SEQUENCE LISTING

<110> DUKE UNIVERSITY
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<120> COMPOSITIONS FOR THE INACTIVATION OF VIRUS REPLICATION AND METHODS OF MAKING AND USING THE SAME

<130> 5667-00184PCT

<150> US 61/940,883
<151> 2014-02-18

<160> 68

<170> PatentIn version 3.5

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<400> 35
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ttatcaactt gaaaaagtgg caccgagtcg gtgcttttt 99

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gtttattttt 130

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<210> 41
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tcggtggaac ct 72

<210> 42
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gcccacccgg ggacg 75

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cgagtcacgg ca 72

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ccggacgagc cc 72

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cgtagaaagt aataatttct tgggtagttt gcagttttaa aattatgttt taaaatggac 180

tatcatatgc ttaccgtaac ttgaaagtat ttcgatttct tggctttata tatcttgtgg 240

aaaggacgaa acacc 255

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gaaagtgatg tcgtgtactg gctccgcctt tttcccgagg gtgggggaga accgtatata 240

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ccacc 185

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cacagaatcc agagggtcaa gaagctcctg ttcgactaca acctgctgac cgaccatagc 240

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Lys Asp Asp Asp Asp Lys Lys Arg Asn Tyr Ile Leu Gly Leu Asp Ile
20 25 30

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Val Ile Asp Ala Gly Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn
    50                  55                  60

Asn Glu Gly Arg Arg Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg
65                  70                  75                  80

Arg Arg His Arg Ile Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn
                85                  90                  95

Leu Leu Thr Asp His Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala
            100                 105                 110

Arg Val Lys Gly Leu Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala
        115                 120                 125

Ala Leu Leu His Leu Ala Lys Arg Arg Gly Val His Asn Val Asn Glu
    130                 135                 140

Val Glu Glu Asp Thr Gly Asn Glu Leu Ser Thr Lys Glu Gln Ile Ser
145                 150                 155                 160

Arg Asn Ser Lys Ala Leu Glu Glu Lys Tyr Val Ala Glu Leu Gln Leu
                165                 170                 175

Glu Arg Leu Lys Lys Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe
            180                 185                 190

Lys Thr Ser Asp Tyr Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln
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Lys Ala Tyr His Gln Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp
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Pro Phe Gly Trp Lys Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly
                245                 250                 255


His Cys Thr Tyr Phe Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr
            260                 265                 270


Asn Ala Asp Leu Tyr Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile
        275                 280                 285


Thr Arg Asp Glu Asn Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile
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Ile Glu Asn Val Phe Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile
305                 310                 315                 320


Ala Lys Glu Ile Leu Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val
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Thr Ser Thr Gly Lys Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp
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Ile Lys Asp Ile Thr Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu
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Leu Asp Gln Ile Ala Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp
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Ile Gln Glu Glu Leu Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu
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Ile Glu Gln Ile Ser Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu
                405                 410                 415
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Ser Leu Lys Ala Ile Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn
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Asp Asn Gln Ile Ala Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys
        435                 440                 445

Val Asp Leu Ser Gln Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp
    450                 455                 460

Phe Ile Leu Ser Pro Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys
465                 470                 475                 480

Val Ile Asn Ala Ile Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile
                485                 490                 495

Ile Glu Leu Ala Arg Glu Lys Asn Ser Lys Asp Ala Gln Lys Met Ile
            500                 505                 510

Asn Glu Met Gln Lys Arg Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu
        515                 520                 525

Ile Ile Arg Thr Thr Gly Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys
    530                 535                 540

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

Ala Ile Pro Leu Glu Asp Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val
                565                 570                 575

Asp His Ile Ile Pro Arg Ser Val Ser Phe Asp Asn Ser Phe Asn Asn
            580                 585                 590

Lys Val Leu Val Lys Gln Glu Glu Asn Ser Lys Lys Gly Asn Arg Thr
        595                 600                 605
```

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Pro Phe Gln Tyr Leu Ser Ser Ser Asp Ser Lys Ile Ser Tyr Glu Thr
    610                 615                 620

Phe Lys Lys His Ile Leu Asn Leu Ala Lys Gly Lys Gly Arg Ile Ser
625                 630                 635                 640

Lys Thr Lys Lys Glu Tyr Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe
                645                 650                 655

Ser Val Gln Lys Asp Phe Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr
            660                 665                 670

Ala Thr Arg Gly Leu Met Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn
        675                 680                 685

Asn Leu Asp Val Lys Val Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe
    690                 695                 700

Leu Arg Arg Lys Trp Lys Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys
705                 710                 715                 720

His His Ala Glu Asp Ala Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe
                725                 730                 735

Lys Glu Trp Lys Lys Leu Asp Lys Ala Lys Lys Val Met Glu Asn Gln
            740                 745                 750

Met Phe Glu Glu Lys Gln Ala Glu Ser Met Pro Glu Ile Glu Thr Glu
        755                 760                 765

Gln Glu Tyr Lys Glu Ile Phe Ile Thr Pro His Gln Ile Lys His Ile
    770                 775                 780

Lys Asp Phe Lys Asp Tyr Lys Tyr Ser His Arg Val Asp Lys Lys Pro
785                 790                 795                 800
```

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Asn Arg Glu Leu Ile Asn Asp Thr Leu Tyr Ser Thr Arg Lys Asp Asp
                805                 810                 815

Lys Gly Asn Thr Leu Ile Val Asn Asn Leu Asn Gly Leu Tyr Asp Lys
            820                 825                 830

Asp Asn Asp Lys Leu Lys Lys Leu Ile Asn Lys Ser Pro Glu Lys Leu
        835                 840                 845

Leu Met Tyr His His Asp Pro Gln Thr Tyr Gln Lys Leu Lys Leu Ile
    850                 855                 860

Met Glu Gln Tyr Gly Asp Glu Lys Asn Pro Leu Tyr Lys Tyr Tyr Glu
865                 870                 875                 880

Glu Thr Gly Asn Tyr Leu Thr Lys Tyr Ser Lys Lys Asp Asn Gly Pro
                885                 890                 895

Val Ile Lys Lys Ile Lys Tyr Tyr Gly Asn Lys Leu Asn Ala His Leu
            900                 905                 910

Asp Ile Thr Asp Asp Tyr Pro Asn Ser Arg Asn Lys Val Val Lys Leu
        915                 920                 925

Ser Leu Lys Pro Tyr Arg Phe Asp Val Tyr Leu Asp Asn Gly Val Tyr
    930                 935                 940

Lys Phe Val Thr Val Lys Asn Leu Asp Val Ile Lys Lys Glu Asn Tyr
945                 950                 955                 960

Tyr Glu Val Asn Ser Lys Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys
                965                 970                 975

Ile Ser Asn Gln Ala Glu Phe Ile Ala Ser Phe Tyr Asn Asn Asp Leu
            980                 985                 990
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Ile Lys Ile Asn Gly Glu Leu Tyr Arg Val Ile Gly Val Asn Asn Asp
995 1000 1005

Leu Leu Asn Arg Ile Glu Val Asn Met Ile Asp Ile Thr Tyr Arg
1010 1015 1020

Glu Tyr Leu Glu Asn Met Asn Asp Lys Arg Pro Pro Arg Ile Ile
1025 1030 1035

Lys Thr Ile Ala Ser Lys Thr Gln Ser Ile Lys Lys Tyr Ser Thr
1040 1045 1050

Asp Ile Leu Gly Asn Leu Tyr Glu Val Lys Ser Lys Lys His Pro
1055 1060 1065

Gln Ile Ile Lys Lys Gly
1070

<210> 58
<211> 4289
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: AAV construct insert (2 sgRNAs; synthetic)

<400> 58
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tcggtggaac ctggagacgg acgtctccgt tttagtactc tggaaacaga atctactaaa 120

acaaggcaaa atgccgtgtt tatctcgtca acttgttggc gagatttttt tctagagagg 180

gcctatttcc catgattcct tcatatttgc atatacgata caaggctgtt agagagataa 240

ttggaattaa tttgactgta aacacaaaga tattagtaca aaatacgtga cgtagaaagt 300

aataatttct tgggtagttt gcagttttaa aattatgttt taaaatggac tatcatatgc 360

ttaccgtaac ttgaaagtat ttcgatttct tggctttata tatcttgtgg aaaggacgaa 420

acaccgggtc ttcgagaaga cccgttttag tactctggaa acagaatcta ctaaaacaag 480

gcaaaatgcc gtgtttatct cgtcaacttg ttggcgagat tttttctcga ggtcggagga 540

tccacaaagg ctagccggtc tatgcattag gtcttgaaag gagtgggaat tggctccggt 600

gcccgtcagt gggcagagcg cacatcgccc acagtccccg agaagttggg gggaggggtc 660

ggcaattgat ccggtgccta gagaaggtgg cgcggggtaa actgggaaag tgatgtcgtg 720

tactggctcc gccttttcc cgagggtggg ggagaaccgt atataagtgc agtagtcgcc 780

gtgaacgttc tttttcgcaa cgggtttgcc gccagaacac aggaagcttg gtaagtgacc 840

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ccagtcaaga ctccagggat ttgagggacg ctgtgggctc ttctcttaca tgtacctttt 960

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atccagaggg tcaagaagct cctgttcgac tacaacctgc tgaccgacca tagcgagctg 1320

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gccctggagg aaaaatatgt cgccgagcta cagctggaga gactcaagaa ggatggcgag 1560

gtcagaggct ccattaacag gttcaagacc tccgactacg tgaaagaagc caagcagctg 1620

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ctgctcgaaa ccaggagaac ctactatgag ggccctggag aaggaagccc cttcggatgg 1740

aaagacatta aggagtggta cgaaatgctg atgggacact gcacctactt ccccgaggag 1800

ctgaggagcg tgaaatatgc ctacaacgcc gatctctaca acgccctgaa cgacctgaac 1860

aatctcgtga ttacaaggga tgagaacgaa aagctggaat attacgaaaa atttcagatc 1920

attgaaaacg tgtttaagca aaagaagaag cccaccctga agcagattgc caaggagatc 1980

ctggtgaacg aagaggacat taaaggctac agagtgacct ccacaggcaa acccgaattt 2040

accaatctga aggtgtatca cgatatcaaa gatatcacag ctagaaagga gatcatcgag 2100

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tccaacctga aaggctacac cggcacccac aacctgtccc tgaaggccat caacctgatc 2280

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ttcatcctca gccccgtcgt gaagaggagc ttcatccagt ccatcaaggt gattaacgct 2460

atcatcaaga agtatggcct ccccaacgac atcatcatcg agctcgctag ggaaaaaaac 2520

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gatgccctca tcattgctaa cgccgacttc atctttaagg agtggaagaa gctcgataag 3240

gccaagaaag tcatggagaa tcaaatgttc gaggagaaac aagccgaatc catgcccgag 3300

attgaaacgg agcaagagta caaggaaata ttcatcaccc ctcaccagat caaacacatc 3360

aaggacttca aagactacaa atatagccat agagtcgata agaagcccaa cagggagctg 3420

atcaacgaca cactctattc caccagaaag gatgataagg gcaacaccct gattgtgaac 3480

aacctgaacg gcctctacga taaggataac gacaagctga agaagctgat taacaagagc 3540

cccgagaaac tgctcatgta ccaccacgac ccccaaacat accagaaact gaagctgatc 3600

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ttacatctgt gtgttggttt tttgtgtgt 4289

<210> 59
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Nuclear localization signal

<400> 59

Leu Glu Ala Pro Lys Lys Lys Arg Lys Val
1 5 10

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Nuclear localization signal

<400> 60

Ala Ala Pro Ala Ala Lys Lys Lys Leu Asp
1 5 10

<210> 61
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Nuclear localization signal

<400> 61

Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
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<210> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Nuclear localization signal

<400> 62

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> Synthetic: ICP4 (Nme)

<400> 63
gcggtggccg gccgcgacgc cacg 24

<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: GFP (Nme)

<400> 64
gtcacgaggg tgggccaggg cacg 24

<210> 65
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: G6P (Nme)

<400> 65
gatctggttc catcttaaag agact 25

<210> 66
<211> 23
<212> DNA
<213> Human papilloma virus

<220>
<221> misc_feature
<222> (1)..(23)
<223> Wild-type E6 partial sequence

<400> 66
cgcgctttga ggatccaaca cgg 23

<210> 67
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic: Mutant E6 partial sequence

<400> 67
cgcgctttga ggaccccacg cgg 23

<210> 68
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: oligonucleotide

<400> 68
gaaatcctgc agaaagacct 20