SEQUENCE LISTING

<110> Bamboo Therapeutics, Inc.
The University of North Carolina at Chapel Hill

<120> Optimized Mini-dystrophin Genes and Expression Cassettes and Their Use

<130> PC45290A

<150> US 62/352,675
<151> 2016-06-21

<150> US 62/516,449
<151> 2017-06-07

<160> 28

<170> PatentIn version 3.5

<210> 1
<211> 3978
<212> DNA
<213> Artificial Sequence

<220>
<223> Hopti-Dys3978 gene

<400> 1
atgctttggt gggaggaagt ggaggactgc tacgagagag aggacgtgca gaagaaaacc 60

ttcaccaagt gggtgaacgc ccagttcagc aagttcggca agcagcacat cgagaacctg 120

ttcagcgacc tgcaggatgg caggagactg ctggacctgc tggagggcct gaccggccag 180

aagctgccca aggagaaggg cagcaccaga gtgcacgccc tgaacaacgt gaacaaggcc 240

ctgagagtgc tgcagaacaa caacgtggac ctggtgaaca tcggcagcac cgacatcgtg 300

gacggcaacc acaagctgac cctgggcctg atctggaaca tcatcctgca ctggcaggtg 360

aagaacgtga tgaagaacat catggccggc ctgcagcaga ccaacagcga gaagatcctg 420

ctgagctggg tgaggcagag caccagaaac tacccccagg tgaacgtgat caacttcacc 480

acctcctgga gcgacggcct ggccctgaac gccctgatcc acagccacag acccgacctg 540

ttcgactgga acagcgtggt gtgtcagcag agcgccaccc agagactgga gcacgccttc 600

aacatcgcca gataccagct gggcatcgag aagctgctgg accccgagga cgtggacacc 660

acctaccccg acaagaaaag catcctcatg tacattacca gcctgttcca ggtgctgccc 720

cagcaggtgt ccatcgaggc catccaggaa gtggaaatgc tgcccaggcc ccccaaagtg 780

accaaggagg agcacttcca gctgcaccac cagatgcact acagccagca gatcacagtg 840

agcctggccc agggctatga gagaaccagc agccccaagc ccagattcaa gagctacgcc 900

tacacccagg ccgcctacgt gaccacctcc gaccccacca gaagcccctt ccccagccag 960

cacctggagg cccccgagga caagagcttc ggcagcagcc tgatggagag cgaagtgaac 1020

ctggacagat accagaccgc cctggaggaa gtgctgtcct ggctgctgag cgccgaggac 1080

accctgcagg cccagggcga gatcagcaac gacgtggaag tggtgaagga ccagttccac 1140

acccacgagg gctacatgat ggatctgacc gcccaccagg gcagagtggg caatatcctg 1200

cagctgggca gcaagctgat cggcaccggc aagctgagcg aggacgagga gaccgaagtg 1260

caggagcaga tgaacctgct gaacagcaga tgggagtgcc tgagagtggc cagcatggag 1320

aagcagagca acctgcacag agtgctgatg gacctgcaga accagaagct gaaggagctg 1380

aacgactggc tgaccaagac cgaggagcgg accagaaaga tggaggagga gcccctgggc 1440

cccgacctgg aggacctgaa gagacaggtg cagcagcaca aagtgctgca ggaggacctg 1500

gagcaggagc aggtgcgcgt gaacagcctg acccacatgg tggtggtcgt ggacgagagc 1560

agcggcgacc acgccacagc cgccctggaa gagcagctga aagtgctggg cgacagatgg 1620

gccaatattt gtaggtggac cgaggacaga tgggtgctgc tgcaggacca gcccgacctg 1680

gcccctggcc tgaccaccat cggcgccagc cccacccaga ccgtgaccct ggtgacccag 1740

cccgtggtga caaaggagac cgccatcagc aagctggaga tgcccagctc cctgatgctg 1800

gaagtgccca cccaccgcct gctccagcag ttccccctgg acctggagaa gttcctggcc 1860

tggctgaccg aggccgaaac caccgccaat gtgctccagg acgccactag aaaggagagg 1920

ctgctggagg acagcaaggg cgtgaaagag ctgatgaagc agtggcagga tctgcagggc 1980

gaaatcgagg cccacaccga cgtgtaccac aacctggacg agaacagcca gaagattctg 2040

aggagcctgg agggcagcga cgacgccgtc ctgctccaga ggaggctgga caacatgaac 2100

ttcaagtgga gcgagctgcg gaagaagagc ctgaacatcc ggagccacct ggaagccagc 2160

agcgaccagt ggaagagact gcacctgagc ctgcaggagc tgctggtgtg gctgcagctg 2220

aaggacgacg agctgagcag acaggccccc atcggcggcg acttccccgc cgtgcagaag 2280

cagaacgacg tgcaccgggc cttcaagagg gagctgaaaa ccaaggaacc cgtgatcatg 2340

agcaccctgg agacagtgcg gatcttcctg accgagcagc ccctggaggg actggagaag 2400

ctgtaccagg agcccagaga gctgcccccc gaggagagag cccagaacgt gaccaggctg 2460

ctgagaaagc aggccgagga agtgaatacc gagtgggaga agctgaatct gcacagcgcc 2520

gactggcaga gaaagatcga cgagaccctg gagagactcc aggaactgca ggaagccacc 2580

gacgagctgg acctgaagct gagacaggcc gaagtgatca agggcagctg gcagcctgtg 2640

ggcgatctgc tgatcgactc cctgcaggat cacctggaga aagtgaaggc cctgcggggc 2700

gagatcgccc ccctgaagga gaatgtgagc cacgtgaacg acctggccag acagctgacc 2760

accctgggca tccagctgag ccctacaac ctgagcacac tggaggatct gaacacccgg 2820

tggaaactgc tgcaggtggc cgtggaggat agagtgaggc agctgcacga agcccacaga 2880

gacttcggcc ctgcctccca gcacttcctg agcaccagcg tgcagggccc ctgggagaga 2940

gccatctccc ccaacaaagt gccctactac atcaaccacg agacccagac cacctgctgg 3000

gaccacccta agatgaccga gctgtatcag agcctggccg acctgaacaa tgtgcggttc 3060

agcgcctaca gaaccgccat gaagctgcgg agactgcaga aggccctgtg cctggatctg 3120

ctgagcctga gcgccgcctg cgacgccctg gaccagcaca acctgaagca gaatgaccag 3180

cccatggaca tcctgcagat catcaactgc ctgaccacaa tctacgaccg gctggaacag 3240

gagcacaaca acctggtgaa tgtgcccctg tgcgtggaca tgtgcctgaa ttggctgctg 3300

aacgtgtacg acaccggcag gaccggcaga atccgcgtgc tgagcttcaa gaccggcatc 3360

atcagcctgt gcaaggccca cctggaggat aagtaccgct acctgttcaa gcaggtggcc 3420

agcagcaccg gcttctgcga tcagaggaga ctgggcctgc tgctgcacga tagcatccag 3480

atccctaggc agctgggcga agtggccagc tttggcggca gcaacatcga gccctctgtg 3540

aggagctgct tccagttcgc caacaacaag cccgagatcg aggccgccct gttcctggac 3600

tggatgaggc tggagcctca gagcatggtg tggctgcctg tgctgcacag agtggccgcc 3660

gccgagaccg ccaagcacca ggccaagtgc aatatctgca aggagtgccc catcatcggc 3720

ttccggtaca ggagcctgaa gcacttcaac tacgacatct gccagagctg ctttttcagc 3780

ggcagagtgg ccaagggcca caaaatgcac taccccatgg tggagtactg caccccccacc 3840

acctccggcg aggatgtgag agacttcgcc aaagtgctga agaataagtt ccggaccaag 3900

cggtactttg ccaagcaccc caggatgggc tacctgcccg tgcagaccgt gctggaaggc 3960

gacaacatgg agacctga 3978

<210> 2
<211> 3837
<212> DNA
<213> Artificial Sequence

<220>
<223> Hopti-Dys3837 gene

<400> 2
atgctttggt gggaggaagt ggaggactgc tacgagagag aggacgtgca gaagaaaacc 60

ttcaccaagt gggtgaacgc ccagttcagc aagttcggca agcagcacat cgagaacctg 120

ttcagcgacc tgcaggatgg caggagactg ctggacctgc tggagggcct gaccggccag 180

aagctgccca aggagaaggg cagcaccaga gtgcacgccc tgaacaacgt gaacaaggcc 240

ctgagagtgc tgcagaacaa caacgtggac ctggtgaaca tcggcagcac cgacatcgtg 300

gacggcaacc acaagctgac cctgggcctg atctggaaca tcatcctgca ctggcaggtg 360

aagaacgtga tgaagaacat catggccggc ctgcagcaga ccaacagcga gaagatcctg 420

ctgagctggg tgaggcagag caccagaaac tacccccagg tgaacgtgat caacttcacc 480

acctcctgga gcgacggcct ggccctgaac gccctgatcc acagccacag acccgacctg 540

ttcgactgga acagcgtggt gtgtcagcag agcgccaccc agagactgga gcacgccttc 600

aacatcgcca gataccagct gggcatcgag aagctgctgg accccgagga cgtggacacc 660

acctaccccg acaagaaaag catcctcatg tacattacca gcctgttcca ggtgctgccc 720

cagcaggtgt ccatcgaggc catccaggaa gtggaaatgc tgcccaggcc ccccaaagtg 780

accaaggagg agcacttcca gctgcaccac cagatgcact acagccagca gatcacagtg 840

agcctggccc agggctatga gagaaccagc agccccaagc ccagattcaa gagctacgcc 900

tacacccagg ccgcctacgt gaccacctcc gaccccacca gaagcccctt ccccagccag 960

cacctggagg cccccgagga caagagcttc ggcagcagcc tgatggagag cgaagtgaac 1020

ctggacagat accagaccgc cctggaggaa gtgctgtcct ggctgctgag cgccgaggac 1080

accctgcagg cccagggcga gatcagcaac gacgtggaag tggtgaagga ccagttccac 1140

acccacgagg gctacatgat ggatctgacc gcccaccagg gcagagtggg caatatcctg 1200

cagctgggca gcaagctgat cggcaccggc aagctgagcg aggacgagga gaccgaagtg 1260

caggagcaga tgaacctgct gaacagcaga tgggagtgcc tgagagtggc cagcatggag 1320

aagcagagca acctgcacag agtgctgatg gacctgcaga accagaagct gaaggagctg 1380

aacgactggc tgaccaagac cgaggagcgg accagaaaga tggaggagga gcccctgggc 1440

cccgacctgg aggacctgaa gagacaggtg cagcagcaca aagtgctgca ggaggacctg 1500

gagcaggagc aggtgcgcgt gaacagcctg acccacatgg tggtggtcgt ggacgagagc 1560

agcggcgacc acgccacagc cgccctggaa gagcagctga aagtgctggg cgacagatgg 1620

gccaatattt gtaggtggac cgaggacaga tgggtgctgc tgcaggacac ccaccgcctg 1680

ctccagcagt tccccctgga cctggagaag ttcctggcct ggctgaccga ggccgaaacc 1740

accgccaatg tgctccagga cgccactaga aaggagaggc tgctggagga cagcaagggc 1800

gtgaaagagc tgatgaagca gtggcaggat ctgcagggcg aaatcgaggc ccacaccgac 1860

gtgtaccaca acctggacga gaacagccag aagattctga ggagcctgga gggcagcgac 1920

gacgccgtcc tgctccagag gaggctggac aacatgaact tcaagtggag cgagctgcgg 1980

aagaagagcc tgaacatccg gagccacctg gaagccagca gcgaccagtg gaagagactg 2040

cacctgagcc tgcaggagct gctggtgtgg ctgcagctga aggacgacga gctgagcaga 2100

caggccccca tcggcggcga cttccccgcc gtgcagaagc agaacgacgt gcaccgggcc 2160

ttcaagaggg agctgaaaac caaggaaccc gtgatcatga gcaccctgga gacagtgcgg 2220

atcttcctga ccgagcagcc cctggaggga ctggagaagc tgtaccagga gcccagagag 2280

ctgccccccg aggagagagc ccagaacgtg accaggctgc tgagaaagca ggccgaggaa 2340

gtgaataccg agtgggagaa gctgaatctg cacagcgccg actggcagag aaagatcgac 2400

gagaccctgg agagactcca ggaactgcag gaagccaccg acgagctgga cctgaagctg 2460

agacaggccg aagtgatcaa gggcagctgg cagcctgtgg gcgatctgct gatcgactcc 2520

ctgcaggatc acctggagaa agtgaaggcc ctgcggggcg agatcgcccc cctgaaggag 2580

aatgtgagcc acgtgaacga cctggccaga cagctgacca ccctgggcat ccagctgagc 2640

ccctacaacc tgagcacact ggaggatctg aacacccggt ggaaactgct gcaggtggcc 2700

gtggaggata gagtgaggca gctgcacgaa gcccacagag acttcggccc tgcctcccag 2760

cacttcctga gcaccagcgt gcagggcccc tgggagagag ccatctcccc caacaaagtg 2820

ccctactaca tcaaccacga gacccagacc acctgctggg accaccctaa gatgaccgag 2880

ctgtatcaga gcctggccga cctgaacaat gtgcggttca gcgcctacag aaccgccatg 2940

aagctgcgga gactgcagaa ggccctgtgc ctggatctgc tgagcctgag cgccgcctgc 3000

gacgccctgg accagcacaa cctgaagcag aatgaccagc ccatggacat cctgcagatc 3060

atcaactgcc tgaccacaat ctacgaccgg ctggaacagg agcacaacaa cctggtgaat 3120

gtgcccctgt gcgtggacat gtgcctgaat tggctgctga acgtgtacga caccggcagg 3180

accggcagaa tccgcgtgct gagcttcaag accggcatca tcagcctgtg caaggcccac 3240

ctggaggata agtaccgcta cctgttcaag caggtggcca gcagcaccgg cttctgcgat 3300

cagaggagac tgggcctgct gctgcacgat agcatccaga tccctaggca gctgggcgaa 3360

gtggccagct ttggcggcag caacatcgag ccctctgtga ggagctgctt ccagttcgcc 3420

aacaacaagc ccgagatcga ggccgccctg ttcctggact ggatgaggct ggagcctcag 3480

agcatggtgt ggctgcctgt gctgcacaga gtggccgccg ccgagaccgc caagcaccag 3540

gccaagtgca atatctgcaa ggagtgcccc atcatcggct tccggtacag gagcctgaag 3600

cacttcaact acgacatctg ccagagctgc tttttcagcg gcagagtggc caagggccac 3660

aaaatgcact accccatggt ggagtactgc acccccacca cctccggcga ggatgtgaga 3720

gacttcgcca aagtgctgaa gaataagttc cggaccaagc ggtactttgc caagcacccc 3780

aggatgggct acctgcccgt gcagaccgtg ctggaaggcg acaacatgga gacctga 3837

<210> 3
<211> 3978
<212> DNA
<213> Artificial Sequence

<220>
<223> Copti-Dys3978 gene

<400> 3
atgctttggt gggaggaagt ggaggactgc tacgagcggg aggacgtgca gaagaaaacc 60

ttcaccaagt gggtgaacgc ccagttcagc aagttcggca agcagcacat cgagaacctg 120

ttcagcgacc tgcaggacgg caggcggctg ctggacctcc tggaaggcct gaccggccag 180

aagctgccca aagagaaggg cagcaccagg gtgcacgccc tgaacaacgt gaacaaggcc 240

ctgagggtgc tgcagaacaa caacgtggac ctggtgaaca tcggcagcac cgacatcgtg 300

gacggcaacc acaagctgac cctgggcctg atctggaaca tcatcctgca ctggcaggtc 360

aagaacgtga tgaagaacat catggccggc ctgcagcaga ccaacagcga gaagatcctg 420

ctgtcctggg tgcggcagag caccaggaac taccccccagg tcaacgtgat caacttcacc 480

acctcttgga gcgacggcct ggccctgaac gccctgatcc acagccacag gcccgacctg 540

ttcgactgga acagcgtggt gtgccagcag agcgccaccc agaggctgga acacgccttc 600

aacatcgcca gataccagct gggcatcgag aagctgctgg atcccgagga cgtggacacc 660

acctaccccg acaagaaaag catcctcatg tacatcacca gcctgttcca ggtgctgccc 720

cagcaggtgt ccatcgaggc catccaggaa gtggagatgc tgcccaggcc ccccaaggtc 780

accaaagagg aacacttcca gctgcaccac cagatgcact acagccagca gatcaccgtg 840

agcctggccc agggctacga gaggaccagc agccccaagc ccaggttcaa gagctacgcc 900

tacacccagg ccgcctacgt gaccacctcc gaccccacca ggtccccctt ccccagccag 960

catctcgaag cccccgagga caagagcttc ggcagcagcc tgatggaaag cgaggtgaac 1020

ctggacagat accagaccgc cctggaagaa gtgctgtctt ggctgctgtc cgccgaggac 1080

accctgcagg cccagggcga gatcagcaac gacgtggagg tcgtgaagga ccagttccac 1140

acccacgagg gctacatgat ggacctgacc gcccaccagg gcagagtggg caacatcctg 1200

cagctgggca gcaagctgat cggcaccggc aagctgtccg aggacgagga aaccgaggtg 1260

caggaacaga tgaacctgct gaacagcaga tgggagtgcc tgagggtggc cagcatggaa 1320

aagcagagca acctgcacag ggtgctgatg gatctgcaga accagaagct caaagagctg 1380

aacgactggc tgaccaagac cgaggaaagg acccggaaga tggaagagga acccctgggc 1440

cccgatctcg aagatctgaa gaggcaggtg cagcagcaca aggtgctgca ggaagatctc 1500

gaacaggaac aggtccgggt caacagcctg acccacatgg tcgtggtggt ggacgagagc 1560

agcggcgacc acgccaccgc tgccctggaa gagcagctga aggtgctggg cgacagatgg 1620

gccaacatct gccggtggac cgaggacaga tgggtcctcc tgcaggacca gcccgacctg 1680

gcccctggcc tgacaaccat cggcgccagc cccacccaga ccgtgaccct ggtgacccag 1740

cccgtggtga ccaaagagac cgccatcagc aagctggaaa tgcccagctc cctgatgctg 1800

gaagtgccca cccacaggct cctccagcag ttccccctgg acctggaaaa gttcctggcc 1860

tggctgaccg aggccgagac caccgccaac gtgctgcagg acgccaccag gaaagagagg 1920

ctgctggaag atagcaaggg cgtgaaagag ctgatgaagc agtggcagga cctgcagggg 1980

gagattgagg cccacaccga cgtgtaccac aacctggacg agaacagcca gaaaatcctg 2040

agaagcctgg aaggcagcga cgacgccgtg ctgctgcaga ggcggctgga caacatgaac 2100

ttcaagtgga gcgagctgag gaagaagagc ctgaacatca ggtcccatct ggaagccagc 2160

agcgaccagt ggaagaggct gcacctgagc ctgcaggaac tgctcgtctg gctgcagctg 2220

aaagacgacg agctgtccag gcaggccccc atcggcggcg acttccccgc cgtgcagaaa 2280

cagaacgacg tgcacagggc cttcaagcgg gagctgaaaa ccaaagagcc cgtgatcatg 2340

agcaccctgg aaaccgtgag gatcttcctg accgagcagc ccctggaagg actggaaaag 2400

ctgtaccagg aacccagaga gctgcccccc gaggaacggg cccagaacgt gaccaggctg 2460

ctgagaaagc aggccgagga agtgaacacc gagtgggaga agctgaacct gcactccgcc 2520

gactggcaga ggaagatcga cgagaccctg gaaaggctcc aggaactgca ggaagccacc 2580

gacgagctgg acctgaagct gagacaggcc gaggtgatca agggcagctg gcagcccgtg 2640

ggcgacctgc tgatcgactc cctgcaggat cacctggaaa aagtgaaggc cctgcggggc 2700

gagatcgccc ccctgaaaga gaacgtcagc cacgtcaacg acctggccag gcagctgacc 2760

accctgggca tccagctgtc cccctacaac ctgtccaccc tggaagatct gaacacaagg 2820

tggaagctgc tgcaggtggc cgtggaggac agagtgaggc agctgcacga ggcccacagg 2880

gacttcggcc ctgcctccca gcacttcctg agcaccagcg tgcagggccc ctgggagagg 2940

gccatctccc ccaacaaggt gccctactac atcaaccacg agacccagac cacctgctgg 3000

gaccacccta agatgaccga gctgtaccag tccctggccg acctgaacaa tgtgcggttc 3060

agcgcctacc ggaccgccat gaagctgagg cggctgcaga aagccctgtg cctggatctg 3120

ctgtccctga gcgccgcctg cgacgccctg gaccagcaca acctgaagca gaacgaccag 3180

cccatggata tcctgcagat catcaactgt ctgaccacca tctacgacag gctggaacag 3240

gaacacaaca acctggtcaa cgtgcccctg tgcgtggaca tgtgcctgaa ctggctgctg 3300

aacgtgtacg acaccggcag gaccggccgg atcagggtgc tgtccttcaa gaccggcatc 3360

atcagcctgt gcaaggccca cctggaagat aagtaccgct acctgttcaa gcaggtggcc 3420

agctctaccg gcttctgcga ccagcggagg ctgggcctgc tgctgcacga cagcatccag 3480

atcccccggc agctgggcga ggtggcctcc ttcggcggca gcaacatcga gcccagcgtg 3540

cggagctgct tccagttcgc caacaacaag cccgagatcg aggccgccct gttcctggac 3600

tggatgcggc tggaacccca gagcatggtc tggctgcccg tgctgcacag agtggctgcc 3660

gccgagaccg ccaagcacca ggccaagtgc aacatctgca aagagtgccc catcatcggc 3720

ttcaggtaca gaagcctgaa gcacttcaac tacgacatct gccagagctg tttcttcagc 3780

ggcagggtgg ccaagggcca caaaatgcac taccccatgg tggagtactg cacccccacc 3840

acctccggcg aggacgtgag ggacttcgcc aaggtgctga agaataagtt ccggaccaag 3900

cggtacttcg ccaaacaccc caggatgggc tacctgcccg tgcagaccgt gctggaaggc 3960

gacaacatgg aaacctga 3978

<210> 4
<211> 606
<212> DNA
<213> Artificial Sequence

<220>
<223> hCK promoter

<400> 4
gaattcggta ccccactacg ggtttaggct gcccatgtaa ggaggcaagg cctggggaca 60

cccgagatgc ctggttataa ttaacccaga catgtggctg ccccccccccc ccccaacacc 120

tgctgcctct aaaaataacc ctgtccctgg tggatcccct gcatgcgaag atcttcgaac 180

aaggctgtgg gggactgagg gcaggctgta acaggcttgg gggccagggc ttatacgtgc 240

ctgggactcc caaagtatta ctgttccatg ttcccggcga agggccagct gtcccccgcc 300

agctagactc agcacttagt ttaggaacca gtgagcaagt cagcccttgg ggcagcccat 360

acaaggccat ggggctgggc aagctgcacg cctgggtccg gggtgggcac ggtgcccggg 420

caacgagctg aaagctcatc tgctctcagg ggcccctccc tggggacagc ccctcctggc 480

tagtcacacc ctgtaggctc ctctatataa cccaggggca caggggctgc cctcattcta 540

ccaccacctc cacagcacag acagacactc aggagccagc cagcgtcgag cggccgatcc 600

gccacc 606

<210> 5
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> hCKplus promoter

<400> 5
gaattcggta ccccactacg ggtctaggct gcccatgtaa ggaggcaagg cctggggaca 60

cccgagatgc ctggttataa ttaaccccaa cacctgctgc ccccccccccc ccaacacctg 120

ctgcctctaa aaataaccct gtccctggtg gatcccctgc atgccccact acgggtttag 180

gctgcccatg taaggaggca aggcctgggg acacccgaga tgcctggtta taattaaccc 240

agacatgtgg ctgccccccc ccccccccaac acctgctgcc tctaaaaata accctgtccc 300

tggtggatcc cctgcatgcg aagatcttcg aacaaggctg tgggggactg agggcaggct 360

gtaacaggct tgggggccag ggcttatacg tgcctgggac tcccaaagta ttactgttcc 420

atgttcccgg cgaagggcca gctgtccccc gccagctaga ctcagcactt agtttaggaa 480

ccagtgagca agtcagccct tggggcagcc catacaaggc catggggctg ggcaagctgc 540

acgcctgggt ccggggtggg cacggtgccc gggcaacgag ctgaaagctc atctgctctc 600

aggggcccct ccctggggac agcccctcct ggctagtcac accctgtagg ctcctctata 660

taacccaggg gcacaggggc tgccctcatt ctaccaccac ctccacagca cagacagaca 720

ctcaggagcc agccagcgtc gagcggccga tccgccacc 759

<210> 6
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polyA

<400> 6
tgaggagctc gagaggccta ataaagagct cagatgcatc gatcagagtg tgttggtttt 60

ttgtgtg 67

<210> 7
<211> 1325
<212> PRT
<213> Artificial Sequence

<220>
<223> Dys3978 protein

<400> 7

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val

```
1               5                   10                  15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
            20                  25                  30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
        35                  40                  45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
    50                  55                  60

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

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
                85                  90                  95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
            100                 105                 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
        115                 120                 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
    130                 135                 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145                 150                 155                 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
                165                 170                 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
            180                 185                 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
        195                 200                 205
```

```
Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
    210                 215                 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225                 230                 235                 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
                245                 250                 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
            260                 265                 270

His Tyr Ser Gln Gln Ile Thr Val Ser Leu Ala Gln Gly Tyr Glu Arg
        275                 280                 285

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
    290                 295                 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305                 310                 315                 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
                325                 330                 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
            340                 345                 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
        355                 360                 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
    370                 375                 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385                 390                 395                 400
```

```
Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
                405                 410                 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
            420                 425                 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Arg Val
        435                 440                 445

Leu Met Asp Leu Gln Asn Gln Lys Leu Lys Glu Leu Asn Asp Trp Leu
    450                 455                 460

Thr Lys Thr Glu Glu Arg Thr Arg Lys Met Glu Glu Glu Pro Leu Gly
465                 470                 475                 480

Pro Asp Leu Glu Asp Leu Lys Arg Gln Val Gln Gln His Lys Val Leu
                485                 490                 495

Gln Glu Asp Leu Glu Gln Glu Gln Val Arg Val Asn Ser Leu Thr His
            500                 505                 510

Met Val Val Val Val Asp Glu Ser Ser Gly Asp His Ala Thr Ala Ala
        515                 520                 525

Leu Glu Glu Gln Leu Lys Val Leu Gly Asp Arg Trp Ala Asn Ile Cys
    530                 535                 540

Arg Trp Thr Glu Asp Arg Trp Val Leu Leu Gln Asp Gln Pro Asp Leu
545                 550                 555                 560

Ala Pro Gly Leu Thr Thr Ile Gly Ala Ser Pro Thr Gln Thr Val Thr
                565                 570                 575

Leu Val Thr Gln Pro Val Val Thr Lys Glu Thr Ala Ile Ser Lys Leu
            580                 585                 590
```

```
Glu Met Pro Ser Ser Leu Met Leu Glu Val Pro Thr His Arg Leu Leu
        595                 600                 605

Gln Gln Phe Pro Leu Asp Leu Glu Lys Phe Leu Ala Trp Leu Thr Glu
    610                 615                 620

Ala Glu Thr Thr Ala Asn Val Leu Gln Asp Ala Thr Arg Lys Glu Arg
625                 630                 635                 640

Leu Leu Glu Asp Ser Lys Gly Val Lys Glu Leu Met Lys Gln Trp Gln
                645                 650                 655

Asp Leu Gln Gly Glu Ile Glu Ala His Thr Asp Val Tyr His Asn Leu
            660                 665                 670

Asp Glu Asn Ser Gln Lys Ile Leu Arg Ser Leu Glu Gly Ser Asp Asp
        675                 680                 685

Ala Val Leu Leu Gln Arg Arg Leu Asp Asn Met Asn Phe Lys Trp Ser
    690                 695                 700

Glu Leu Arg Lys Lys Ser Leu Asn Ile Arg Ser His Leu Glu Ala Ser
705                 710                 715                 720

Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu Leu Val
                725                 730                 735

Trp Leu Gln Leu Lys Asp Asp Glu Leu Ser Arg Gln Ala Pro Ile Gly
            740                 745                 750

Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala Phe
        755                 760                 765

Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu Glu
    770                 775                 780

Thr Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly Leu Glu Lys
```

785 790 795 800

Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln Asn
805 810 815

Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr Glu Trp
820 825 830

Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile Asp Glu
835 840 845

Thr Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu Leu Asp
850 855 860

Leu Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln Pro Val
865 870 875 880

Gly Asp Leu Leu Ile Asp Ser Leu Gln Asp His Leu Glu Lys Val Lys
885 890 895

Ala Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser His Val
900 905 910

Asn Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu Ser Pro
915 920 925

Tyr Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp Lys Leu Leu
930 935 940

Gln Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu Ala His Arg
945 950 955 960

Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser Val Gln Gly
965 970 975

Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr Tyr Ile Asn
980 985 990

```
His Glu Thr Gln Thr Thr Cys Trp  Asp His Pro Lys Met  Thr Glu Leu
        995                 1000                1005

Tyr Gln  Ser Leu Ala Asp Leu  Asn Asn Val Arg Phe  Ser Ala Tyr
    1010                1015                1020

Arg Thr  Ala Met Lys Leu Arg  Arg Leu Gln Lys Ala  Leu Cys Leu
    1025                1030                1035

Asp Leu  Leu Ser Leu Ser Ala  Ala Cys Asp Ala Leu  Asp Gln His
    1040                1045                1050

Asn Leu  Lys Gln Asn Asp Gln  Pro Met Asp Ile Leu  Gln Ile Ile
    1055                1060                1065

Asn Cys  Leu Thr Thr Ile Tyr  Asp Arg Leu Glu Gln  Glu His Asn
    1070                1075                1080

Asn Leu  Val Asn Val Pro Leu  Cys Val Asp Met Cys  Leu Asn Trp
    1085                1090                1095

Leu Leu  Asn Val Tyr Asp Thr  Gly Arg Thr Gly Arg  Ile Arg Val
    1100                1105                1110

Leu Ser  Phe Lys Thr Gly Ile  Ile Ser Leu Cys Lys  Ala His Leu
    1115                1120                1125

Glu Asp  Lys Tyr Arg Tyr Leu  Phe Lys Gln Val Ala  Ser Ser Thr
    1130                1135                1140

Gly Phe  Cys Asp Gln Arg Arg  Leu Gly Leu Leu Leu  His Asp Ser
    1145                1150                1155

Ile Gln  Ile Pro Arg Gln Leu  Gly Glu Val Ala Ser  Phe Gly Gly
    1160                1165                1170
```

```
Ser Asn  Ile Glu Pro Ser Val  Arg Ser Cys Phe Gln  Phe Ala Asn
    1175                 1180                 1185

Asn Lys  Pro Glu Ile Glu Ala  Ala Leu Phe Leu Asp  Trp Met Arg
    1190                 1195                 1200

Leu Glu  Pro Gln Ser Met Val  Trp Leu Pro Val Leu  His Arg Val
    1205                 1210                 1215

Ala Ala  Ala Glu Thr Ala Lys  His Gln Ala Lys Cys  Asn Ile Cys
    1220                 1225                 1230

Lys Glu  Cys Pro Ile Ile Gly  Phe Arg Tyr Arg Ser  Leu Lys His
    1235                 1240                 1245

Phe Asn  Tyr Asp Ile Cys Gln  Ser Cys Phe Phe Ser  Gly Arg Val
    1250                 1255                 1260

Ala Lys  Gly His Lys Met His  Tyr Pro Met Val Glu  Tyr Cys Thr
    1265                 1270                 1275

Pro Thr  Thr Ser Gly Glu Asp  Val Arg Asp Phe Ala  Lys Val Leu
    1280                 1285                 1290

Lys Asn  Lys Phe Arg Thr Lys  Arg Tyr Phe Ala Lys  His Pro Arg
    1295                 1300                 1305

Met Gly  Tyr Leu Pro Val Gln  Thr Val Leu Glu Gly  Asp Asn Met
    1310                 1315                 1320

Glu Thr
    1325
```

<210> 8
<211> 1278
<212> PRT
<213> Artificial Sequence

<220>
<223> Dys3837 protein

<400> 8

```
Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1               5                  10                  15


Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
            20                  25                  30


Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
        35                  40                  45


Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
    50                  55                  60


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


Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
                85                  90                  95


Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
            100                 105                 110


Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
        115                 120                 125


Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
    130                 135                 140


Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145                 150                 155                 160


Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
                165                 170                 175
```

```
Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
            180                 185                 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
        195                 200                 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
    210                 215                 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225                 230                 235                 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
                245                 250                 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
            260                 265                 270

His Tyr Ser Gln Gln Ile Thr Val Ser Leu Ala Gln Gly Tyr Glu Arg
        275                 280                 285

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
    290                 295                 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305                 310                 315                 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
                325                 330                 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
            340                 345                 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
        355                 360                 365
```

```
Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
    370                 375                 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385                 390                 395                 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
                405                 410                 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
            420                 425                 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Arg Val
        435                 440                 445

Leu Met Asp Leu Gln Asn Gln Lys Leu Lys Glu Leu Asn Asp Trp Leu
    450                 455                 460

Thr Lys Thr Glu Glu Arg Thr Arg Lys Met Glu Glu Glu Pro Leu Gly
465                 470                 475                 480

Pro Asp Leu Glu Asp Leu Lys Arg Gln Val Gln Gln His Lys Val Leu
                485                 490                 495

Gln Glu Asp Leu Glu Gln Glu Gln Val Arg Val Asn Ser Leu Thr His
            500                 505                 510

Met Val Val Val Val Asp Glu Ser Ser Gly Asp His Ala Thr Ala Ala
        515                 520                 525

Leu Glu Glu Gln Leu Lys Val Leu Gly Asp Arg Trp Ala Asn Ile Cys
    530                 535                 540

Arg Trp Thr Glu Asp Arg Trp Val Leu Leu Gln Asp Thr His Arg Leu
545                 550                 555                 560

Leu Gln Gln Phe Pro Leu Asp Leu Glu Lys Phe Leu Ala Trp Leu Thr
```

565 570 575

Glu Ala Glu Thr Thr Ala Asn Val Leu Gln Asp Ala Thr Arg Lys Glu
580 585 590

Arg Leu Leu Glu Asp Ser Lys Gly Val Lys Glu Leu Met Lys Gln Trp
595 600 605

Gln Asp Leu Gln Gly Glu Ile Glu Ala His Thr Asp Val Tyr His Asn
610 615 620

Leu Asp Glu Asn Ser Gln Lys Ile Leu Arg Ser Leu Glu Gly Ser Asp
625 630 635 640

Asp Ala Val Leu Leu Gln Arg Arg Leu Asp Asn Met Asn Phe Lys Trp
645 650 655

Ser Glu Leu Arg Lys Lys Ser Leu Asn Ile Arg Ser His Leu Glu Ala
660 665 670

Ser Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu Leu
675 680 685

Val Trp Leu Gln Leu Lys Asp Asp Glu Leu Ser Arg Gln Ala Pro Ile
690 695 700

Gly Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala
705 710 715 720

Phe Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu
725 730 735

Glu Thr Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly Leu Glu
740 745 750

Lys Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln
755 760 765

```
Asn Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr Glu
    770                 775                 780

Trp Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile Asp
785                 790                 795                 800

Glu Thr Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu Leu
                805                 810                 815

Asp Leu Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln Pro
            820                 825                 830

Val Gly Asp Leu Leu Ile Asp Ser Leu Gln Asp His Leu Glu Lys Val
        835                 840                 845

Lys Ala Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser His
    850                 855                 860

Val Asn Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu Ser
865                 870                 875                 880

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

Leu Gln Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu Ala His
            900                 905                 910

Arg Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser Val Gln
        915                 920                 925

Gly Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr Tyr Ile
    930                 935                 940

Asn His Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met Thr Glu
945                 950                 955                 960
```

```
Leu Tyr Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser Ala Tyr
               965                 970                 975

Arg Thr Ala Met Lys Leu Arg Arg Leu Gln Lys Ala Leu Cys Leu Asp
           980                 985                 990

Leu Leu Ser Leu Ser Ala Ala Cys  Asp Ala Leu Asp Gln  His Asn Leu
        995                 1000                1005

Lys Gln  Asn Asp Gln Pro Met  Asp Ile Leu Gln Ile  Ile Asn Cys
    1010                1015                1020

Leu Thr  Thr Ile Tyr Asp Arg  Leu Glu Gln Glu His  Asn Asn Leu
    1025                1030                1035

Val Asn  Val Pro Leu Cys Val  Asp Met Cys Leu Asn  Trp Leu Leu
    1040                1045                1050

Asn Val  Tyr Asp Thr Gly Arg  Thr Gly Arg Ile Arg  Val Leu Ser
    1055                1060                1065

Phe Lys  Thr Gly Ile Ile Ser  Leu Cys Lys Ala His  Leu Glu Asp
    1070                1075                1080

Lys Tyr  Arg Tyr Leu Phe Lys  Gln Val Ala Ser Ser  Thr Gly Phe
    1085                1090                1095

Cys Asp  Gln Arg Arg Leu Gly  Leu Leu Leu His Asp  Ser Ile Gln
    1100                1105                1110

Ile Pro  Arg Gln Leu Gly Glu  Val Ala Ser Phe Gly  Gly Ser Asn
    1115                1120                1125

Ile Glu  Pro Ser Val Arg Ser  Cys Phe Gln Phe Ala  Asn Asn Lys
    1130                1135                1140
```

Pro Glu Ile Glu Ala Ala Leu Phe Leu Asp Trp Met Arg Leu Glu
1145 1150 1155

Pro Gln Ser Met Val Trp Leu Pro Val Leu His Arg Val Ala Ala
1160 1165 1170

Ala Glu Thr Ala Lys His Gln Ala Lys Cys Asn Ile Cys Lys Glu
1175 1180 1185

Cys Pro Ile Ile Gly Phe Arg Tyr Arg Ser Leu Lys His Phe Asn
1190 1195 1200

Tyr Asp Ile Cys Gln Ser Cys Phe Phe Ser Gly Arg Val Ala Lys
1205 1210 1215

Gly His Lys Met His Tyr Pro Met Val Glu Tyr Cys Thr Pro Thr
1220 1225 1230

Thr Ser Gly Glu Asp Val Arg Asp Phe Ala Lys Val Leu Lys Asn
1235 1240 1245

Lys Phe Arg Thr Lys Arg Tyr Phe Ala Lys His Pro Arg Met Gly
1250 1255 1260

Tyr Leu Pro Val Gln Thr Val Leu Glu Gly Asp Asn Met Glu Thr
1265 1270 1275

<210> 9
<211> 4953
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV vector genome with Hopti-Dys3978 gene

<400> 9
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctagatc tgaattcggt accccactac gggtttaggc 180

tgcccatgta aggaggcaag gcctggggac acccgagatg cctggttata attaacccag 240

acatgtggct gccccccccc cccccaacac ctgctgcctc taaaaataac cctgtccctg 300

gtggatcccc tgcatgcgaa gatcttcgaa caaggctgtg ggggactgag ggcaggctgt 360

aacaggcttg ggggccaggg cttatacgtg cctgggactc ccaaagtatt actgttccat 420

gttcccggcg aagggccagc tgtcccccgc cagctagact cagcacttag tttaggaacc 480

agtgagcaag tcagcccttg gggcagccca tacaaggcca tggggctggg caagctgcac 540

gcctgggtcc ggggtgggca cggtgcccgg gcaacgagct gaaagctcat ctgctctcag 600

gggcccctcc ctggggacag cccctcctgg ctagtcacac cctgtaggct cctctatata 660

acccaggggc acaggggctg ccctcattct accaccacct ccacagcaca gacagacact 720

caggagccag ccagcgtcga gcggccgatc cgccaccatg ctttggtggg aggaagtgga 780

ggactgctac gagagagagg acgtgcagaa gaaaaccttc accaagtggg tgaacgccca 840

gttcagcaag ttcggcaagc agcacatcga gaacctgttc agcgacctgc aggatggcag 900

gagactgctg gacctgctgg agggcctgac cggccagaag ctgcccaagg agaagggcag 960

caccagagtg cacgccctga acaacgtgaa caaggccctg agagtgctgc agaacaacaa 1020

cgtggacctg gtgaacatcg gcagcaccga catcgtggac ggcaaccaca agctgaccct 1080

gggcctgatc tggaacatca tcctgcactg gcaggtgaag aacgtgatga agaacatcat 1140

ggccggcctg cagcagacca acagcgagaa gatcctgctg agctgggtga ggcagagcac 1200

cagaaactac ccccaggtga acgtgatcaa cttcaccacc tcctggagcg acggcctggc 1260

cctgaacgcc ctgatccaca gccacagacc cgacctgttc gactggaaca gcgtggtgtg 1320

tcagcagagc gccacccaga gactggagca cgccttcaac atcgccagat accagctggg 1380

catcgagaag ctgctggacc ccgaggacgt ggacaccacc taccccgaca agaaaagcat 1440

cctcatgtac attaccagcc tgttccaggt gctgccccag caggtgtcca tcgaggccat 1500

ccaggaagtg gaaatgctgc ccaggccccc caaagtgacc aaggaggagc acttccagct 1560

gcaccaccag atgcactaca gccagcagat cacagtgagc ctggcccagg gctatgagag 1620

aaccagcagc cccaagccca gattcaagag ctacgcctac acccaggccg cctacgtgac 1680

cacctccgac cccaccagaa gccccttccc cagccagcac ctggaggccc ccgaggacaa 1740

gagcttcggc agcagcctga tggagagcga agtgaacctg gacagatacc agaccgccct 1800

ggaggaagtg ctgtcctggc tgctgagcgc cgaggacacc ctgcaggccc agggcgagat 1860

cagcaacgac gtggaagtgg tgaaggacca gttccacacc cacgagggct acatgatgga 1920

tctgaccgcc caccagggca gagtgggcaa tatcctgcag ctgggcagca agctgatcgg 1980

caccggcaag ctgagcgagg acgaggagac cgaagtgcag gagcagatga acctgctgaa 2040

cagcagatgg gagtgcctga gagtggccag catggagaag cagagcaacc tgcacagagt 2100

gctgatggac ctgcagaacc agaagctgaa ggagctgaac gactggctga ccaagaccga 2160

ggagcggacc agaaagatgg aggaggagcc cctgggcccc gacctggagg acctgaagag 2220

acaggtgcag cagcacaaag tgctgcagga ggacctggag caggagcagg tgcgcgtgaa 2280

cagcctgacc cacatggtgg tggtcgtgga cgagagcagc ggcgaccacg ccacagccgc 2340

cctggaagag cagctgaaag tgctgggcga cagatgggcc aatatttgta ggtggaccga 2400

ggacagatgg gtgctgctgc aggaccagcc cgacctggcc cctggcctga ccaccatcgg 2460

cgccagcccc acccagaccg tgaccctggt gacccagccc gtggtgacaa aggagaccgc 2520

catcagcaag ctggagatgc ccagctccct gatgctggaa gtgcccaccc accgcctgct 2580

ccagcagttc cccctggacc tggagaagtt cctggcctgg ctgaccgagg ccgaaaccac 2640

cgccaatgtg ctccaggacg ccactagaaa ggagaggctg ctggaggaca gcaagggcgt 2700

gaaagagctg atgaagcagt ggcaggatct gcagggcgaa atcgaggccc acaccgacgt 2760

gtaccacaac ctggacgaga acagccagaa gattctgagg agcctggagg gcagcgacga 2820

cgccgtcctg ctccagagga ggctggacaa catgaacttc aagtggagcg agctgcggaa 2880

gaagagcctg aacatccgga gccacctgga agccagcagc gaccagtgga agagactgca 2940

cctgagcctg caggagctgc tggtgtggct gcagctgaag gacgacgagc tgagcagaca 3000

ggcccccatc ggcggcgact tccccgccgt gcagaagcag aacgacgtgc accgggcctt 3060

caagagggag ctgaaaacca aggaacccgt gatcatgagc accctggaga cagtgcggat 3120

cttcctgacc gagcagcccc tggagggact ggagaagctg taccaggagc ccagagagct 3180

gccccccgag gagagagccc agaacgtgac caggctgctg agaaagcagg ccgaggaagt 3240

gaataccgag tgggagaagc tgaatctgca cagcgccgac tggcagagaa agatcgacga 3300

gaccctggag agactccagg aactgcagga agccaccgac gagctggacc tgaagctgag 3360

acaggccgaa gtgatcaagg gcagctggca gcctgtgggc gatctgctga tcgactccct 3420

gcaggatcac ctggagaaag tgaaggccct gcggggcgag atcgcccccc tgaaggagaa 3480

tgtgagccac gtgaacgacc tggccagaca gctgaccacc ctgggcatcc agctgagccc 3540

ctacaacctg agcacactgg aggatctgaa cacccggtgg aaactgctgc aggtggccgt 3600

ggaggataga gtgaggcagc tgcacgaagc ccacagagac ttcggccctg cctcccagca 3660

cttcctgagc accagcgtgc agggcccctg ggagagagcc atctccccca acaaagtgcc 3720

ctactacatc aaccacgaga cccagaccac ctgctgggac caccctaaga tgaccgagct 3780

gtatcagagc ctggccgacc tgaacaatgt gcggttcagc gcctacagaa ccgccatgaa 3840

gctgcggaga ctgcagaagg ccctgtgcct ggatctgctg agcctgagcg ccgcctgcga 3900

cgccctggac cagcacaacc tgaagcagaa tgaccagccc atggacatcc tgcagatcat 3960

caactgcctg accacaatct acgaccggct ggaacaggag cacaacaacc tggtgaatgt 4020

gcccctgtgc gtggacatgt gcctgaattg gctgctgaac gtgtacgaca ccggcaggac 4080

cggcagaatc cgcgtgctga gcttcaagac cggcatcatc agcctgtgca aggcccacct 4140

ggaggataag taccgctacc tgttcaagca ggtggccagc agcaccggct tctgcgatca 4200

gaggagactg ggcctgctgc tgcacgatag catccagatc cctaggcagc tgggcgaagt 4260

ggccagcttt ggcggcagca acatcgagcc ctctgtgagg agctgcttcc agttcgccaa 4320

caacaagccc gagatcgagg ccgccctgtt cctggactgg atgaggctgg agcctcagag 4380

catggtgtgg ctgcctgtgc tgcacagagt ggccgccgcc gagaccgcca agcaccaggc 4440

caagtgcaat atctgcaagg agtgccccat catcggcttc cggtacagga gcctgaagca 4500

cttcaactac gacatctgcc agagctgctt tttcagcggc agagtggcca agggccacaa 4560

aatgcactac cccatggtgg agtactgcac ccccaccacc tccggcgagg atgtgagaga 4620

cttcgccaaa gtgctgaaga ataagttccg gaccaagcgg tactttgcca agcaccccag 4680

gatgggctac ctgcccgtgc agaccgtgct ggaaggcgac aacatggaga cctgatgagg 4740

agctcgagag gcctaataaa gagctcagat gcatcgatca gagtgtgttg gttttttgtg 4800

tgagatctag gaacccctag tgatggagtt ggccactccc tctctgcgcg ctcgctcgct 4860

cactgaggcc gcccgggcaa agcccgggcg tcgggcgacc tttggtcgcc cggcctcagt 4920

gagcgagcga gcgcgcagag agggagtggc caa 4953

<210> 10
<211> 4812
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV vector genome with Hopti-Dys3837 gene

<400> 10
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctagatc tgaattcggt accccactac gggtttaggc 180

tgcccatgta aggaggcaag gcctggggac acccgagatg cctggttata attaacccag 240

acatgtggct gccccccccc cccccaacac ctgctgcctc taaaaataac cctgtccctg 300

gtggatcccc tgcatgcgaa gatcttcgaa caaggctgtg ggggactgag ggcaggctgt 360

aacaggcttg ggggccaggg cttatacgtg cctgggactc ccaaagtatt actgttccat 420

gttcccggcg aagggccagc tgtcccccgc cagctagact cagcacttag tttaggaacc 480

agtgagcaag tcagcccttg gggcagccca tacaaggcca tggggctggg caagctgcac 540

gcctgggtcc ggggtgggca cggtgcccgg gcaacgagct gaaagctcat ctgctctcag 600

gggcccctcc ctggggacag cccctcctgg ctagtcacac cctgtaggct cctctatata 660

acccaggggc acaggggctg ccctcattct accaccacct ccacagcaca gacagacact 720

caggagccag ccagcgtcga gcggccgatc cgccaccatg ctttggtggg aggaagtgga 780

ggactgctac gagagagagg acgtgcagaa gaaaaccttc accaagtggg tgaacgccca 840

gttcagcaag ttcggcaagc agcacatcga gaacctgttc agcgacctgc aggatggcag 900

gagactgctg gacctgctgg agggcctgac cggccagaag ctgcccaagg agaagggcag 960

caccagagtg cacgccctga acaacgtgaa caaggccctg agagtgctgc agaacaacaa 1020

cgtggacctg gtgaacatcg gcagcaccga catcgtggac ggcaaccaca agctgaccct 1080

gggcctgatc tggaacatca tcctgcactg gcaggtgaag aacgtgatga agaacatcat 1140

ggccggcctg cagcagacca acagcgagaa gatcctgctg agctgggtga ggcagagcac 1200

cagaaactac ccccaggtga acgtgatcaa cttcaccacc tcctggagcg acggcctggc 1260

cctgaacgcc ctgatccaca gccacagacc cgacctgttc gactggaaca gcgtggtgtg 1320

tcagcagagc gccacccaga gactggagca cgccttcaac atcgccagat accagctggg 1380

catcgagaag ctgctggacc ccgaggacgt ggacaccacc taccccgaca agaaaagcat 1440

cctcatgtac attaccagcc tgttccaggt gctgccccag caggtgtcca tcgaggccat 1500

ccaggaagtg gaaatgctgc ccaggccccc caaagtgacc aaggaggagc acttccagct 1560

gcaccaccag atgcactaca gccagcagat cacagtgagc ctggcccagg gctatgagag 1620

aaccagcagc cccaagccca gattcaagag ctacgcctac acccaggccg cctacgtgac 1680

cacctccgac cccaccagaa gccccttccc cagccagcac ctggaggccc ccgaggacaa 1740

gagcttcggc agcagcctga tggagagcga agtgaacctg gacagatacc agaccgccct 1800

ggaggaagtg ctgtcctggc tgctgagcgc cgaggacacc ctgcaggccc agggcgagat 1860

cagcaacgac gtggaagtgg tgaaggacca gttccacacc cacgagggct acatgatgga 1920

tctgaccgcc caccagggca gagtgggcaa tatcctgcag ctgggcagca agctgatcgg 1980

caccggcaag ctgagcgagg acgaggagac cgaagtgcag gagcagatga acctgctgaa 2040

cagcagatgg gagtgcctga gagtggccag catggagaag cagagcaacc tgcacagagt 2100

gctgatggac ctgcagaacc agaagctgaa ggagctgaac gactggctga ccaagaccga 2160

ggagcggacc agaaagatgg aggaggagcc cctgggcccc gacctggagg acctgaagag 2220

acaggtgcag cagcacaaag tgctgcagga ggacctggag caggagcagg tgcgcgtgaa 2280

cagcctgacc cacatggtgg tggtcgtgga cgagagcagc ggcgaccacg ccacagccgc 2340

cctggaagag cagctgaaag tgctgggcga cagatgggcc aatatttgta ggtggaccga 2400

ggacagatgg gtgctgctgc aggacaccca ccgcctgctc cagcagttcc ccctggacct 2460

ggagaagttc ctggcctggc tgaccgaggc cgaaaccacc gccaatgtgc tccaggacgc 2520

cactagaaag gagaggctgc tggaggacag caagggcgtg aaagagctga tgaagcagtg 2580

gcaggatctg cagggcgaaa tcgaggccca caccgacgtg taccacaacc tggacgagaa 2640

cagccagaag attctgagga gcctggaggg cagcgacgac gccgtcctgc tccagaggag 2700

gctggacaac atgaacttca agtggagcga gctgcggaag aagagcctga acatccggag 2760

ccacctggaa gccagcagcg accagtggaa gagactgcac ctgagcctgc aggagctgct 2820

ggtgtggctg cagctgaagg acgacgagct gagcagacag gcccccatcg gcggcgactt 2880

ccccgccgtg cagaagcaga acgacgtgca ccgggccttc aagagggagc tgaaaaccaa 2940

ggaacccgtg atcatgagca ccctggagac agtgcggatc ttcctgaccg agcagcccct 3000

ggagggactg gagaagctgt accaggagcc cagagagctg ccccccgagg agagagccca 3060

gaacgtgacc aggctgctga gaaagcaggc cgaggaagtg aataccgagt gggagaagct 3120

gaatctgcac agcgccgact ggcagagaaa gatcgacgag accctggaga gactccagga 3180

actgcaggaa gccaccgacg agctggacct gaagctgaga caggccgaag tgatcaaggg 3240

cagctggcag cctgtgggcg atctgctgat cgactccctg caggatcacc tggagaaagt 3300

gaaggccctg cggggcgaga tcgcccccct gaaggagaat gtgagccacg tgaacgacct 3360

ggccagacag ctgaccaccc tgggcatcca gctgagcccc tacaacctga gcacactgga 3420

ggatctgaac acccggtgga aactgctgca ggtggccgtg gaggatagag tgaggcagct 3480

gcacgaagcc cacagagact tcggccctgc ctcccagcac ttcctgagca ccagcgtgca 3540

gggcccctgg gagagagcca tctcccccaa caaagtgccc tactacatca accacgagac 3600

ccagaccacc tgctgggacc accctaagat gaccgagctg tatcagagcc tggccgacct 3660

gaacaatgtg cggttcagcg cctacagaac cgccatgaag ctgcggagac tgcagaaggc 3720

cctgtgcctg gatctgctga gcctgagcgc cgcctgcgac gccctggacc agcacaacct 3780

gaagcagaat gaccagccca tggacatcct gcagatcatc aactgcctga ccacaatcta 3840

cgaccggctg gaacaggagc acaacaacct ggtgaatgtg cccctgtgcg tggacatgtg 3900

cctgaattgg ctgctgaacg tgtacgacac cggcaggacc ggcagaatcc gcgtgctgag 3960

cttcaagacc ggcatcatca gcctgtgcaa ggcccacctg gaggataagt accgctacct 4020

gttcaagcag gtggccagca gcaccggctt ctgcgatcag aggagactgg gcctgctgct 4080

gcacgatagc atccagatcc ctaggcagct gggcgaagtg gccagctttg gcggcagcaa 4140

catcgagccc tctgtgagga gctgcttcca gttcgccaac aacaagcccg agatcgaggc 4200

cgccctgttc ctggactgga tgaggctgga gcctcagagc atggtgtggc tgcctgtgct 4260

gcacagagtg gccgccgccg agaccgccaa gcaccaggcc aagtgcaata tctgcaagga 4320

gtgccccatc atcggcttcc ggtacaggag cctgaagcac ttcaactacg acatctgcca 4380

gagctgcttt ttcagcggca gagtggccaa gggccacaaa atgcactacc ccatggtgga 4440

gtactgcacc cccaccacct ccggcgagga tgtgagagac ttcgccaaag tgctgaagaa 4500

taagttccgg accaagcggt actttgccaa gcaccccagg atgggctacc tgcccgtgca 4560

gaccgtgctg gaaggcgaca acatggagac ctgatgagga gctcgagagg cctaataaag 4620

agctcagatg catcgatcag agtgtgttgg ttttttgtgt gagatctagg aacccctagt 4680

gatggagttg gccactccct ctctgcgcgc tcgctcgctc actgaggccg cccgggcaaa 4740

gcccgggcgt cgggcgacct ttggtcgccc ggcctcagtg agcgagcgag cgcgcagaga 4800

gggagtggcc aa 4812

<210> 11
<211> 4965
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV vector genome with Hopti-Dys3837 gene

<400> 11

ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctagatc tgaattcggt accccactac gggtctaggc 180

tgcccatgta aggaggcaag gcctggggac acccgagatg cctggttata attaacccca 240

acacctgctg ccccccccccc cccaacacct gctgcctcta aaaataaccc tgtccctggt 300

ggatcccctg catgccccac tacgggttta ggctgcccat gtaaggaggc aaggcctggg 360

gacacccgag atgcctggtt ataattaacc cagacatgtg gctgcccccc ccccccccaa 420

cacctgctgc ctctaaaaat aaccctgtcc ctggtggatc ccctgcatgc gaagatcttc 480

gaacaaggct gtgggggact gagggcaggc tgtaacaggc ttgggggcca gggcttatac 540

gtgcctggga ctcccaaagt attactgttc catgttcccg gcgaagggcc agctgtcccc 600

cgccagctag actcagcact tagtttagga accagtgagc aagtcagccc ttggggcagc 660

ccatacaagg ccatggggct gggcaagctg cacgcctggg tccggggtgg gcacggtgcc 720

cgggcaacga gctgaaagct catctgctct caggggcccc tccctgggga cagcccctcc 780

tggctagtca caccctgtag gctcctctat ataacccagg ggcacagggg ctgccctcat 840

tctaccacca cctccacagc acagacagac actcaggagc cagccagcgt cgagcggccg 900

atccgccacc atgctttggt gggaggaagt ggaggactgc tacgagagag aggacgtgca 960

gaagaaaacc ttcaccaagt gggtgaacgc ccagttcagc aagttcggca agcagcacat 1020

cgagaacctg ttcagcgacc tgcaggatgg caggagactg ctggacctgc tggagggcct 1080

gaccggccag aagctgccca aggagaaggg cagcaccaga gtgcacgccc tgaacaacgt 1140

gaacaaggcc ctgagagtgc tgcagaacaa caacgtggac ctggtgaaca tcggcagcac 1200

cgacatcgtg gacggcaacc acaagctgac cctgggcctg atctggaaca tcatcctgca 1260

ctggcaggtg aagaacgtga tgaagaacat catggccggc ctgcagcaga ccaacagcga 1320

gaagatcctg ctgagctggg tgaggcagag caccagaaac tacccccagg tgaacgtgat 1380

caacttcacc acctcctgga gcgacggcct ggccctgaac gccctgatcc acagccacag 1440

acccgacctg ttcgactgga acagcgtggt gtgtcagcag agcgccaccc agagactgga 1500

gcacgccttc aacatcgcca gataccagct gggcatcgag aagctgctgg accccgagga 1560

cgtggacacc acctaccccg acaagaaaag catcctcatg tacattacca gcctgttcca 1620

ggtgctgccc cagcaggtgt ccatcgaggc catccaggaa gtggaaatgc tgcccaggcc 1680

ccccaaagtg accaaggagg agcacttcca gctgcaccac cagatgcact acagccagca 1740

gatcacagtg agcctggccc agggctatga gagaaccagc agccccaagc ccagattcaa 1800

gagctacgcc tacacccagg ccgcctacgt gaccacctcc gaccccacca gaagcccctt 1860

ccccagccag cacctggagg cccccgagga caagagcttc ggcagcagcc tgatggagag 1920

cgaagtgaac ctggacagat accagaccgc cctggaggaa gtgctgtcct ggctgctgag 1980

cgccgaggac accctgcagg cccagggcga gatcagcaac gacgtggaag tggtgaagga 2040

ccagttccac acccacgagg gctacatgat ggatctgacc gcccaccagg gcagagtggg 2100

caatatcctg cagctgggca gcaagctgat cggcaccggc aagctgagcg aggacgagga 2160

gaccgaagtg caggagcaga tgaacctgct gaacagcaga tgggagtgcc tgagagtggc 2220

cagcatggag aagcagagca acctgcacag agtgctgatg gacctgcaga accagaagct 2280

gaaggagctg aacgactggc tgaccaagac cgaggagcgg accagaaaga tggaggagga 2340

gcccctgggc cccgacctgg aggacctgaa gagacaggtg cagcagcaca aagtgctgca 2400

ggaggacctg gagcaggagc aggtgcgcgt gaacagcctg acccacatgg tggtggtcgt 2460

ggacgagagc agcggcgacc acgccacagc cgccctggaa gagcagctga aagtgctggg 2520

cgacagatgg gccaatattt gtaggtggac cgaggacaga tgggtgctgc tgcaggacac 2580

ccaccgcctg ctccagcagt tccccctgga cctggagaag ttcctggcct ggctgaccga 2640

ggccgaaacc accgccaatg tgctccagga cgccactaga aaggagaggc tgctggagga 2700

cagcaagggc gtgaaagagc tgatgaagca gtggcaggat ctgcagggcg aaatcgaggc 2760

ccacaccgac gtgtaccaca acctggacga gaacagccag aagattctga ggagcctgga 2820

gggcagcgac gacgccgtcc tgctccagag gaggctggac aacatgaact tcaagtggag 2880

cgagctgcgg aagaagagcc tgaacatccg gagccacctg gaagccagca gcgaccagtg 2940

gaagagactg cacctgagcc tgcaggagct gctggtgtgg ctgcagctga aggacgacga 3000

gctgagcaga caggccccca tcggcggcga cttccccgcc gtgcagaagc agaacgacgt 3060

gcaccgggcc ttcaagaggg agctgaaaac caaggaaccc gtgatcatga gcaccctgga 3120

gacagtgcgg atcttcctga ccgagcagcc cctggaggga ctggagaagc tgtaccagga 3180

gcccagagag ctgccccccg aggagagagc ccagaacgtg accaggctgc tgagaaagca 3240

ggccgaggaa gtgaataccg agtgggagaa gctgaatctg cacagcgccg actggcagag 3300

aaagatcgac gagaccctgg agagactcca ggaactgcag gaagccaccg acgagctgga 3360

cctgaagctg agacaggccg aagtgatcaa gggcagctgg cagcctgtgg gcgatctgct 3420

gatcgactcc ctgcaggatc acctggagaa agtgaaggcc ctgcggggcg agatcgcccc 3480

cctgaaggag aatgtgagcc acgtgaacga cctggccaga cagctgacca ccctgggcat 3540

ccagctgagc ccctacaacc tgagcacact ggaggatctg aacacccggt ggaaactgct 3600

gcaggtggcc gtggaggata gagtgaggca gctgcacgaa gcccacagag acttcggccc 3660

tgcctcccag cacttcctga gcaccagcgt gcagggcccc tgggagagag ccatctcccc 3720

caacaaagtg ccctactaca tcaaccacga gacccagacc acctgctggg accaccctaa 3780

gatgaccgag ctgtatcaga gcctggccga cctgaacaat gtgcggttca gcgcctacag 3840

aaccgccatg aagctgcgga gactgcagaa ggccctgtgc ctggatctgc tgagcctgag 3900

cgccgcctgc gacgccctgg accagcacaa cctgaagcag aatgaccagc ccatggacat 3960

cctgcagatc atcaactgcc tgaccacaat ctacgaccgg ctggaacagg agcacaacaa 4020

cctggtgaat gtgcccctgt gcgtggacat gtgcctgaat tggctgctga acgtgtacga 4080

caccggcagg accggcagaa tccgcgtgct gagcttcaag accggcatca tcagcctgtg 4140

caaggcccac ctggaggata agtaccgcta cctgttcaag caggtggcca gcagcaccgg 4200

cttctgcgat cagaggagac tgggcctgct gctgcacgat agcatccaga tccctaggca 4260

gctgggcgaa gtggccagct ttggcggcag caacatcgag ccctctgtga ggagctgctt 4320

ccagttcgcc aacaacaagc ccgagatcga ggccgccctg ttcctggact ggatgaggct 4380

ggagcctcag agcatggtgt ggctgcctgt gctgcacaga gtggccgccg ccgagaccgc 4440

caagcaccag gccaagtgca atatctgcaa ggagtgcccc atcatcggct tccggtacag 4500

gagcctgaag cacttcaact acgacatctg ccagagctgc tttttcagcg gcagagtggc 4560

caagggccac aaaatgcact accccatggt ggagtactgc acccccacca cctccggcga 4620

ggatgtgaga gacttcgcca aagtgctgaa gaataagttc cggaccaagc ggtactttgc 4680

caagcacccc aggatgggct acctgcccgt gcagaccgtg ctggaaggcg acaacatgga 4740

gacctgatga ggagctcgag aggcctaata aagagctcag atgcatcgat cagagtgtgt 4800

tggtttttg tgtgagatct aggaacccct agtgatggag ttggccactc cctctctgcg 4860

cgctcgctcg ctcactgagg ccgcccgggc aaagcccggg cgtcgggcga cctttggtcg 4920

cccggcctca gtgagcgagc gagcgcgcag agagggagtg gccaa 4965

<210> 12
<211> 4955
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV vector genome with Copti-Dys3978 gene

<400> 12
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctcagat ctgaattcgg taccccacta cgggtttagg 180

ctgcccatgt aaggaggcaa ggcctgggga cacccgagat gcctggttat aattaaccca 240

gacatgtggc tgccccccc ccccccaaca cctgctgcct ctaaaaataa ccctgtccct 300

ggtggatccc ctgcatgcga agatcttcga acaaggctgt gggggactga gggcaggctg 360

taacaggctt gggggccagg gcttatacgt gcctgggact cccaaagtat tactgttcca 420

tgttcccggc gaagggccag ctgtcccccg ccagctagac tcagcactta gtttaggaac 480

cagtgagcaa gtcagccctt ggggcagccc atacaaggcc atggggctgg gcaagctgca 540

cgcctgggtc cggggtgggc acggtgcccg ggcaacgagc tgaaagctca tctgctctca 600

ggggccctc cctggggaca gcccctcctg gctagtcaca ccctgtaggc tcctctatat 660

aacccagggg cacaggggct gccctcattc taccaccacc tccacagcac agacagacac 720

tcaggagcca gccagcgtcg agcggccgcc accatgcttt ggtgggagga agtggaggac 780

tgctacgagc gggaggacgt gcagaagaaa accttcacca agtgggtgaa cgcccagttc 840

agcaagttcg gcaagcagca catcgagaac ctgttcagcg acctgcagga cggcaggcgg 900

ctgctggacc tcctggaagg cctgaccggc cagaagctgc ccaaagagaa gggcagcacc 960

agggtgcacg ccctgaacaa cgtgaacaag gccctgaggg tgctgcagaa caacaacgtg 1020

gacctggtga acatcggcag caccgacatc gtggacggca accacaagct gaccctgggc 1080

ctgatctgga acatcatcct gcactggcag gtcaagaacg tgatgaagaa catcatggcc 1140

ggcctgcagc agaccaacag cgagaagatc ctgctgtcct gggtgcggca gagcaccagg 1200

aactaccccc aggtcaacgt gatcaacttc accacctctt ggagcgacgg cctggccctg 1260

aacgccctga tccacagcca caggcccgac ctgttcgact ggaacagcgt ggtgtgccag 1320

cagagcgcca cccagaggct ggaacacgcc ttcaacatcg ccagatacca gctgggcatc 1380

gagaagctgc tggatcccga ggacgtggac accacctacc ccgacaagaa aagcatcctc 1440

atgtacatca ccagcctgtt ccaggtgctg ccccagcagg tgtccatcga ggccatccag 1500

gaagtggaga tgctgcccag gccccccaag gtcaccaaag aggaacactt ccagctgcac 1560

caccagatgc actacagcca gcagatcacc gtgagcctgg cccagggcta cgagaggacc 1620

agcagcccca agcccaggtt caagagctac gcctacaccc aggccgccta cgtgaccacc 1680

tccgacccca ccaggtcccc cttccccagc cagcatctcg aagcccccga ggacaagagc 1740

ttcggcagca gcctgatgga aagcgaggtg aacctggaca gataccagac cgccctggaa 1800

gaagtgctgt cttggctgct gtccgccgag gacaccctgc aggcccaggg cgagatcagc 1860

aacgacgtgg aggtcgtgaa ggaccagttc cacacccacg agggctacat gatggacctg 1920

accgcccacc agggcagagt gggcaacatc ctgcagctgg gcagcaagct gatcggcacc 1980

ggcaagctgt ccgaggacga ggaaaccgag gtgcaggaac agatgaacct gctgaacagc 2040

agatgggagt gcctgagggt ggccagcatg gaaaagcaga gcaacctgca cagggtgctg 2100

atggatctgc agaaccagaa gctcaaagag ctgaacgact ggctgaccaa gaccgaggaa 2160

aggacccgga agatggaaga ggaacccctg ggccccgatc tcgaagatct gaagaggcag 2220

gtgcagcagc acaaggtgct gcaggaagat ctcgaacagg aacaggtccg ggtcaacagc 2280

ctgacccaca tggtcgtggt ggtggacgag agcagcggcg accacgccac cgctgccctg 2340

gaagagcagc tgaaggtgct gggcgacaga tgggccaaca tctgccggtg gaccgaggac 2400

agatgggtcc tcctgcagga ccagcccgac ctggcccctg gcctgacaac catcggcgcc 2460

agccccaccc agaccgtgac cctggtgacc cagcccgtgg tgaccaaaga gaccgccatc 2520

agcaagctgg aaatgcccag ctccctgatg ctggaagtgc ccacccacag gctcctccag 2580

cagttccccc tggacctgga aaagttcctg gcctggctga ccgaggccga gaccaccgcc 2640

aacgtgctgc aggacgccac caggaaagag aggctgctgg aagatagcaa gggcgtgaaa 2700

gagctgatga agcagtggca ggacctgcag ggggagattg aggcccacac cgacgtgtac 2760

cacaacctgg acgagaacag ccagaaaatc ctgagaagcc tggaaggcag cgacgacgcc 2820

gtgctgctgc agaggcggct ggacaacatg aacttcaagt ggagcgagct gaggaagaag 2880

agcctgaaca tcaggtccca tctggaagcc agcagcgacc agtggaagag gctgcacctg 2940

agcctgcagg aactgctcgt ctggctgcag ctgaaagacg acgagctgtc caggcaggcc 3000

cccatcggcg gcgacttccc cgccgtgcag aaacagaacg acgtgcacag ggccttcaag 3060

cgggagctga aaaccaaaga gcccgtgatc atgagcaccc tggaaaccgt gaggatcttc 3120

ctgaccgagc agcccctgga aggactggaa aagctgtacc aggaacccag agagctgccc 3180

cccgaggaac gggcccagaa cgtgaccagg ctgctgagaa agcaggccga ggaagtgaac 3240

accgagtggg agaagctgaa cctgcactcc gccgactggc agaggaagat cgacgagacc 3300

ctggaaaggc tccaggaact gcaggaagcc accgacgagc tggacctgaa gctgagacag 3360

gccgaggtga tcaagggcag ctggcagccc gtgggcgacc tgctgatcga ctccctgcag 3420

gatcacctgg aaaaagtgaa ggccctgcgg ggcgagatcg ccccccctgaa agagaacgtc 3480

agccacgtca acgacctggc caggcagctg accaccctgg gcatccagct gtcccctac 3540

aacctgtcca ccctggaaga tctgaacaca aggtggaagc tgctgcaggt ggccgtggag 3600

gacagagtga ggcagctgca cgaggcccac agggacttcg gccctgcctc ccagcacttc 3660

ctgagcacca gcgtgcaggg cccctgggag agggccatct cccccaacaa ggtgccctac 3720

tacatcaacc acgagaccca gaccacctgc tgggaccacc ctaagatgac cgagctgtac 3780

cagtccctgg ccgacctgaa caatgtgcgg ttcagcgcct accggaccgc catgaagctg 3840

aggcggctgc agaaagccct gtgcctggat ctgctgtccc tgagcgccgc ctgcgacgcc 3900

ctggaccagc acaacctgaa gcagaacgac cagcccatgg atatcctgca gatcatcaac 3960

tgtctgacca ccatctacga caggctggaa caggaacaca acaacctggt caacgtgccc 4020

ctgtgcgtgg acatgtgcct gaactggctg ctgaacgtgt acgacaccgg caggaccggc 4080

cggatcaggg tgctgtcctt caagaccggc atcatcagcc tgtgcaaggc ccacctggaa 4140

gataagtacc gctacctgtt caagcaggtg gccagctcta ccggcttctg cgaccagcgg 4200

aggctgggcc tgctgctgca cgacagcatc cagatccccc ggcagctggg cgaggtggcc 4260

tccttcggcg gcagcaacat cgagcccagc gtgcggagct gcttccagtt cgccaacaac 4320

aagcccgaga tcgaggccgc cctgttcctg gactggatgc ggctggaacc ccagagcatg 4380

gtctggctgc ccgtgctgca cagagtggct gccgccgaga ccgccaagca ccaggccaag 4440

tgcaacatct gcaaagagtg ccccatcatc ggcttcaggt acagaagcct gaagcacttc 4500

aactacgaca tctgccagag ctgtttcttc agcggcaggg tggccaaggg ccacaaaatg 4560

cactacccca tggtggagta ctgcaccccc accacctccg gcgaggacgt gagggacttc 4620

gccaaggtgc tgaagaataa gttccggacc aagcggtact tcgccaaaca ccccaggatg 4680

ggctacctgc ccgtgcagac cgtgctggaa ggcgacaaca tggaaacctg ataacacgcg 4740

tcgactcgag aggcctaata aagagctcag atgcatcgat cagagtgtgt tggtttttg 4800

tgtgagatct aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg 4860

ctcactgagg ccgcccgggc aaagcccggg cgtcgggcga cctttggtcg cccggcctca 4920

gtgagcgagc gagcgcgcag agagggagtg gccaa 4955

<210> 13
<211> 736
<212> PRT
<213> adeno-associated virus 9

<400> 13

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


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


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
```

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

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

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 14
<211> 145
<212> DNA
<213> adeno-associated virus 2

<400> 14
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcct 145

<210> 15
<211> 145
<212> DNA
<213> adeno-associated virus 2

<400> 15
aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctcactgagg 60

ccgcccgggc aaagcccggg cgtcgggcga cctttggtcg cccggcctca gtgagcgagc 120

gagcgcgcag agagggagtg gccaa 145

<210> 16
<211> 577
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic enhancer and promoter

<400> 16
ccactacggg tctaggctgc ccatgtaagg aggcaaggcc tggggacacc cgagatgcct 60

ggttataatt aacccagaca tgtggctgcc ccccccccc ccaacacctg ctgcctctaa 120

aaataaccct gtccctggtg gatcccctgc atgcgaagat cttcgaacaa ggctgtgggg 180

gactgagggc aggctgtaac aggcttgggg gccagggctt atacgtgcct gggactccca 240

aagtattact gttccatgtt cccggcgaag ggccagctgt cccccgccag ctagactcag 300

cacttagttt aggaaccagt gagcaagtca gcccttgggg cagcccatac aaggccatgg 360

ggctgggcaa gctgcacgcc tgggtccggg gtgggcacgg tgcccgggca acgagctgaa 420

agctcatctg ctctcagggg cccctccctg gggacagccc ctcctggcta gtcacaccct 480

gtaggctcct ctatataacc caggggcaca ggggctgccc tcattctacc accacctcca 540

cagcacagac agacactcag gagccagcca gcgtcga 577

<210> 17
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic transcription terminator

<400> 17
aggcctaata aagagctcag atgcatcgat cagagtgtgt tggtttttg tgtg 54

<210> 18
<211> 4955
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV vector genome with Hopti-Dys3978 gene

<400> 18
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctcagat ctgaattcgg taccccacta cgggtctagg 180

ctgcccatgt aaggaggcaa ggcctgggga cacccgagat gcctggttat aattaaccca 240

gacatgtggc tgccccccc ccccccaaca cctgctgcct ctaaaaataa ccctgtccct 300

ggtggatccc ctgcatgcga agatcttcga acaaggctgt gggggactga gggcaggctg 360

taacaggctt gggggccagg gcttatacgt gcctgggact cccaaagtat tactgttcca 420

tgttcccggc gaagggccag ctgtcccccg ccagctagac tcagcactta gtttaggaac 480

cagtgagcaa gtcagccctt ggggcagccc atacaaggcc atggggctgg gcaagctgca 540

cgcctgggtc cggggtgggc acggtgcccg ggcaacgagc tgaaagctca tctgctctca 600

ggggcccctc cctggggaca gcccctcctg gctagtcaca ccctgtaggc tcctctatat 660

aacccagggg cacaggggct gccctcattc taccaccacc tccacagcac agacagacac 720

tcaggagcca gccagcgtcg agcggccgat ccgccaccat gctttggtgg gaggaagtgg 780

aggactgcta cgagagagag gacgtgcaga agaaaacctt caccaagtgg gtgaacgccc 840

agttcagcaa gttcggcaag cagcacatcg agaacctgtt cagcgacctg caggatggca 900

ggagactgct ggacctgctg gagggcctga ccggccagaa gctgcccaag gagaagggca 960

gcaccagagt gcacgccctg aacaacgtga acaaggccct gagagtgctg cagaacaaca 1020

acgtggacct ggtgaacatc ggcagcaccg acatcgtgga cggcaaccac aagctgaccc 1080

tgggcctgat ctggaacatc atcctgcact ggcaggtgaa gaacgtgatg aagaacatca 1140

tggccggcct gcagcagacc aacagcgaga agatcctgct gagctgggtg aggcagagca 1200

ccagaaacta cccccaggtg aacgtgatca acttcaccac ctcctggagc gacggcctgg 1260

ccctgaacgc cctgatccac agccacagac ccgacctgtt cgactggaac agcgtggtgt 1320

gtcagcagag cgccacccag agactggagc acgccttcaa catcgccaga taccagctgg 1380

gcatcgagaa gctgctggac cccgaggacg tggacaccac ctaccccgac aagaaaagca 1440

tcctcatgta cattaccagc ctgttccagg tgctgcccca gcaggtgtcc atcgaggcca 1500

tccaggaagt ggaaatgctg cccaggcccc ccaaagtgac caaggaggag cacttccagc 1560

tgcaccacca gatgcactac agccagcaga tcacagtgag cctggcccag ggctatgaga 1620

gaaccagcag ccccaagccc agattcaaga gctacgccta cacccaggcc gcctacgtga 1680

ccacctccga ccccaccaga agccccttcc ccagccagca cctggaggcc cccgaggaca 1740

agagcttcgg cagcagcctg atggagagcg aagtgaacct ggacagatac cagaccgccc 1800

tggaggaagt gctgtcctgg ctgctgagcg ccgaggacac cctgcaggcc cagggcgaga 1860

tcagcaacga cgtggaagtg gtgaaggacc agttccacac ccacgagggc tacatgatgg 1920

atctgaccgc ccaccagggc agagtgggca atatcctgca gctgggcagc aagctgatcg 1980

gcaccggcaa gctgagcgag gacgaggaga ccgaagtgca ggagcagatg aacctgctga 2040

acagcagatg ggagtgcctg agagtggcca gcatggagaa gcagagcaac ctgcacagag 2100

tgctgatgga cctgcagaac cagaagctga aggagctgaa cgactggctg accaagaccg 2160

aggagcggac cagaaagatg gaggaggagc ccctgggccc cgacctggag gacctgaaga 2220

gacaggtgca gcagcacaaa gtgctgcagg aggacctgga gcaggagcag gtgcgcgtga 2280

acagcctgac ccacatggtg gtggtcgtgg acgagagcag cggcgaccac gccacagccg 2340

ccctggaaga gcagctgaaa gtgctgggcg acagatgggc caatatttgt aggtggaccg 2400

aggacagatg ggtgctgctg caggaccagc ccgacctggc ccctggcctg accaccatcg 2460

gcgccagccc cacccagacc gtgaccctgg tgacccagcc cgtggtgaca aaggagaccg 2520

ccatcagcaa gctggagatg cccagctccc tgatgctgga agtgcccacc caccgcctgc 2580

tccagcagtt ccccctggac ctggagaagt tcctggcctg gctgaccgag gccgaaacca 2640

ccgccaatgt gctccaggac gccactagaa aggagaggct gctggaggac agcaagggcg 2700

tgaaagagct gatgaagcag tggcaggatc tgcagggcga aatcgaggcc cacaccgacg 2760

tgtaccacaa cctggacgag aacagccaga agattctgag gagcctggag ggcagcgacg 2820

acgccgtcct gctccagagg aggctggaca acatgaactt caagtggagc gagctgcgga 2880

agaagagcct gaacatccgg agccacctgg aagccagcag cgaccagtgg aagagactgc 2940

acctgagcct gcaggagctg ctggtgtggc tgcagctgaa ggacgacgag ctgagcagac 3000

aggcccccat cggcggcgac ttccccgccg tgcagaagca gaacgacgtg caccgggcct 3060

tcaagaggga gctgaaaacc aaggaacccg tgatcatgag caccctggag acagtgcgga 3120

tcttcctgac cgagcagccc ctggagggac tggagaagct gtaccaggag cccagagagc 3180

tgccccccga ggagagagcc cagaacgtga ccaggctgct gagaaagcag gccgaggaag 3240

tgaataccga gtgggagaag ctgaatctgc acagcgccga ctggcagaga aagatcgacg 3300

agaccctgga gagactccag gaactgcagg aagccaccga cgagctggac ctgaagctga 3360

gacaggccga agtgatcaag ggcagctggc agcctgtggg cgatctgctg atcgactccc 3420

tgcaggatca cctggagaaa gtgaaggccc tgcggggcga gatcgccccc ctgaaggaga 3480

atgtgagcca cgtgaacgac ctggccagac agctgaccac cctgggcatc cagctgagcc 3540

cctacaacct gagcacactg gaggatctga acacccggtg gaaactgctg caggtggccg 3600

tggaggatag agtgaggcag ctgcacgaag cccacagaga cttcggccct gcctcccagc 3660

acttcctgag caccagcgtg cagggcccct gggagagagc catctccccc aacaaagtgc 3720

cctactacat caaccacgag acccagacca cctgctggga ccaccctaag atgaccgagc 3780

tgtatcagag cctggccgac ctgaacaatg tgcggttcag cgcctacaga accgccatga 3840

agctgcggag actgcagaag gccctgtgcc tggatctgct gagcctgagc gccgcctgcg 3900

acgccctgga ccagcacaac ctgaagcaga atgaccagcc catggacatc ctgcagatca 3960

tcaactgcct gaccacaatc tacgaccggc tggaacagga gcacaacaac ctggtgaatg 4020

tgcccctgtg cgtggacatg tgcctgaatt ggctgctgaa cgtgtacgac accggcagga 4080

ccggcagaat ccgcgtgctg agcttcaaga ccggcatcat cagcctgtgc aaggcccacc 4140

tggaggataa gtaccgctac ctgttcaagc aggtggccag cagcaccggc ttctgcgatc 4200

agaggagact gggcctgctg ctgcacgata gcatccagat ccctaggcag ctgggcgaag 4260

tggccagctt tggcggcagc aacatcgagc cctctgtgag gagctgcttc cagttcgcca 4320

acaacaagcc cgagatcgag gccgccctgt tcctggactg gatgaggctg gagcctcaga 4380

gcatggtgtg gctgcctgtg ctgcacagag tggccgccgc cgagaccgcc aagcaccagg 4440

ccaagtgcaa tatctgcaag gagtgcccca tcatcggctt ccggtacagg agcctgaagc 4500

acttcaacta cgacatctgc cagagctgct ttttcagcgg cagagtggcc aagggccaca 4560

aaatgcacta ccccatggtg gagtactgca cccccaccac ctccggcgag gatgtgagag 4620

acttcgccaa agtgctgaag aataagttcc ggaccaagcg gtactttgcc aagcacccca 4680

ggatgggcta cctgcccgtg cagaccgtgc tggaaggcga caacatggag acctgatgag 4740

gagctcgaga ggcctaataa agagctcaga tgcatcgatc agagtgtgtt ggtttttgt 4800

gtgagatctg aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg 4860

ctcactgagg ccgcccgggc aaagcccggg cgtcgggcga cctttggtcg cccggcctca 4920

gtgagcgagc gagcgcgcag agagggagtg gccaa 4955

<210> 19
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
ccaacaaagt gccctactac atc 23

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
ggttgtgctg gtccagggcg t 21

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
ccgagctgta tcagagcctg gcc 23

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
gcgaaagtgg aaaagccaag t 21

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 23
gccacatcaa caggactctt gtag 24

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
caaagcctaa aagacagcgg caagttgaat 30

<210> 25
<211> 3685
<212> PRT
<213> Homo sapiens

<400> 25

Met Leu Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

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

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

```
Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
            100                 105                 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met
        115                 120                 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
    130                 135                 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145                 150                 155                 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
                165                 170                 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
            180                 185                 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
        195                 200                 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
    210                 215                 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225                 230                 235                 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
                245                 250                 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
            260                 265                 270

His Tyr Ser Gln Gln Ile Thr Val Ser Leu Ala Gln Gly Tyr Glu Arg
        275                 280                 285

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
```

290 295 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305 310 315 320

His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
325 330 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
340 345 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
355 360 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
370 375 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385 390 395 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
405 410 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
420 425 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Arg Val
435 440 445

Leu Met Asp Leu Gln Asn Gln Lys Leu Lys Glu Leu Asn Asp Trp Leu
450 455 460

Thr Lys Thr Glu Glu Arg Thr Arg Lys Met Glu Glu Glu Pro Leu Gly
465 470 475 480

Pro Asp Leu Glu Asp Leu Lys Arg Gln Val Gln Gln His Lys Val Leu
485 490 495

```
Gln Glu Asp Leu Glu Gln Glu Gln Val Arg Val Asn Ser Leu Thr His
            500                 505                 510

Met Val Val Val Val Asp Glu Ser Ser Gly Asp His Ala Thr Ala Ala
        515                 520                 525

Leu Glu Glu Gln Leu Lys Val Leu Gly Asp Arg Trp Ala Asn Ile Cys
    530                 535                 540

Arg Trp Thr Glu Asp Arg Trp Val Leu Leu Gln Asp Ile Leu Leu Lys
545                 550                 555                 560

Trp Gln Arg Leu Thr Glu Glu Gln Cys Leu Phe Ser Ala Trp Leu Ser
                565                 570                 575

Glu Lys Glu Asp Ala Val Asn Lys Ile His Thr Thr Gly Phe Lys Asp
            580                 585                 590

Gln Asn Glu Met Leu Ser Ser Leu Gln Lys Leu Ala Val Leu Lys Ala
        595                 600                 605

Asp Leu Glu Lys Lys Lys Gln Ser Met Gly Lys Leu Tyr Ser Leu Lys
    610                 615                 620

Gln Asp Leu Leu Ser Thr Leu Lys Asn Lys Ser Val Thr Gln Lys Thr
625                 630                 635                 640

Glu Ala Trp Leu Asp Asn Phe Ala Arg Cys Trp Asp Asn Leu Val Gln
                645                 650                 655

Lys Leu Glu Lys Ser Thr Ala Gln Ile Ser Gln Ala Val Thr Thr Thr
            660                 665                 670

Gln Pro Ser Leu Thr Gln Thr Thr Val Met Glu Thr Val Thr Thr Val
        675                 680                 685
```

```
Thr Thr Arg Glu Gln Ile Leu Val Lys His Ala Gln Glu Glu Leu Pro
    690                 695                 700

Pro Pro Pro Pro Gln Lys Lys Arg Gln Ile Thr Val Asp Ser Glu Ile
705                 710                 715                 720

Arg Lys Arg Leu Asp Val Asp Ile Thr Glu Leu His Ser Trp Ile Thr
                725                 730                 735

Arg Ser Glu Ala Val Leu Gln Ser Pro Glu Phe Ala Ile Phe Arg Lys
            740                 745                 750

Glu Gly Asn Phe Ser Asp Leu Lys Glu Lys Val Asn Ala Ile Glu Arg
        755                 760                 765

Glu Lys Ala Glu Lys Phe Arg Lys Leu Gln Asp Ala Ser Arg Ser Ala
    770                 775                 780

Gln Ala Leu Val Glu Gln Met Val Asn Glu Gly Val Asn Ala Asp Ser
785                 790                 795                 800

Ile Lys Gln Ala Ser Glu Gln Leu Asn Ser Arg Trp Ile Glu Phe Cys
                805                 810                 815

Gln Leu Leu Ser Glu Arg Leu Asn Trp Leu Glu Tyr Gln Asn Asn Ile
            820                 825                 830

Ile Ala Phe Tyr Asn Gln Leu Gln Gln Leu Glu Gln Met Thr Thr Thr
        835                 840                 845

Ala Glu Asn Trp Leu Lys Ile Gln Pro Thr Thr Pro Ser Glu Pro Thr
    850                 855                 860

Ala Ile Lys Ser Gln Leu Lys Ile Cys Lys Asp Glu Val Asn Arg Leu
865                 870                 875                 880
```

```
Ser Gly Leu Gln Pro Gln Ile Glu Arg Leu Lys Ile Gln Ser Ile Ala
               885                 890                 895

Leu Lys Glu Lys Gly Gln Gly Pro Met Phe Leu Asp Ala Asp Phe Val
            900                 905                 910

Ala Phe Thr Asn His Phe Lys Gln Val Phe Ser Asp Val Gln Ala Arg
        915                 920                 925

Glu Lys Glu Leu Gln Thr Ile Phe Asp Thr Leu Pro Pro Met Arg Tyr
    930                 935                 940

Gln Glu Thr Met Ser Ala Ile Arg Thr Trp Val Gln Gln Ser Glu Thr
945                 950                 955                 960

Lys Leu Ser Ile Pro Gln Leu Ser Val Thr Asp Tyr Glu Ile Met Glu
               965                 970                 975

Gln Arg Leu Gly Glu Leu Gln Ala Leu Gln Ser Ser Leu Gln Glu Gln
            980                 985                 990

Gln Ser Gly Leu Tyr Tyr Leu Ser  Thr Thr Val Lys Glu  Met Ser Lys
        995                 1000                1005

Lys Ala  Pro Ser Glu Ile Ser  Arg Lys Tyr Gln Ser  Glu Phe Glu
    1010                1015                1020

Glu Ile  Glu Gly Arg Trp Lys  Lys Leu Ser Ser Gln  Leu Val Glu
    1025                1030                1035

His Cys  Gln Lys Leu Glu Glu  Gln Met Asn Lys Leu  Arg Lys Ile
    1040                1045                1050

Gln Asn  His Ile Gln Thr Leu  Lys Lys Trp Met Ala  Glu Val Asp
    1055                1060                1065

Val Phe  Leu Lys Glu Glu Trp  Pro Ala Leu Gly Asp  Ser Glu Ile
```

```
    1070                1075                1080

Leu Lys  Lys Gln Leu Lys Gln  Cys Arg Leu Leu Val  Ser Asp Ile
    1085                1090                1095

Gln Thr  Ile Gln Pro Ser Leu  Asn Ser Val Asn Glu  Gly Gly Gln
    1100                1105                1110

Lys Ile  Lys Asn Glu Ala Glu  Pro Glu Phe Ala Ser  Arg Leu Glu
    1115                1120                1125

Thr Glu  Leu Lys Glu Leu Asn  Thr Gln Trp Asp His  Met Cys Gln
    1130                1135                1140

Gln Val  Tyr Ala Arg Lys Glu  Ala Leu Lys Gly Gly  Leu Glu Lys
    1145                1150                1155

Thr Val  Ser Leu Gln Lys Asp  Leu Ser Glu Met His  Glu Trp Met
    1160                1165                1170

Thr Gln  Ala Glu Glu Glu Tyr  Leu Glu Arg Asp Phe  Glu Tyr Lys
    1175                1180                1185

Thr Pro  Asp Glu Leu Gln Lys  Ala Val Glu Glu Met  Lys Arg Ala
    1190                1195                1200

Lys Glu  Glu Ala Gln Gln Lys  Glu Ala Lys Val Lys  Leu Leu Thr
    1205                1210                1215

Glu Ser  Val Asn Ser Val Ile  Ala Gln Ala Pro Pro  Val Ala Gln
    1220                1225                1230

Glu Ala  Leu Lys Lys Glu Leu  Glu Thr Leu Thr Thr  Asn Tyr Gln
    1235                1240                1245

Trp Leu  Cys Thr Arg Leu Asn  Gly Lys Cys Lys Thr  Leu Glu Glu
    1250                1255                1260
```

```
Val Trp  Ala Cys Trp His Glu  Leu Leu Ser Tyr Leu  Glu Lys Ala
    1265                1270                1275

Asn Lys  Trp Leu Asn Glu Val  Glu Phe Lys Leu Lys  Thr Thr Glu
    1280                1285                1290

Asn Ile  Pro Gly Gly Ala Glu  Glu Ile Ser Glu Val  Leu Asp Ser
    1295                1300                1305

Leu Glu  Asn Leu Met Arg His  Ser Glu Asp Asn Pro  Asn Gln Ile
    1310                1315                1320

Arg Ile  Leu Ala Gln Thr Leu  Thr Asp Gly Gly Val  Met Asp Glu
    1325                1330                1335

Leu Ile  Asn Glu Glu Leu Glu  Thr Phe Asn Ser Arg  Trp Arg Glu
    1340                1345                1350

Leu His  Glu Glu Ala Val Arg  Arg Gln Lys Leu Leu  Glu Gln Ser
    1355                1360                1365

Ile Gln  Ser Ala Gln Glu Thr  Glu Lys Ser Leu His  Leu Ile Gln
    1370                1375                1380

Glu Ser  Leu Thr Phe Ile Asp  Lys Gln Leu Ala Ala  Tyr Ile Ala
    1385                1390                1395

Asp Lys  Val Asp Ala Ala Gln  Met Pro Gln Glu Ala  Gln Lys Ile
    1400                1405                1410

Gln Ser  Asp Leu Thr Ser His  Glu Ile Ser Leu Glu  Glu Met Lys
    1415                1420                1425

Lys His  Asn Gln Gly Lys Glu  Ala Ala Gln Arg Val  Leu Ser Gln
    1430                1435                1440
```

```
Ile Asp  Val Ala Gln Lys Lys  Leu Gln Asp Val Ser  Met Lys Phe
    1445                1450                1455

Arg Leu  Phe Gln Lys Pro Ala  Asn Phe Glu Gln Arg  Leu Gln Glu
    1460                1465                1470

Ser Lys  Met Ile Leu Asp Glu  Val Lys Met His Leu  Pro Ala Leu
    1475                1480                1485

Glu Thr  Lys Ser Val Glu Gln  Glu Val Val Gln Ser  Gln Leu Asn
    1490                1495                1500

His Cys  Val Asn Leu Tyr Lys  Ser Leu Ser Glu Val  Lys Ser Glu
    1505                1510                1515

Val Glu  Met Val Ile Lys Thr  Gly Arg Gln Ile Val  Gln Lys Lys
    1520                1525                1530

Gln Thr  Glu Asn Pro Lys Glu  Leu Asp Glu Arg Val  Thr Ala Leu
    1535                1540                1545

Lys Leu  His Tyr Asn Glu Leu  Gly Ala Lys Val Thr  Glu Arg Lys
    1550                1555                1560

Gln Gln  Leu Glu Lys Cys Leu  Lys Leu Ser Arg Lys  Met Arg Lys
    1565                1570                1575

Glu Met  Asn Val Leu Thr Glu  Trp Leu Ala Ala Thr  Asp Met Glu
    1580                1585                1590

Leu Thr  Lys Arg Ser Ala Val  Glu Gly Met Pro Ser  Asn Leu Asp
    1595                1600                1605

Ser Glu  Val Ala Trp Gly Lys  Ala Thr Gln Lys Glu  Ile Glu Lys
    1610                1615                1620
```

```
Gln Lys  Val His Leu Lys Ser  Ile Thr Glu Val Gly  Glu Ala Leu
    1625                1630                1635

Lys Thr  Val Leu Gly Lys Lys  Glu Thr Leu Val Glu  Asp Lys Leu
    1640                1645                1650

Ser Leu  Leu Asn Ser Asn Trp  Ile Ala Val Thr Ser  Arg Ala Glu
    1655                1660                1665

Glu Trp  Leu Asn Leu Leu Leu  Glu Tyr Gln Lys His  Met Glu Thr
    1670                1675                1680

Phe Asp  Gln Asn Val Asp His  Ile Thr Lys Trp Ile  Ile Gln Ala
    1685                1690                1695

Asp Thr  Leu Leu Asp Glu Ser  Glu Lys Lys Lys Pro  Gln Gln Lys
    1700                1705                1710

Glu Asp  Val Leu Lys Arg Leu  Lys Ala Glu Leu Asn  Asp Ile Arg
    1715                1720                1725

Pro Lys  Val Asp Ser Thr Arg  Asp Gln Ala Ala Asn  Leu Met Ala
    1730                1735                1740

Asn Arg  Gly Asp His Cys Arg  Lys Leu Val Glu Pro  Gln Ile Ser
    1745                1750                1755

Glu Leu  Asn His Arg Phe Ala  Ala Ile Ser His Arg  Ile Lys Thr
    1760                1765                1770

Gly Lys  Ala Ser Ile Pro Leu  Lys Glu Leu Glu Gln  Phe Asn Ser
    1775                1780                1785

Asp Ile  Gln Lys Leu Leu Glu  Pro Leu Glu Ala Glu  Ile Gln Gln
    1790                1795                1800

Gly Val  Asn Leu Lys Glu Glu  Asp Phe Asn Lys Asp  Met Asn Glu
```

```
    1805                1810                1815

Asp Asn  Glu Gly Thr Val Lys  Glu Leu Leu Gln Arg  Gly Asp Asn
    1820                1825                1830

Leu Gln  Gln Arg Ile Thr Asp  Glu Arg Lys Arg Glu  Glu Ile Lys
    1835                1840                1845

Ile Lys  Gln Gln Leu Leu Gln  Thr Lys His Asn Ala  Leu Lys Asp
    1850                1855                1860

Leu Arg  Ser Gln Arg Arg Lys  Lys Ala Leu Glu Ile  Ser His Gln
    1865                1870                1875

Trp Tyr  Gln Tyr Lys Arg Gln  Ala Asp Asp Leu Leu  Lys Cys Leu
    1880                1885                1890

Asp Asp  Ile Glu Lys Lys Leu  Ala Ser Leu Pro Glu  Pro Arg Asp
    1895                1900                1905

Glu Arg  Lys Ile Lys Glu Ile  Asp Arg Glu Leu Gln  Lys Lys Lys
    1910                1915                1920

Glu Glu  Leu Asn Ala Val Arg  Arg Gln Ala Glu Gly  Leu Ser Glu
    1925                1930                1935

Asp Gly  Ala Ala Met Ala Val  Glu Pro Thr Gln Ile  Gln Leu Ser
    1940                1945                1950

Lys Arg  Trp Arg Glu Ile Glu  Ser Lys Phe Ala Gln  Phe Arg Arg
    1955                1960                1965

Leu Asn  Phe Ala Gln Ile His  Thr Val Arg Glu Glu  Thr Met Met
    1970                1975                1980

Val Met  Thr Glu Asp Met Pro  Leu Glu Ile Ser Tyr  Val Pro Ser
    1985                1990                1995
```

```
Thr Tyr  Leu Thr Glu Ile Thr  His Val Ser Gln Ala  Leu Leu Glu
    2000                2005                2010

Val Glu  Gln Leu Leu Asn Ala  Pro Asp Leu Cys Ala  Lys Asp Phe
    2015                2020                2025

Glu Asp  Leu Phe Lys Gln Glu  Glu Ser Leu Lys Asn  Ile Lys Asp
    2030                2035                2040

Ser Leu  Gln Gln Ser Ser Gly  Arg Ile Asp Ile Ile  His Ser Lys
    2045                2050                2055

Lys Thr  Ala Ala Leu Gln Ser  Ala Thr Pro Val Glu  Arg Val Lys
    2060                2065                2070

Leu Gln  Glu Ala Leu Ser Gln  Leu Asp Phe Gln Trp  Glu Lys Val
    2075                2080                2085

Asn Lys  Met Tyr Lys Asp Arg  Gln Gly Arg Phe Asp  Arg Ser Val
    2090                2095                2100

Glu Lys  Trp Arg Arg Phe His  Tyr Asp Ile Lys Ile  Phe Asn Gln
    2105                2110                2115

Trp Leu  Thr Glu Ala Glu Gln  Phe Leu Arg Lys Thr  Gln Ile Pro
    2120                2125                2130

Glu Asn  Trp Glu His Ala Lys  Tyr Lys Trp Tyr Leu  Lys Glu Leu
    2135                2140                2145

Gln Asp  Gly Ile Gly Gln Arg  Gln Thr Val Val Arg  Thr Leu Asn
    2150                2155                2160

Ala Thr  Gly Glu Glu Ile Ile  Gln Gln Ser Ser Lys  Thr Asp Ala
    2165                2170                2175
```

```
Ser Ile  Leu Gln Glu Lys Leu  Gly Ser Leu Asn Leu  Arg Trp Gln
    2180                2185                2190

Glu Val  Cys Lys Gln Leu Ser  Asp Arg Lys Lys Arg  Leu Glu Glu
    2195                2200                2205

Gln Lys  Asn Ile Leu Ser Glu  Phe Gln Arg Asp Leu  Asn Glu Phe
    2210                2215                2220

Val Leu  Trp Leu Glu Glu Ala  Asp Asn Ile Ala Ser  Ile Pro Leu
    2225                2230                2235

Glu Pro  Gly Lys Glu Gln Gln  Leu Lys Glu Lys Leu  Glu Gln Val
    2240                2245                2250

Lys Leu  Leu Val Glu Glu Leu  Pro Leu Arg Gln Gly  Ile Leu Lys
    2255                2260                2265

Gln Leu  Asn Glu Thr Gly Gly  Pro Val Leu Val Ser  Ala Pro Ile
    2270                2275                2280

Ser Pro  Glu Glu Gln Asp Lys  Leu Glu Asn Lys Leu  Lys Gln Thr
    2285                2290                2295

Asn Leu  Gln Trp Ile Lys Val  Ser Arg Ala Leu Pro  Glu Lys Gln
    2300                2305                2310

Gly Glu  Ile Glu Ala Gln Ile  Lys Asp Leu Gly Gln  Leu Glu Lys
    2315                2320                2325

Lys Leu  Glu Asp Leu Glu Glu  Gln Leu Asn His Leu  Leu Leu Trp
    2330                2335                2340

Leu Ser  Pro Ile Arg Asn Gln  Leu Glu Ile Tyr Asn  Gln Pro Asn
    2345                2350                2355
```

```
Gln Glu  Gly Pro Phe Asp Val  Gln Glu Thr Glu Ile  Ala Val Gln
    2360                2365                2370

Ala Lys  Gln Pro Asp Val Glu  Glu Ile Leu Ser Lys  Gly Gln His
    2375                2380                2385

Leu Tyr  Lys Glu Lys Pro Ala  Thr Gln Pro Val Lys  Arg Lys Leu
    2390                2395                2400

Glu Asp  Leu Ser Ser Glu Trp  Lys Ala Val Asn Arg  Leu Leu Gln
    2405                2410                2415

Glu Leu  Arg Ala Lys Gln Pro  Asp Leu Ala Pro Gly  Leu Thr Thr
    2420                2425                2430

Ile Gly  Ala Ser Pro Thr Gln  Thr Val Thr Leu Val  Thr Gln Pro
    2435                2440                2445

Val Val  Thr Lys Glu Thr Ala  Ile Ser Lys Leu Glu  Met Pro Ser
    2450                2455                2460

Ser Leu  Met Leu Glu Val Pro  Ala Leu Ala Asp Phe  Asn Arg Ala
    2465                2470                2475

Trp Thr  Glu Leu Thr Asp Trp  Leu Ser Leu Leu Asp  Gln Val Ile
    2480                2485                2490

Lys Ser  Gln Arg Val Met Val  Gly Asp Leu Glu Asp  Ile Asn Glu
    2495                2500                2505

Met Ile  Ile Lys Gln Lys Ala  Thr Met Gln Asp Leu  Glu Gln Arg
    2510                2515                2520

Arg Pro  Gln Leu Glu Glu Leu  Ile Thr Ala Ala Gln  Asn Leu Lys
    2525                2530                2535

Asn Lys  Thr Ser Asn Gln Glu  Ala Arg Thr Ile Ile  Thr Asp Arg
```

```
    2540                2545                2550

Ile Glu  Arg Ile Gln Asn Gln  Trp Asp Glu Val Gln  Glu His Leu
    2555                2560                2565

Gln Asn  Arg Arg Gln Gln Leu  Asn Glu Met Leu Lys  Asp Ser Thr
    2570                2575                2580

Gln Trp  Leu Glu Ala Lys Glu  Glu Ala Glu Gln Val  Leu Gly Gln
    2585                2590                2595

Ala Arg  Ala Lys Leu Glu Ser  Trp Lys Glu Gly Pro  Tyr Thr Val
    2600                2605                2610

Asp Ala  Ile Gln Lys Lys Ile  Thr Glu Thr Lys Gln  Leu Ala Lys
    2615                2620                2625

Asp Leu  Arg Gln Trp Gln Thr  Asn Val Asp Val Ala  Asn Asp Leu
    2630                2635                2640

Ala Leu  Lys Leu Leu Arg Asp  Tyr Ser Ala Asp Asp  Thr Arg Lys
    2645                2650                2655

Val His  Met Ile Thr Glu Asn  Ile Asn Ala Ser Trp  Arg Ser Ile
    2660                2665                2670

His Lys  Arg Val Ser Glu Arg  Glu Ala Ala Leu Glu  Glu Thr His
    2675                2680                2685

Arg Leu  Leu Gln Gln Phe Pro  Leu Asp Leu Glu Lys  Phe Leu Ala
    2690                2695                2700

Trp Leu  Thr Glu Ala Glu Thr  Thr Ala Asn Val Leu  Gln Asp Ala
    2705                2710                2715

Thr Arg  Lys Glu Arg Leu Leu  Glu Asp Ser Lys Gly  Val Lys Glu
    2720                2725                2730
```

```
Leu Met  Lys Gln Trp Gln Asp  Leu Gln Gly Glu Ile  Glu Ala His
    2735                2740                2745

Thr Asp  Val Tyr His Asn Leu  Asp Glu Asn Ser Gln  Lys Ile Leu
    2750                2755                2760

Arg Ser  Leu Glu Gly Ser Asp  Asp Ala Val Leu Leu  Gln Arg Arg
    2765                2770                2775

Leu Asp  Asn Met Asn Phe Lys  Trp Ser Glu Leu Arg  Lys Lys Ser
    2780                2785                2790

Leu Asn  Ile Arg Ser His Leu  Glu Ala Ser Ser Asp  Gln Trp Lys
    2795                2800                2805

Arg Leu  His Leu Ser Leu Gln  Glu Leu Leu Val Trp  Leu Gln Leu
    2810                2815                2820

Lys Asp  Asp Glu Leu Ser Arg  Gln Ala Pro Ile Gly  Gly Asp Phe
    2825                2830                2835

Pro Ala  Val Gln Lys Gln Asn  Asp Val His Arg Ala  Phe Lys Arg
    2840                2845                2850

Glu Leu  Lys Thr Lys Glu Pro  Val Ile Met Ser Thr  Leu Glu Thr
    2855                2860                2865

Val Arg  Ile Phe Leu Thr Glu  Gln Pro Leu Glu Gly  Leu Glu Lys
    2870                2875                2880

Leu Tyr  Gln Glu Pro Arg Glu  Leu Pro Pro Glu Glu  Arg Ala Gln
    2885                2890                2895

Asn Val  Thr Arg Leu Leu Arg  Lys Gln Ala Glu Glu  Val Asn Thr
    2900                2905                2910
```

```
Glu Trp  Glu Lys Leu Asn Leu  His Ser Ala Asp Trp  Gln Arg Lys
    2915                2920                2925

Ile Asp  Glu Thr Leu Glu Arg  Leu Gln Glu Leu Gln  Glu Ala Thr
    2930                2935                2940

Asp Glu  Leu Asp Leu Lys Leu  Arg Gln Ala Glu Val  Ile Lys Gly
    2945                2950                2955

Ser Trp  Gln Pro Val Gly Asp  Leu Leu Ile Asp Ser  Leu Gln Asp
    2960                2965                2970

His Leu  Glu Lys Val Lys Ala  Leu Arg Gly Glu Ile  Ala Pro Leu
    2975                2980                2985

Lys Glu  Asn Val Ser His Val  Asn Asp Leu Ala Arg  Gln Leu Thr
    2990                2995                3000

Thr Leu  Gly Ile Gln Leu Ser  Pro Tyr Asn Leu Ser  Thr Leu Glu
    3005                3010                3015

Asp Leu  Asn Thr Arg Trp Lys  Leu Leu Gln Val Ala  Val Glu Asp
    3020                3025                3030

Arg Val  Arg Gln Leu His Glu  Ala His Arg Asp Phe  Gly Pro Ala
    3035                3040                3045

Ser Gln  His Phe Leu Ser Thr  Ser Val Gln Gly Pro  Trp Glu Arg
    3050                3055                3060

Ala Ile  Ser Pro Asn Lys Val  Pro Tyr Tyr Ile Asn  His Glu Thr
    3065                3070                3075

Gln Thr  Thr Cys Trp Asp His  Pro Lys Met Thr Glu  Leu Tyr Gln
    3080                3085                3090
```

```
Ser Leu  Ala Asp Leu Asn Asn  Val Arg Phe Ser Ala  Tyr Arg Thr
    3095                 3100                 3105

Ala Met  Lys Leu Arg Arg Leu  Gln Lys Ala Leu Cys  Leu Asp Leu
    3110                 3115                 3120

Leu Ser  Leu Ser Ala Ala Cys  Asp Ala Leu Asp Gln  His Asn Leu
    3125                 3130                 3135

Lys Gln  Asn Asp Gln Pro Met  Asp Ile Leu Gln Ile  Ile Asn Cys
    3140                 3145                 3150

Leu Thr  Thr Ile Tyr Asp Arg  Leu Glu Gln Glu His  Asn Asn Leu
    3155                 3160                 3165

Val Asn  Val Pro Leu Cys Val  Asp Met Cys Leu Asn  Trp Leu Leu
    3170                 3175                 3180

Asn Val  Tyr Asp Thr Gly Arg  Thr Gly Arg Ile Arg  Val Leu Ser
    3185                 3190                 3195

Phe Lys  Thr Gly Ile Ile Ser  Leu Cys Lys Ala His  Leu Glu Asp
    3200                 3205                 3210

Lys Tyr  Arg Tyr Leu Phe Lys  Gln Val Ala Ser Ser  Thr Gly Phe
    3215                 3220                 3225

Cys Asp  Gln Arg Arg Leu Gly  Leu Leu Leu His Asp  Ser Ile Gln
    3230                 3235                 3240

Ile Pro  Arg Gln Leu Gly Glu  Val Ala Ser Phe Gly  Gly Ser Asn
    3245                 3250                 3255

Ile Glu  Pro Ser Val Arg Ser  Cys Phe Gln Phe Ala  Asn Asn Lys
    3260                 3265                 3270

Pro Glu  Ile Glu Ala Ala Leu  Phe Leu Asp Trp Met  Arg Leu Glu
```

```
    3275                3280                3285

Pro Gln  Ser Met Val Trp Leu  Pro Val Leu His Arg  Val Ala Ala
    3290                3295                3300

Ala Glu  Thr Ala Lys His Gln  Ala Lys Cys Asn Ile  Cys Lys Glu
    3305                3310                3315

Cys Pro  Ile Ile Gly Phe Arg  Tyr Arg Ser Leu Lys  His Phe Asn
    3320                3325                3330

Tyr Asp  Ile Cys Gln Ser Cys  Phe Phe Ser Gly Arg  Val Ala Lys
    3335                3340                3345

Gly His  Lys Met His Tyr Pro  Met Val Glu Tyr Cys  Thr Pro Thr
    3350                3355                3360

Thr Ser  Gly Glu Asp Val Arg  Asp Phe Ala Lys Val  Leu Lys Asn
    3365                3370                3375

Lys Phe  Arg Thr Lys Arg Tyr  Phe Ala Lys His Pro  Arg Met Gly
    3380                3385                3390

Tyr Leu  Pro Val Gln Thr Val  Leu Glu Gly Asp Asn  Met Glu Thr
    3395                3400                3405

Pro Val  Thr Leu Ile Asn Phe  Trp Pro Val Asp Ser  Ala Pro Ala
    3410                3415                3420

Ser Ser  Pro Gln Leu Ser His  Asp Asp Thr His Ser  Arg Ile Glu
    3425                3430                3435

His Tyr  Ala Ser Arg Leu Ala  Glu Met Glu Asn Ser  Asn Gly Ser
    3440                3445                3450

Tyr Leu  Asn Asp Ser Ile Ser  Pro Asn Glu Ser Ile  Asp Asp Glu
    3455                3460                3465
```

```
His Leu  Leu Ile Gln His Tyr  Cys Gln Ser Leu Asn  Gln Asp Ser
    3470                3475                3480

Pro Leu  Ser Gln Pro Arg Ser  Pro Ala Gln Ile Leu  Ile Ser Leu
    3485                3490                3495

Glu Ser  Glu Glu Arg Gly Glu  Leu Glu Arg Ile Leu  Ala Asp Leu
    3500                3505                3510

Glu Glu  Glu Asn Arg Asn Leu  Gln Ala Glu Tyr Asp  Arg Leu Lys
    3515                3520                3525

Gln Gln  His Glu His Lys Gly  Leu Ser Pro Leu Pro  Ser Pro Pro
    3530                3535                3540

Glu Met  Met Pro Thr Ser Pro  Gln Ser Pro Arg Asp  Ala Glu Leu
    3545                3550                3555

Ile Ala  Glu Ala Lys Leu Leu  Arg Gln His Lys Gly  Arg Leu Glu
    3560                3565                3570

Ala Arg  Met Gln Ile Leu Glu  Asp His Asn Lys Gln  Leu Glu Ser
    3575                3580                3585

Gln Leu  His Arg Leu Arg Gln  Leu Leu Glu Gln Pro  Gln Ala Glu
    3590                3595                3600

Ala Lys  Val Asn Gly Thr Thr  Val Ser Ser Pro Ser  Thr Ser Leu
    3605                3610                3615

Gln Arg  Ser Asp Ser Ser Gln  Pro Met Leu Leu Arg  Val Val Gly
    3620                3625                3630

Ser Gln  Thr Ser Asp Ser Met  Gly Glu Glu Asp Leu  Leu Ser Pro
    3635                3640                3645
```

Pro Gln Asp Thr Ser Thr Gly Leu Glu Glu Val Met Glu Gln Leu
    3650   3655   3660

Asn Asn Ser Phe Pro Ser Ser Arg Gly Arg Asn Thr Pro Gly Lys
    3665   3670   3675

Pro Met Arg Glu Asp Thr Met
    3680   3685

<210> 26
<211> 3978
<212> DNA
<213> Artificial Sequence

<220>
<223> Non-codon optimized Dys3978 gene

<400> 26
atgctttggt gggaagaagt agaggactgt tatgaaagag aagatgttca aaagaaaaca 60

ttcacaaaat gggtaaatgc acaattttct aagtttggga agcagcatat tgagaacctc 120

ttcagtgacc tacaggatgg gaggcgcctc ctagacctcc tcgaaggcct gacagggcaa 180

aaactgccaa aagaaaaagg atccacaaga gttcatgccc tgaacaatgt caacaaggca 240

ctgcgggttt tgcagaacaa taatgttgat ttagtgaata ttggaagtac tgacatcgta 300

gatggaaatc ataaactgac tcttggtttg atttggaata taatcctcca ctggcaggtc 360

aaaaatgtaa tgaaaaatat catggctgga ttgcaacaaa ccaacagtga aaagattctc 420

ctgagctggg tccgacaatc aactcgtaat tatccacagg ttaatgtaat caacttcacc 480

accagctggt ctgatggcct ggctttgaat gctctcatcc atagtcatag gccagaccta 540

tttgactgga atagtgtggt ttgccagcag tcagccacac aacgactgga acatgcattc 600

aacatcgcca gatatcaatt aggcatagag aaactactcg atcctgaaga tgttgatacc 660

acctatccag ataagaagtc catcttaatg tacatcacat cactcttcca agttttgcct 720

caacaagtga gcattgaagc catccaggaa gtggaaatgt tgccaaggcc acctaaagtg 780

actaaagaag aacattttca gttacatcat caaatgcact attctcaaca gatcacggtc 840

agtctagcac agggatatga gagaacttct tcccctaagc ctcgattcaa gagctatgcc 900

tacacacagg ctgcttatgt caccacctct gaccctacac ggagcccatt tccttcacag 960

catttggaag ctcctgaaga caagtcattt ggcagttcat tgatggagag tgaagtaaac 1020

ctggaccgtt atcaaacagc tttagaagaa gtattatcgt ggcttctttc tgctgaggac 1080

acattgcaag cacaaggaga gatttctaat gatgtggaag tggtgaaaga ccagtttcat 1140

actcatgagg ggtacatgat ggatttgaca gcccatcagg gccgggttgg taatattcta 1200

caattgggaa gtaagctgat tggaacagga aaattatcag aagatgaaga aactgaagta 1260

caagagcaga tgaatctcct aaattcaaga tgggaatgcc tcagggtagc tagcatggaa 1320

aaacaaagca atttacatag agttttaatg gatctccaga atcagaaact gaaagagttg 1380

aatgactggc taacaaaaac agaagaaaga acaaggaaaa tggaggaaga gcctcttgga 1440

cctgatcttg aagacctaaa acgccaagta caacaacata aggtgcttca agaagatcta 1500

gaacaagaac aagtcagggt caattctctc actcacatgg tggtggtagt tgatgaatct 1560

agtggagatc acgcaactgc tgctttggaa gaacaactta aggtattggg agatcgatgg 1620

gcaaacatct gtagatggac agaagaccgc tgggttcttt tacaagacca gcctgaccta 1680

gctcctggac tgaccactat tggagcctct cctactcaga ctgttactct ggtgacacaa 1740

cctgtggtta ctaaggaaac tgccatctcc aaactagaaa tgccatcttc cttgatgttg 1800

gaggtaccta ctcatagatt actgcaacag ttcccccctgg acctggaaaa gtttcttgcc 1860

tggcttacag aagctgaaac aactgccaat gtcctacagg atgctacccg taaggaaagg 1920

ctcctagaag actccaaggg agtaaaagag ctgatgaaac aatggcaaga cctccaaggt 1980

gaaattgaag ctcacacaga tgtttatcac aacctggatg aaaacagcca aaaaatcctg 2040

agatccctgg aaggttccga tgatgcagtc ctgttacaaa gacgtttgga taacatgaac 2100

ttcaagtgga gtgaacttcg gaaaaagtct ctcaacatta ggtcccattt ggaagccagt 2160

tctgaccagt ggaagcgtct gcacctttct ctgcaggaac ttctggtgtg gctacagctg 2220

aaagatgatg aattaagccg gcaggcacct attggaggcg actttccagc agttcagaag 2280

cagaacgatg tacatagggc cttcaagagg gaattgaaaa ctaaagaacc tgtaatcatg 2340

agtactcttg agactgtacg aatatttctg acagagcagc ctttggaagg actagagaaa 2400

ctctaccagg agcccagaga gctgcctcct gaggagagag cccagaatgt cactcggctt 2460

ctacgaaagc aggctgagga ggtcaatact gagtgggaaa aattgaacct gcactccgct 2520

gactggcaga gaaaaataga tgagaccctt gaaagactcc aggaacttca agaggccacg 2580

gatgagctgg acctcaagct gcgccaagct gaggtgatca agggatcctg gcagcccgtg 2640

ggcgatctcc tcattgactc tctccaagat cacctcgaga aagtcaaggc acttcgagga 2700

gaaattgcgc ctctgaaaga gaacgtgagc cacgtcaatg accttgctcg ccagcttacc 2760

actttgggca ttcagctctc accgtataac ctcagcactc tggaagacct gaacaccaga 2820

tggaagcttc tgcaggtggc cgtcgaggac cgagtcaggc agctgcatga agcccacagg 2880

gactttggtc cagcatctca gcactttctt tccacgtctg tccagggtcc ctgggagaga 2940

gccatctcgc caaacaaagt gccctactat atcaaccacg agactcaaac aacttgctgg 3000

gaccatccca aaatgacaga gctctaccag tctttagctg acctgaataa tgtcagattc 3060

tcagcttata ggactgccat gaaactccga agactgcaga aggccctttg cttggatctc 3120

ttgagcctgt cagctgcatg tgatgccttg gaccagcaca acctcaagca aaatgaccag 3180

cccatggata tcctgcagat tattaattgt ttgaccacta tttatgaccg cctggagcaa 3240

gagcacaaca atttggtcaa cgtccctctc tgcgtggata tgtgtctgaa ctggctgctg 3300

aatgtttatg atacgggacg aacagggagg atccgtgtcc tgtcttttaa aactggcatc 3360

atttccctgt gtaaagcaca tttggaagac aagtacagat acctttttcaa gcaagtggca 3420

agttcaacag gattttgtga ccagcgcagg ctgggcctcc ttctgcatga ttctatccaa 3480

attccaagac agttgggtga agttgcatcc tttgggggca gtaacattga gccaagtgtc 3540

cggagctgct tccaatttgc taataataag ccagagatcg aagcggccct cttcctagac 3600

tggatgagac tggaacccca gtccatggtg tggctgcccg tcctgcacag agtggctgct 3660

gcagaaactg ccaagcatca ggccaaatgt aacatctgca aagagtgtcc aatcattgga 3720

ttcaggtaca ggagtctaaa gcactttaat tatgacatct gccaaagctg ctttttttct 3780

ggtcgagttg caaaaggcca taaaatgcac tatcccatgg tggaatattg cactccgact 3840

acatcaggag aagatgttcg agactttgcc aaggtactaa aaaacaaatt tcgaaccaaa 3900

aggtattttg cgaagcatcc ccgaatgggc tacctgccag tgcagactgt cttagagggg 3960

gacaacatgg aaacttag 3978

<210> 27
<211> 1329
<212> PRT
<213> Artificial Sequence

<220>
<223> Delta3990 protein

<400> 27

Met Val Trp Trp Glu Glu Val Glu Asp Cys Tyr Glu Arg Glu Asp Val
1 5 10 15

Gln Lys Lys Thr Phe Thr Lys Trp Val Asn Ala Gln Phe Ser Lys Phe
20 25 30

Gly Lys Gln His Ile Glu Asn Leu Phe Ser Asp Leu Gln Asp Gly Arg
35 40 45

Arg Leu Leu Asp Leu Leu Glu Gly Leu Thr Gly Gln Lys Leu Pro Lys
50 55 60

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

Leu Arg Val Leu Gln Asn Asn Asn Val Asp Leu Val Asn Ile Gly Ser
85 90 95

Thr Asp Ile Val Asp Gly Asn His Lys Leu Thr Leu Gly Leu Ile Trp
100 105 110

Asn Ile Ile Leu His Trp Gln Val Lys Asn Val Met Lys Asn Ile Met

115 120 125

Ala Gly Leu Gln Gln Thr Asn Ser Glu Lys Ile Leu Leu Ser Trp Val
130 135 140

Arg Gln Ser Thr Arg Asn Tyr Pro Gln Val Asn Val Ile Asn Phe Thr
145 150 155 160

Thr Ser Trp Ser Asp Gly Leu Ala Leu Asn Ala Leu Ile His Ser His
165 170 175

Arg Pro Asp Leu Phe Asp Trp Asn Ser Val Val Cys Gln Gln Ser Ala
180 185 190

Thr Gln Arg Leu Glu His Ala Phe Asn Ile Ala Arg Tyr Gln Leu Gly
195 200 205

Ile Glu Lys Leu Leu Asp Pro Glu Asp Val Asp Thr Thr Tyr Pro Asp
210 215 220

Lys Lys Ser Ile Leu Met Tyr Ile Thr Ser Leu Phe Gln Val Leu Pro
225 230 235 240

Gln Gln Val Ser Ile Glu Ala Ile Gln Glu Val Glu Met Leu Pro Arg
245 250 255

Pro Pro Lys Val Thr Lys Glu Glu His Phe Gln Leu His His Gln Met
260 265 270

His Tyr Ser Gln Gln Ile Thr Val Ser Leu Ala Gln Gly Tyr Glu Arg
275 280 285

Thr Ser Ser Pro Lys Pro Arg Phe Lys Ser Tyr Ala Tyr Thr Gln Ala
290 295 300

Ala Tyr Val Thr Thr Ser Asp Pro Thr Arg Ser Pro Phe Pro Ser Gln
305 310 315 320

```
His Leu Glu Ala Pro Glu Asp Lys Ser Phe Gly Ser Ser Leu Met Glu
                325                 330                 335

Ser Glu Val Asn Leu Asp Arg Tyr Gln Thr Ala Leu Glu Glu Val Leu
            340                 345                 350

Ser Trp Leu Leu Ser Ala Glu Asp Thr Leu Gln Ala Gln Gly Glu Ile
        355                 360                 365

Ser Asn Asp Val Glu Val Val Lys Asp Gln Phe His Thr His Glu Gly
    370                 375                 380

Tyr Met Met Asp Leu Thr Ala His Gln Gly Arg Val Gly Asn Ile Leu
385                 390                 395                 400

Gln Leu Gly Ser Lys Leu Ile Gly Thr Gly Lys Leu Ser Glu Asp Glu
                405                 410                 415

Glu Thr Glu Val Gln Glu Gln Met Asn Leu Leu Asn Ser Arg Trp Glu
            420                 425                 430

Cys Leu Arg Val Ala Ser Met Glu Lys Gln Ser Asn Leu His Arg Val
        435                 440                 445

Leu Met Asp Leu Gln Asn Gln Lys Leu Lys Glu Leu Asn Asp Trp Leu
    450                 455                 460

Thr Lys Thr Glu Glu Arg Thr Arg Lys Met Glu Glu Glu Pro Leu Gly
465                 470                 475                 480

Pro Asp Leu Glu Asp Leu Lys Arg Gln Val Gln Gln His Lys Val Leu
                485                 490                 495

Gln Glu Asp Leu Glu Gln Glu Gln Val Arg Val Asn Ser Leu Thr His
            500                 505                 510
```

```
Met Val Val Val Val Asp Glu Ser Ser Gly Asp His Ala Thr Ala Ala
        515                 520                 525

Leu Glu Glu Gln Leu Lys Val Leu Gly Asp Arg Trp Ala Asn Ile Cys
    530                 535                 540

Arg Trp Thr Glu Asp Arg Trp Val Leu Leu Gln Asp Gln Pro Asp Leu
545                 550                 555                 560

Ala Pro Gly Leu Thr Thr Ile Gly Ala Ser Pro Thr Gln Thr Val Thr
                565                 570                 575

Leu Val Thr Gln Pro Val Val Thr Lys Glu Thr Ala Ile Ser Lys Leu
            580                 585                 590

Glu Met Pro Ser Ser Leu Met Leu Glu Val Pro Thr His Arg Leu Leu
        595                 600                 605

Gln Gln Phe Pro Leu Asp Leu Glu Lys Phe Leu Ala Trp Leu Thr Glu
    610                 615                 620

Ala Glu Thr Thr Ala Asn Val Leu Gln Asp Ala Thr Arg Lys Glu Arg
625                 630                 635                 640

Leu Leu Glu Asp Ser Lys Gly Val Lys Glu Leu Met Lys Gln Trp Gln
                645                 650                 655

Asp Leu Gln Gly Glu Ile Glu Ala His Thr Asp Val Tyr His Asn Leu
            660                 665                 670

Asp Glu Asn Ser Gln Lys Ile Leu Arg Ser Leu Glu Gly Ser Asp Asp
        675                 680                 685

Ala Val Leu Leu Gln Arg Arg Leu Asp Asn Met Asn Phe Lys Trp Ser
    690                 695                 700
```

```
Glu Leu Arg Lys Lys Ser Leu Asn Ile Arg Ser His Leu Glu Ala Ser
705                 710                 715                 720

Ser Asp Gln Trp Lys Arg Leu His Leu Ser Leu Gln Glu Leu Leu Val
                725                 730                 735

Trp Leu Gln Leu Lys Asp Asp Glu Leu Ser Arg Gln Ala Pro Ile Gly
            740                 745                 750

Gly Asp Phe Pro Ala Val Gln Lys Gln Asn Asp Val His Arg Ala Phe
        755                 760                 765

Lys Arg Glu Leu Lys Thr Lys Glu Pro Val Ile Met Ser Thr Leu Glu
    770                 775                 780

Thr Val Arg Ile Phe Leu Thr Glu Gln Pro Leu Glu Gly Leu Glu Lys
785                 790                 795                 800

Leu Tyr Gln Glu Pro Arg Glu Leu Pro Pro Glu Glu Arg Ala Gln Asn
                805                 810                 815

Val Thr Arg Leu Leu Arg Lys Gln Ala Glu Glu Val Asn Thr Glu Trp
            820                 825                 830

Glu Lys Leu Asn Leu His Ser Ala Asp Trp Gln Arg Lys Ile Asp Glu
        835                 840                 845

Thr Leu Glu Arg Leu Gln Glu Leu Gln Glu Ala Thr Asp Glu Leu Asp
    850                 855                 860

Leu Lys Leu Arg Gln Ala Glu Val Ile Lys Gly Ser Trp Gln Pro Val
865                 870                 875                 880

Gly Asp Leu Leu Ile Asp Ser Leu Gln Asp His Leu Glu Lys Val Lys
                885                 890                 895

Ala Leu Arg Gly Glu Ile Ala Pro Leu Lys Glu Asn Val Ser His Val
```

900 905 910

Asn Asp Leu Ala Arg Gln Leu Thr Thr Leu Gly Ile Gln Leu Ser Pro
915 920 925

Tyr Asn Leu Ser Thr Leu Glu Asp Leu Asn Thr Arg Trp Lys Leu Leu
930 935 940

Gln Val Ala Val Glu Asp Arg Val Arg Gln Leu His Glu Ala His Arg
945 950 955 960

Asp Phe Gly Pro Ala Ser Gln His Phe Leu Ser Thr Ser Val Gln Gly
965 970 975

Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val Pro Tyr Tyr Ile Asn
980 985 990

His Glu Thr Gln Thr Thr Cys Trp Asp His Pro Lys Met Thr Glu Leu
995 1000 1005

Tyr Gln Ser Leu Ala Asp Leu Asn Asn Val Arg Phe Ser Ala Tyr
1010 1015 1020

Arg Thr Ala Met Lys Leu Arg Arg Leu Gln Lys Ala Leu Cys Leu
1025 1030 1035

Asp Leu Leu Ser Leu Ser Ala Ala Cys Asp Ala Leu Asp Gln His
1040 1045 1050

Asn Leu Lys Gln Asn Asp Gln Pro Met Asp Ile Leu Gln Ile Ile
1055 1060 1065

Asn Cys Leu Thr Thr Ile Tyr Asp Arg Leu Glu Gln Glu His Asn
1070 1075 1080

Asn Leu Val Asn Val Pro Leu Cys Val Asp Met Cys Leu Asn Trp
1085 1090 1095

```
Leu Leu  Asn Val Tyr Asp Thr  Gly Arg Thr Gly Arg  Ile Arg Val
    1100                1105                1110

Leu Ser  Phe Lys Thr Gly Ile  Ile Ser Leu Cys Lys  Ala His Leu
    1115                1120                1125

Glu Asp  Lys Tyr Arg Tyr Leu  Phe Lys Gln Val Ala  Ser Ser Thr
    1130                1135                1140

Gly Phe  Cys Asp Gln Arg Arg  Leu Gly Leu Leu Leu  His Asp Ser
    1145                1150                1155

Ile Gln  Ile Pro Arg Gln Leu  Gly Glu Val Ala Ser  Phe Gly Gly
    1160                1165                1170

Ser Asn  Ile Glu Pro Ser Val  Arg Ser Cys Phe Gln  Phe Ala Asn
    1175                1180                1185

Asn Lys  Pro Glu Ile Glu Ala  Ala Leu Phe Leu Asp  Trp Met Arg
    1190                1195                1200

Leu Glu  Pro Gln Ser Met Val  Trp Leu Pro Val Leu  His Arg Val
    1205                1210                1215

Ala Ala  Ala Glu Thr Ala Lys  His Gln Ala Lys Cys  Asn Ile Cys
    1220                1225                1230

Lys Glu  Cys Pro Ile Ile Gly  Phe Arg Tyr Arg Ser  Leu Lys His
    1235                1240                1245

Phe Asn  Tyr Asp Ile Cys Gln  Ser Cys Phe Phe Ser  Gly Arg Val
    1250                1255                1260

Ala Lys  Gly His Lys Met His  Tyr Pro Met Val Glu  Tyr Cys Thr
    1265                1270                1275
```

Pro Thr Thr Ser Gly Glu Asp Val Arg Asp Phe Ala Lys Val Leu
    1280   1285   1290

Lys Asn Lys Phe Arg Thr Lys Arg Tyr Phe Ala Lys His Pro Arg
    1295   1300   1305

Met Gly Tyr Leu Pro Val Gln Thr Val Leu Glu Gly Asp Asn Met
    1310   1315   1320

Glu Thr Pro Asp Thr Met
    1325

<210> 28
<211> 3990
<212> DNA
<213> Artificial Sequence

<220>
<223> Delta3990 gene

<400> 28
atggtttggt gggaagaagt agaggactgt tatgaaagag aagatgttca aaagaaaaca 60

ttcacaaaat gggtaaatgc acaattttct aagtttggga agcagcatat tgagaacctc 120

ttcagtgacc tacaggatgg gaggcgcctc ctagacctcc tcgaaggcct gacagggcaa 180

aaactgccaa aagaaaaagg atccacaaga gttcatgccc tgaacaatgt caacaaggca 240

ctgcgggttt tgcagaacaa taatgttgat ttagtgaata ttggaagtac tgacatcgta 300

gatggaaatc ataaactgac tcttggtttg atttggaata taatcctcca ctggcaggtc 360

aaaaatgtaa tgaaaaatat catggctgga ttgcaacaaa ccaacagtga aaagattctc 420

ctgagctggg tccgacaatc aactcgtaat tatccacagg ttaatgtaat caacttcacc 480

accagctggt ctgatggcct ggctttgaat gctctcatcc atagtcatag gccagaccta 540

tttgactgga atagtgtggt ttgccagcag tcagccacac aacgactgga acatgcattc 600

aacatcgcca gatatcaatt aggcatagag aaactactcg atcctgaaga tgttgatacc 660

acctatccag ataagaagtc catcttaatg tacatcacat cactcttcca agttttgcct 720

caacaagtga gcattgaagc catccaggaa gtggaaatgt tgccaaggcc acctaaagtg 780

actaaagaag aacattttca gttacatcat caaatgcact attctcaaca gatcacggtc 840

agtctagcac agggatatga gagaacttct tcccctaagc ctcgattcaa gagctatgcc 900

tacacacagg ctgcttatgt caccacctct gaccctacac ggagcccatt tccttcacag 960

catttggaag ctcctgaaga caagtcattt ggcagttcat tgatggagag tgaagtaaac 1020

ctggaccgtt atcaaacagc tttagaagaa gtattatcgt ggcttctttc tgctgaggac 1080

acattgcaag cacaaggaga gatttctaat gatgtggaag tggtgaaaga ccagtttcat 1140

actcatgagg ggtacatgat ggatttgaca gcccatcagg gccgggttgg taatattcta 1200

caattgggaa gtaagctgat tggaacagga aaattatcag aagatgaaga aactgaagta 1260

caagagcaga tgaatctcct aaattcaaga tgggaatgcc tcagggtagc tagcatggaa 1320

aaacaaagca atttacatag agttttaatg gatctccaga atcagaaact gaaagagttg 1380

aatgactggc taacaaaaac agaagaaaga acaaggaaaa tggaggaaga gcctcttgga 1440

cctgatcttg aagacctaaa acgccaagta caacaacata aggtgcttca agaagatcta 1500

gaacaagaac aagtcagggt caattctctc actcacatgg tggtggtagt tgatgaatct 1560

agtggagatc acgcaactgc tgctttggaa gaacaactta aggtattggg agatcgatgg 1620

gcaaacatct gtagatggac agaagaccgc tgggttcttt tacaagacca gcctgaccta 1680

gctcctggac tgaccactat tggagcctct cctactcaga ctgttactct ggtgacacaa 1740

cctgtggtta ctaaggaaac tgccatctcc aaactagaaa tgccatcttc cttgatgttg 1800

gaggtaccta ctcatagatt actgcaacag ttccccctgg acctggaaaa gtttcttgcc 1860

tggcttacag aagctgaaac aactgccaat gtcctacagg atgctacccg taaggaaagg 1920

ctcctagaag actccaaggg agtaaaagag ctgatgaaac aatggcaaga cctccaaggt 1980

gaaattgaag ctcacacaga tgtttatcac aacctggatg aaaacagcca aaaaatcctg 2040

agatccctgg aaggttccga tgatgcagtc ctgttacaaa gacgtttgga taacatgaac 2100

ttcaagtgga gtgaacttcg gaaaaagtct ctcaacatta ggtcccattt ggaagccagt 2160

tctgaccagt ggaagcgtct gcacctttct ctgcaggaac ttctggtgtg gctacagctg 2220

aaagatgatg aattaagccg gcaggcacct attggaggcg actttccagc agttcagaag 2280

cagaacgatg tacatagggc cttcaagagg gaattgaaaa ctaaagaacc tgtaatcatg 2340

agtactcttg agactgtacg aatatttctg acagagcagc ctttggaagg actagagaaa 2400

ctctaccagg agcccagaga gctgcctcct gaggagagag cccagaatgt cactcggctt 2460

ctacgaaagc aggctgagga ggtcaatact gagtgggaaa aattgaacct gcactccgct 2520

gactggcaga gaaaaatага tgagaccctt gaaagactcc aggaacttca agaggccacg 2580

gatgagctgg acctcaagct gcgccaagct gaggtgatca agggatcctg gcagcccgtg 2640

ggcgatctcc tcattgactc tctccaagat cacctcgaga aagtcaaggc acttcgagga 2700

gaaattgcgc ctctgaaaga gaacgtgagc cacgtcaatg accttgctcg ccagcttacc 2760

actttgggca ttcagctctc accgtataac ctcagcactc tggaagacct gaacaccaga 2820

tggaagcttc tgcaggtggc cgtcgaggac cgagtcaggc agctgcatga agcccacagg 2880

gactttggtc cagcatctca gcactttctt tccacgtctg tccagggtcc ctgggagaga 2940

gccatctcgc caaacaaagt gccctactat atcaaccacg agactcaaac aacttgctgg 3000

gaccatccca aaatgacaga gctctaccag tctttagctg acctgaataa tgtcagattc 3060

tcagcttata ggactgccat gaaactccga agactgcaga aggccctttg cttggatctc 3120

ttgagcctgt cagctgcatg tgatgccttg gaccagcaca acctcaagca aaatgaccag 3180

cccatggata tcctgcagat tattaattgt ttgaccacta tttatgaccg cctggagcaa 3240

gagcacaaca atttggtcaa cgtccctctc tgcgtggata tgtgtctgaa ctggctgctg 3300

aatgtttatg atacgggacg aacagggagg atccgtgtcc tgtcttttaa aactggcatc 3360

atttccctgt gtaaagcaca tttggaagac aagtacagat acctttтcaa gcaagtggca 3420

agttcaacag gattttgtga ccagcgcagg ctgggcctcc ttctgcatga ttctatccaa 3480

attccaagac agttgggtga agttgcatcc tttgggggca gtaacattga gccaagtgtc 3540

cggagctgct tccaatttgc taataataag ccagagatcg aagcggccct cttcctagac 3600

tggatgagac tggaacccca gtccatggtg tggctgcccg tcctgcacag agtggctgct 3660

gcagaaactg ccaagcatca ggccaaatgt aacatctgca aagagtgtcc aatcattgga 3720

ttcaggtaca ggagtctaaa gcactttaat tatgacatct gccaaagctg ctttttttct 3780

ggtcgagttg caaaaggcca taaaatgcac tatcccatgg tggaatattg cactccgact 3840

acatcaggag aagatgttcg agactttgcc aaggtactaa aaaacaaatt tcgaaccaaa 3900

aggtattttg cgaagcatcc ccgaatgggc tacctgccag tgcagactgt cttagagggg 3960

gacaacatgg aaactcccga cacaatgtag 3990