cctaaagtgg caacccagac tgttggtggt gtagagcttc 240

ctgtagccgc atggcgttcg tacttaaata tggaactaac cattccaatt ttcgctacga 300

attccgactg cgagcttatt gttaaggcaa tgcaaggtct cctaaaagat ggaaacccga 360

ttccctcagc aatcgcagca aactccggca tctactaa 398

<210> 3
<211> 130
<212> PRT
<213> Bacteriophage MS2

<400> 3

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr
130

<210> 4
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Bacteriophage MS2 coat protein and pac sequence cloning cassette

<220>
<221> gene
<222> (42)..(435)

<220>
<221> stem_loop
<222> (454)..(472)

<400> 4
acaagtttgt acaaaaaagc aggctaagaa ggagatatac atatggcttc taactttact 60

cagttcgttc tcgtcgacaa tggcggaact ggcgacgtga ctgtcgcccc aagcaacttc 120

gctaacgggg tcgctgaatg gatcagctct aactcgcgtt cacaggctta caaagtaacc 180

tgtagcgttc gtcagagctc tgcgcagaat cgcaaataca ccatcaaagt cgaggtgcct 240

aaagtggcaa cccagactgt tggtggtgta gagcttcctg tagccgcatg gcgttcgtac 300

ttaaatatgg aactaaccat tccaattttc gctacgaatt ccgactgcga gcttattgtt 360

aaggcaatgc aaggtctcct aaaagatgga aacccgattc cctcagcaat cgcagcaaac 420

tccggcatct actaatagac gccggccatt caaacatgag gattacccat gtacccagct 480

<210> 5
<211> 165
<212> DNA
<213> Artificial Sequence

<220>
<223> T7-Rz2

<220>
<221> promoter
<222> (1)..(18)
<223> T7

<220>
<221> stem_loop
<222> (19)..(67)
<223> shRNA

<220>
<221> misc_RNA
<222> (68)..(130)
<223> HDV ribozyme

<220>
<221> misc_feature
<222> (131)..(140)
<223> AT spacer

<220>
<221> stem_loop
<222> (141)..(159)
<223> MS2 specific packing sequence

<220>
<221> misc_feature
<222> (160)..(165)
<223> NcoI restriction site

<400> 5
taatacgact cactataggc ttgtgatgct tcagccaaat caagagtttg gctgaagcat 60

cacaagcggc cggcatggtc ccagcctcct cgctggcgcc ggctgggcaa cattcgtggc 120

gaatgggacc atatatatat acatgaggat tacccatgtc catgg 165

<210> 6
<211> 221
<212> DNA
<213> Artificial Sequence

<220>
<223> T7-Rz3

<220>
<221> promoter
<222> (1)..(18)
<223> T7

<220>
<221> misc_RNA
<222> (19)..(74)
<223> Hammerhead ribozyme

<220>
<221> stem_loop
<222> (75)..(123)
<223> shRNA

<220>
<221> misc_RNA
<222> (124)..(186)
<223> HDV ribozyme

<220>
<221> misc_feature
<222> (187)..(196)
<223> AT spacer

<220>
<221> stem_loop
<222> (197)..(215)
<223> MS2 specific packing sequence

<220>

<221> misc_feature
<222> (216)..(221)
<223> NcoI restriction site

<400> 6
taatacgact cactataggg gagagcacac aagcctgatg agtccgtgag gacgaaacgg 60

tacccggtac cgtcgcttgt gatgcttcag ccaaatcaag agtttggctg aagcatcaca 120

agcggccggc atggtcccag cctcctcgct ggcgccggct gggcaacatt cgtggcgaat 180

gggaccatat atatatacat gaggattacc catgtccatg g 221

<210> 7
<211> 179
<212> DNA
<213> Artificial Sequence

<220>
<223> T7-Rz6

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriciton site

<220>
<221> promoter
<222> (7)..(24)
<223> T7

<220>
<221> stem_loop
<222> (25)..(74)
<223> shRNA

<220>
<221> misc_RNA
<222> (75)..(137)
<223> HDV ribozyme

<220>
<221> stem_loop
<222> (147)..(165)
<223> MS2 specific packing sequence

<220>
<221> misc_feature
<222> (174)..(179)
<223> NcoI restriciton site

<400> 7
ggatcctaat acgactcact ataggcaagc tgaccctgaa gttctcaaga ggaacttcag 60

ggtcagcttg ccaaggccgg catggtccca gcctcctcgc tggcgccggc tgggcaacat 120

tcgtggcgaa tgggaccacg cttcaaacat gaggattacc catgtcgaag cgaccatgg 179

<210> 8
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> T7-Rz8

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(24)
<223> T7

<220>
<221> misc_RNA
<222> (25)..(84)
<223> Hammerhead ribozyme

<220>
<221> misc_feature
<222> (85)..(105)
<223> sense strand siRNA

<220>
<221> misc_RNA
<222> (106)..(168)
<223> HDV ribozyme

<220>
<221> misc_feature
<222> (169)..(172)
<223> AT spacer

<220>
<221> misc_RNA
<222> (173)..(239)
<223> Hammerhead ribozyme

<220>
<221> misc_feature
<222> (240)..(262)
<223> antisense strand siRNA

<220>
<221> misc_RNA
<222> (263)..(325)
<223> HDV ribozyme

<220>
<221> stem_loop
<222> (263)..(325)
<223> MS2 specific packing sequence

<220>
<221> misc_feature
<222> (263)..(325)
<223> NcoI restriction site

<400> 8
ggatcctaat acgactcact atagggagaa tgaacttcag ggtcagcttg ctgatgaggc 60

gcttcggcgc cgaaacaccg tgtccaagct gaccctgaag ttcatggccg gcatggtccc 120

agcctcctcg ctggcgccgg ctgggcaaca ttcgtggcga atgggaccat tagccaagct 180

gaccctgaag ttcatctgat gagactccga attcggagtc gaaacacggt aaccgtgtca 240

tgaacttcag ggtcagcttg gcggccggca tggtcccagc ctcctcgctg gcgccggctg 300

ggcaacattc gtggcgaatg ggacccattc aaacatgagg attacccatg tcgaagccat 360

gg 362

<210> 9
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> T7-Rz1

<220>
<221> promoter
<222> (1)..(18)
<223> T7

<220>
<221> misc_RNA
<222> (19)..(64)
<223> Hammerhead ribozyme

<220>
<221> misc_RNA
<222> (65)..(113)
<223> siRNA

<220>
<221> misc_RNA
<222> (114)..(162)
<223> Hammerhead ribozyme

<220>
<221> misc_feature
<222> (163)..(168)
<223> NcoI restriction site

<400> 9
taatacgact cactataggc tcgagcaagc ctgatgaggc gcttcggcgc cgaaacaccg 60

tgtcgcttgt gatgcttcag ccaaatcaag agtttggctg aagcatcaca agctcaccgg 120

atgtgctctc cggtctgatg agtccgtgag gacgaaagct tgccatgg 168

<210> 10
<211> 251
<212> DNA
<213> Artificial Sequence

<220>
<223> T7-Rz4

<220>
<221> promoter
<222> (1)..(18)
<223> T7

<220>
<221> misc_RNA
<222> (19)..(98)
<223> Hammerhead ribozyme

<220>
<221> misc_RNA

<222> (99)..(146)
<223> siRNA

<220>
<221> misc_RNA
<222> (147)..(245)
<223> Hammerhead ribozyme

<220>
<221> misc_feature
<222> (246)..(251)
<223> NcoI restriction site

<400> 10
taatacgact cactataggg agaacgccgg ccattcaaat agtaaataat agagggtcag 60

cttgctgatg aggcgcttcg gcgccgaaac accgtgtcca agctgaccct gaagttcatc 120

aagagtgaac ttcagggtca gcttgtcacc ggatgtgctc tccggtctga tgagtccgtg 180

aggacgaaac aagctgaccc tgaagttcac tacgccggcc attcaaacat gaggattacc 240

catgtccatg g 251

<210> 11
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> long sense strand RNA

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(26)
<223> T7

<220>
<221> misc_RNA
<222> (27)..(318)
<223> long sense strand RNA

<220>
<221> stem_loop
<222> (319)..(337)
<223> MS2 specific packing sequence

<220>
<221> terminator
<222> (338)..(468)
<223> Transcription terminator

<400> 11
ggatcctaat acgactcact atagggagat gggtggtgat cttggacaga tctacaggcg 60

attggtcaca gctgtgaacg agattgagaa gagggttcca ttttctcacg acgacaggct 120

tggatttctc accttctgtc caaccaatct tggaaccact gtccgggcat cagtccatat 180

taaggtgccc aagctggctg ccaacaaggc aaaacttgag gaagttgctg cacgatacaa 240

ccttcaggtc cgtggtactc gaggagaaca cacagaagct gagggaggag tctatgacat 300

ctcaaacaag aggaggaaac atgaggatca cccatgtgcg gccgcgctgc caccgctgag 360

caataactag cataacccct tggggcctct aaacgggtct tgaggggttt tttgctgaaa 420

cctcaggcat ttgagaagca cacggtcaca ctgcttccgg tagtcaat 468

<210> 12
<211> 467
<212> DNA
<213> Artificial Sequence

<220>
<223> long antisense strand RNA

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(26)
<223> T7

<220>
<221> misc_RNA
<222> (27)..(317)
<223> long antisense RNA

<220>
<221> stem_loop
<222> (318)..(336)
<223> MS2 specific packing sequence

<220>
<221> terminator
<222> (337)..(467)
<223> Transcription terminator

<400> 12
ggatcctaat acgactcact atagggtcct cctcttgttt gagatgtcat agactcctcc 60

ctcagcttct gtgtgttctc ctcgagtacc acggacctga aggttgtatc gtgcagcaac 120

ttcctcaagt tttgccttgt tggcagccag cttgggcacc ttaatatgga ctgatgcccg 180

gacagtggtt ccaagattgg ttggacagaa ggtgagaaat ccaagcctgt cgtcgtgaga 240

aaatggaacc ctcttctcaa tctcgttcac agctgtgacc aatcgcctgt agatctgtcc 300

aagatcacca cccatctaca tgaggatcac ccatgtgcgg ccgcgctgcc accgctgagc 360

aataactagc ataacccctt ggggcctcta aacgggtctt gaggggtttt ttgctgaaac 420

ctcaggcatt tgagaagcac acggtcacac tgcttccggt agtcaat 467

<210> 13
<211> 319
<212> DNA
<213> Artificial Sequence

<220>
<223> long bulged RNA

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(26)
<223> T7

<220>
<221> stem_loop
<222> (27)..(45)
<223> MS2 specific packing sequence

<220>
<221> misc_RNA
<222> (46)..(146)
<223> antisense strand long bulged RNA

<220>
<221> misc_RNA
<222> (147)..(155)
<223> loop region of long bulged RNA

<220>
<221> misc_RNA
<222> (156)..(256)
<223> sense strand long bulged RNA

<220>
<221> misc_feature
<222> (179)..(181)
<223> bulge

<220>
<221> misc_feature
<222> (205)..(207)
<223> bulge

<220>
<221> misc_feature
<222> (231)..(233)
<223> bulge

<220>
<221> misc_RNA
<222> (257)..(319)
<223> HDV ribozyme

<400> 13
ggatcctaat acgactcact atagggacat gaggatcacc catgtggaca gatctacagg 60

cgataatacc tgagattgag aagagggttc aatacctcga cgacaggctt ggatttaata 120

cctgggcatc agtccatatt aaaatacctg acccatattt taatatggac tgatgccccc 180

atattaaatc caagcctgtc gtcgccatat tgaaccctct tctcaatctc ccatattatc 240

gcctgtagat ctgtccggcc ggcatggtcc cagcctcctc gctggcgccg gctgggcaac 300

attcgtggcg aatgggacc 319

<210> 14
<211> 157

<212> DNA
<213> Artificial Sequence

<220>
<223> A. tristis shRNA (single)

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriciton site

<220>
<221> promoter
<222> (7)..(26)
<223> T7

<220>
<221> stem_loop
<222> (27)..(45)
<223> MS2 specific packing sequence

<220>
<221> misc_RNA
<222> (46)..(66)
<223> sense strand siRNA

<220>
<221> misc_RNA
<222> (67)..(73)
<223> loop of siRNA

<220>
<221> misc_RNA
<222> (74)..(94)
<223> antisense strand siRNA

<220>
<221> misc_RNA
<222> (95)..(157)
<223> HDV ribozyme

<400> 14
ggatcctaat acgactcact atagggacat gaggatcacc catgtaaggg catcagtcca 60

tattaatcaa gagttaatat ggactgatgc ccttggccgg catggtccca gcctcctcgc 120

tggcgccggc tgggcaacat tcgtggcgaa tgggacc 157

<210> 15
<211> 233
<212> DNA
<213> Artificial Sequence

<220>
<223> A. tristis shRNA (multiple)

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(26)
<223> T7

<220>
<221> stem_loop
<222> (27)..(45)
<223> MS2 specific pac

<220>
<221> misc_feature
<222> (46)..(54)
<223> TAA spacer

<220>
<221> misc_RNA
<222> (55)..(75)
<223> sense strand first siRNA

<220>
<221> misc_RNA
<222> (76)..(82)
<223> loop of first siRNA

<220>
<221> misc_RNA
<222> (83)..(105)
<223> antisense strand first siRNA

<220>
<221> misc_feature
<222> (106)..(112)
<223> TAA spacer

<220>
<221> misc_RNA
<222> (113)..(133)
<223> sense strand second siRNA

<220>
<221> misc_RNA
<222> (134)..(140)
<223> loop of second siRNA

<220>
<221> misc_RNA
<222> (141)..(163)
<223> antisense strand second siRNA

<220>
<221> misc_feature
<222> (164)..(170)
<223> TA spacer

<220>
<221> misc_RNA
<222> (171)..(233)
<223> HDV ribozyme

<400> 15
ggatcctaat acgactcact atagggacat gaggatcacc catgtaataa taataagggc 60

atcagtccat attaatcaag agttaatatg gactgatgcc cttcataata ataagaagtt 120

gctgcacgat acatcaagag tgtatcgtgc agcaacttct tcataataat ggccggcatg 180

gtcccagcct cctcgctggc gccggctggg caacattcgt ggcgaatggg acc 233

<210> 16
<211> 176

<212> DNA
<213> Artificial Sequence

<220>
<223> half looped shRNA

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(26)
<223> T7

<220>
<221> stem_loop
<222> (27)..(45)
<223> MS2 specific packing sequence

<220>
<221> misc_RNA
<222> (46)..(66)
<223> sense strand siRNA

<220>
<221> misc_RNA
<222> (67)..(69)
<223> first half loop

<220>
<221> stem_loop
<222> (70)..(87)
<223> second MS2 specific packing sequence

<220>
<221> misc_RNA
<222> (88)..(92)
<223> second half loop

<220>
<221> misc_RNA
<222> (93)..(113)
<223> antisense strand siRNA

<220>
<221> misc_RNA
<222> (114)..(176)
<223> HDV ribozyme

<400> 16
ggatcctaat acgactcact atagggacat gaggatcacc catgtaaggg catcagtcca 60

tattaatcaa catgaggatc acccatgtag agttaatatg gactgatgcc cttggccggc 120

atggtcccag cctcctcgct ggcgccggct gggcaacatt cgtggcgaat gggacc 176

<210> 17
<211> 982
<212> DNA
<213> Artificial Sequence

<220>
<223> bacterial expression construct (E. coli)

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(25)
<223> T7

<220>
<221> stem_loop
<222> (33)..(52)
<223> first MS2 specific packing sequence

<220>
<221> misc_feature
<222> (53)..(74)
<223> first MS2 sequence spacer

<220>
<221> gene
<222> (75)..(794)
<223> EGFP gene

<220>
<221> misc_feature
<222> (795)..(809)
<223> second MS2 sequence spacer

<220>
<221> stem_loop
<222> (810)..(828)
<223> second MS2 specific packing sequence

<220>
<221> misc_feature
<222> (829)..(843)
<223> third MS2 sequence spacer

<220>
<221> misc_RNA
<222> (844)..(906)
<223> HDV ribozyme

<220>
<221> misc_feature
<222> (907)..(914)
<223> NotI restriction site

<220>
<221> terminator
<222> (915)..(982)
<223> Transcription terminator

<400> 17
ggatcctaat acgactcact ataggccatt cacacatgag gatcacccat gtggaagaca 60

acggagtttg aagcatggtg agcaagggcg aggagctgtt caccggggtg gtgcccatcc 120

tggtcgagct ggacggcgac gtaaacggcc acaagttcag cgtgtccggc gagggcgagg 180

gcgatgccac ctacggcaag ctgaccctga agttcatctg caccaccggc aagctgcccg 240

tgccctggcc caccctcgtg accaccctga cctacggcgt gcagtgcttc agccgctacc 300

ccgaccacat gaagcagcac gacttcttca agtccgccat gcccgaaggc tacgtccagg 360

agcgcaccat cttcttcaag gacgacggca actacaagac ccgcgccgag gtgaagttcg 420

agggcgacac cctggtgaac cgcatcgagc tgaagggcat cgacttcaag gaggacggca 480

acatcctggg gcacaagctg gagtacaact acaacagcca caacgtctat atcatggccg 540

acaagcagaa gaacggcatc aaggtgaact tcaagatccg ccacaacatc gaggacggca 600

gcgtgcagct cgccgaccac taccagcaga acaccccat cggcgacggc cccgtgctgc 660

tgcccgacaa ccactacctg agcacccagt ccgccctgag caaagacccc aacgagaagc 720

gcgatcacat ggtcctgctg gagttcgtga ccgccgccgg gatcactctc ggcatggacg 780

agctgtacaa gtagacgccg gccattcaga catgaggatc acccatgtcg aagacaacaa 840

agaggccggc atggtcccag cctcctcgct ggcgccggct gggcaacatt cgtggcgaat 900

gggaccgcgg ccgcgctgcc accgctgagc aataactagc ataacccctt ggggcctcta 960

aacgggtctt gaggggtttt tt 982

<210> 18
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
<223> dicotyledenous plant expression construct

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(18)
<223> T7

<220>
<221> misc_feature
<222> (19)..(33)
<223> first MS2 sequence spacer

<220>
<221> stem_loop
<222> (34)..(53)
<223> first MS2 specific packing sequence

<220>
<221> misc_feature
<222> (54)..(63)
<223> second MS2 sequence spacer

<220>
<221> misc_feature
<222> (64)..(139)
<223> first Carnation Italian ringspot virus sequence

<220>
<221> gene
<222> (140)..(859)
<223> EGFP gene

<220>
<221> misc_feature
<222> (860)..(1210)
<223> second Carnation Italian ringspot virus sequence

<220>
<221> misc_feature
<222> (1211)..(1225)
<223> third MS2 sequence spacer

<220>
<221> stem_loop
<222> (1226)..(1244)
<223> second MS2 specific packing sequence

<220>
<221> misc_feature
<222> (1245)..(1259)
<223> fourth MS2 sequence spacer

<220>
<221> misc_RNA
<222> (1260)..(1322)
<223> HDV ribozyme

<220>
<221> misc_feature
<222> (1323)..(1330)
<223> NotI restriction site

<220>
<221> terminator
<222> (1331)..(1398)
<223> Transcription terminator

<400> 18
ggatcctaat acgactcact ataggccatt cacacatgag gatcacccat gtggaagaca 60

acagaaatat ctcaggattt gaccgtccgg tgagttgcgc ttatcacttg cgtaaggtat 120

ttctctcttc attgttcata tggtgagcaa gggcgaggag ctgttcaccg gggtggtgcc 180

catcctggtc gagctggacg gcgacgtaaa cggccacaag ttcagcgtgt ccggcgaggg 240

cgagggcgat gccacctacg gcaagctgac cctgaagttc atctgcacca ccggcaagct 300

gcccgtgccc tggcccaccc tcgtgaccac cctgacctac ggcgtgcagt gcttcagccg 360

ctaccccgac cacatgaagc agcacgactt cttcaagtcc gccatgcccg aaggctacgt 420

ccaggagcgc accatcttct tcaaggacga cggcaactac aagacccgcg ccgaggtgaa 480

gttcgagggc gacaccctgg tgaaccgcat cgagctgaag ggcatcgact tcaaggagga 540

cggcaacatc ctggggcaca agctggagta caactacaac agccacaacg tctatatcat 600

ggccgacaag cagaagaacg gcatcaaggt gaacttcaag atccgccaca acatcgagga 660

cggcagcgtg cagctcgccg accactacca gcagaacacc cccatcggcg acggccccgt 720

gctgctgccc gacaaccact acctgagcac ccagtccgcc ctgagcaaag accccaacga 780

gaagcgcgat cacatggtcc tgctggagtt cgtgaccgcc gccgggatca ctctcggcat 840

ggacgagctg tacaagtagg ttcgctgaaa cgagtgtaaa tctggcatag catacaggtt 900

actcttgttg ggttctagat gttatgatga cgagtcggtt cgggctccgc actaggtttg 960

gtcacctagg ggatggagat atggaaaggg tctcgtgtgc tgttagacgg tcgtaagacg 1020

cgcttgcaac atgggcctat gaccggataa gtcatagcaa tactagccaa catgaatagg 1080

attcctgttt acgaaagtta gatgtcactt gtggaaacgg acccagacac ggttgatctc 1140

accttcgggg gggctataga gatcgctgga agcactaccg gacaaccgga acattgcaga 1200

aatgcagccc acgccggcca ttcagacatg aggatcaccc atgtcgaaga caacaaagag 1260

gccggcatgg tcccagcctc ctcgctggcg ccggctgggc aacattcgtg gcgaatggga 1320

ccgcggccgc gctgccaccg ctgagcaata actagcataa ccccttgggg cctctaaacg 1380

ggtcttgagg ggtttttt 1398

<210> 19
<211> 1246
<212> DNA
<213> Artificial Sequence

<220>
<223> monocotyledenous plant expression construct

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(24)
<223> T7

<220>
<221> misc_feature
<222> (25)..(33)
<223> first MS2 sequence spacer

<220>
<221> stem_loop
<222> (34)..(52)
<223> first MS2 specific packing sequence

<220>
<221> misc_feature
<222> (53)..(62)
<223> second MS2 sequence spacer

<220>
<221> misc_feature
<222> (63)..(139)
<223> first Carnation Italian ringspot virus sequence

<220>
<221> gene
<222> (140)..(859)
<223> EGFP coding sequence

<220>
<221> misc_feature
<222> (860)..(1058)
<223> second Carnation Italian ringspot virus sequence

<220>
<221> misc_feature

<222> (959)..(971)
<223> Maize necrotic streak virus sequence

<220>
<221> misc_feature
<222> (1059)..(1073)
<223> third MS2 sequence spacer

<220>
<221> stem_loop
<222> (1074)..(1092)
<223> second MS2 specific packing sequence

<220>
<221> misc_feature
<222> (1093)..(1107)
<223> fourth MS2 sequence spacer

<220>
<221> misc_RNA
<222> (1108)..(1170)
<223> HDV ribozyme

<220>
<221> misc_feature
<222> (1171)..(1178)
<223> NotI restriction site

<220>
<221> terminator
<222> (1179)..(1246)
<223> Transcription termnator

<400> 19
ggatcctaat acgactcact ataggccatt cacacatgag gatcacccat gtggaagaca 60

acagaaatat ctcaggattt gaccgtccgg tgagttgcgc ttatcacttg cgtaaggtat 120

ttctctcttc attgttcata tggtgagcaa gggcgaggag ctgttcaccg gggtggtgcc 180

catcctggtc gagctggacg gcgacgtaaa cggccacaag ttcagcgtgt ccggcgaggg 240

cgagggcgat gccacctacg gcaagctgac cctgaagttc atctgcacca ccggcaagct 300

gcccgtgccc tggcccaccc tcgtgaccac cctgacctac ggcgtgcagt gcttcagccg 360

ctaccccgac cacatgaagc agcacgactt cttcaagtcc gccatgcccg aaggctacgt 420

ccaggagcgc accatcttct tcaaggacga cggcaactac aagacccgcg ccgaggtgaa 480

gttcgagggc gacaccctgg tgaaccgcat cgagctgaag ggcatcgact tcaaggagga 540

cggcaacatc ctggggcaca agctggagta caactacaac agccacaacg tctatatcat 600

ggccgacaag cagaagaacg gcatcaaggt gaacttcaag atccgccaca acatcgagga 660

cggcagcgtg cagctcgccg accactacca gcagaacacc cccatcggcg acggccccgt 720

gctgctgccc gacaaccact acctgagcac ccagtccgcc ctgagcaaag accccaacga 780

gaagcgcgat cacatggtcc tgctggagtt cgtgaccgcc gccgggatca ctctcggcat 840

ggacgagctg tacaagtagt gtctgatgat gtgaggaacg tggactgtga tgtggtggtg 900

cggtaccatg gctggtcacc atggtaatgc gtagggcaac acagttcatt aagactcact 960

gatgatggca ccagacacgg ttgatctcac cttcgggggg gctatagaga tcgctggaag 1020

cactaccgga caaccggaac attgcagaaa tgcagcccac gccggccatt cagacatgag 1080

gatcacccat gtcgaagaca acaaagaggc cggcatggtc ccagcctcct cgctggcgcc 1140

ggctgggcaa cattcgtggc gaatgggacc gcggccgcgc tgccaccgct gagcaataac 1200

tagcataacc ccttggggcc tctaaacggg tcttgagggg ttttt 1246

<210> 20
<211> 1774
<212> DNA
<213> Artificial Sequence

<220>
<223> mammalian expression construct

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI restriction site

<220>
<221> promoter
<222> (7)..(24)
<223> T7

<220>
<221> misc_feature
<222> (25)..(33)
<223> first MS2 sequence spacer

<220>
<221> stem_loop
<222> (34)..(52)
<223> first MS2 specific packing sequence

<220>
<221> misc_feature
<222> (53)..(62)
<223> second MS2 sequence spacer

<220>
<221> misc_feature
<222> (63)..(561)
<223> Encephalomyocarditis virus IRES sequence

<220>
<221> gene
<222> (562)..(1343)
<223> EGFP gene

<220>
<221> polyA_signal
<222> (1344)..(1586)
<223> SV40 late poly(A) signal sequence

<220>
<221> misc_feature
<222> (1587)..(1601)
<223> third MS2 sequence spacer

<220>
<221> stem_loop
<222> (1602)..(1620)
<223> second MS2 specific packing sequence

<220>
<221> misc_feature
<222> (1621)..(1635)
<223> fourth MS2 sequence spacer

<220>
<221> misc_RNA
<222> (1636)..(1698)
<223> HDV ribozyme

<220>
<221> misc_feature
<222> (1699)..(1706)
<223> NotI restriction site

<220>
<221> terminator
<222> (1707)..(1774)
<223> Transcription terminator

<400> 20
ggatcctaat acgactcact ataggccatt cacacatgag gatcacccat gtggaagaca 60

accccccccc taacgttact ggccgaagcc gcttggaata aggccggtgt gcgtttgtct 120

atatgttatt ttccaccata ttgccgtctt ttggcaatgt gagggcccgg aaacctggcc 180

ctgtcttctt gacgagcatt cctaggggtc tttcccctct cgccaaagga atgcaaggtc 240

tgttgaatgt cgtgaaggaa gcagttcctc tggaagcttc ttgaagacaa acaacgtctg 300

tagcgaccct ttgcaggcag cggaaccccc cacctggcga caggtgcctc tgcggccaaa 360

agccacgtgt ataagataca cctgcaaagg cggcacaacc ccagtgccac gttgtgagtt 420

ggatagttgt ggaaagagtc aaatggctct cctcaagcgt attcaacaag gggctgaagg 480

atgcccagaa ggtaccccat tgtatgggat ctgatctggg gcctcggtgc acatgcttta 540

catgtgttta gtcgaggtta aaaaacgtct aggcccccccg aaccacgggg acgtggtttt 600

cctttgaaaa acacgatgat aatatggtga gcaagggcga ggagctgttc accggggtgg 660

tgcccatcct ggtcgagctg gacggcgacg taaacggcca caagttcagc gtgtccggcg 720

agggcgaggg cgatgccacc tacggcaagc tgaccctgaa gttcatctgc accaccggca 780

agctgcccgt gccctggccc accctcgtga ccaccctgac ctacggcgtg cagtgcttca 840

gccgctaccc cgaccacatg aagcagcacg acttcttcaa gtccgccatg cccgaaggct 900

acgtccagga gcgcaccatc ttcttcaagg acgacggcaa ctacaagacc cgcgccgagg 960

tgaagttcga gggcgacacc ctggtgaacc gcatcgagct gaagggcatc gacttcaagg 1020

aggacggcaa catcctgggg cacaagctgg agtacaacta caacagccac aacgtctata 1080

tcatggccga caagcagaag aacggcatca aggtgaactt caagatccgc cacaacatcg 1140

aggacggcag cgtgcagctc gccgaccact accagcagaa cacccccatc ggcgacggcc 1200

ccgtgctgct gcccgacaac cactacctga gcacccagtc cgccctgagc aaagacccca 1260

acgagaagcg cgatcacatg gtcctgctgg agttcgtgac cgccgccggg atcactctcg 1320

gcatggacga gctgtacaag tagttctaga gcggccgctt cgagcagaca tgataagata 1380

cattgatgag tttggacaaa ccacaactag aatgcagtga aaaaaatgct ttatttgtga 1440

aatttgtgat gctattgctt tatttgtaac cattataagc tgcaataaac aagttaacaa 1500

caacaattgc attcatttta tgtttcaggt tcaggggggag gtgtgggagg ttttttaaag 1560

caagtaaaac ctctacaaat gtggtaacgc cggccattca gacatgagga tcacccatgt 1620

cgaagacaac aaagaggccg gcatggtccc agcctcctcg ctggcgccgg ctgggcaaca 1680

ttcgtggcga atgggaccgc ggccgcgctg ccaccgctga gcaataacta gcataacccc 1740

ttggggcctc taaacgggtc ttgaggggtt tttt 1774