SEQUENCE LISTING

<110> THE WISTAR INSTITUTE OF ANATOMY AND BIOLOGY
Muthumani, Kar
Weiner, David

<120> VACCINES AGAINST AFRICAN SWINE FEVER VIRUS, AND METHODS OF USING SAME

<130> 206194-0040-00WO

<150> US 62/950,194
<151> 2019-12-19

<160> 33

<170> PatentIn version 3.5

<210> 1
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aactccggcc ggatcgtgac caccgccatc aagaccctgc tgagcaccgt gaagtacgac 180

atcgtgaagt ccgccaggat ctacgcagga cagggataca ccgagcacca ggcccaggag 240

gagtggaaca tgatcctgca cgtgctgttc gaggaggaga cagagtccag cgcctccagc 300

gagaacatcc acgagaagaa cgacaacgag acaaacgagt gcaccagcag cttcgagaca 360

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cagaagaccg tgcagcacat cgagcagtac ggcaaggccc ccgacttcaa caaagtgatc 480

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gacagcgagt tcttccagcc cgtgtaccca aggcactacg gagagtgtct gtccccagtg 660

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gtgaccgaca gactggtcat ggccaccggc ggcccagcag cagcaccagc agcagccagc 1020

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aactccctc 1149

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<223> Chemically Synthesized, synthetic ASFV-p32 and p54 immunogen

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Asp Phe Ile Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe Lys Thr
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Asp Leu Arg Ser Ser Ser Gln Val Val Phe His Ala Gly Ser Leu Tyr
20 25 30

Asn Trp Phe Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val Thr Thr
35 40 45

Ala Ile Lys Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val Lys Ser
50 55 60

Ala Arg Ile Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala Gln Glu
65 70 75 80

Glu Trp Asn Met Ile Leu His Val Leu Phe Glu Glu Glu Thr Glu Ser
85 90 95

Ser Ala Ser Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu Thr Asn
100 105 110

Glu Cys Thr Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro Ser Ser
115 120 125

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Glu Val Pro Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys Thr Val
    130                 135                 140

Gln His Ile Glu Gln Tyr Gly Lys Ala Pro Asp Phe Asn Lys Val Ile
145                 150                 155                 160

Arg Ala His Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu Lys Glu
                165                 170                 175

Glu Glu Lys Glu Val Val Arg Leu Met Val Ile Lys Leu Leu Lys Lys
            180                 185                 190

Lys Arg Gly Arg Lys Arg Arg Ser Asp Ser Glu Phe Phe Gln Pro Val
        195                 200                 205

Tyr Pro Arg His Tyr Gly Glu Cys Leu Ser Pro Val Thr Thr Pro Ser
    210                 215                 220

Phe Phe Ser Thr His Met Tyr Thr Ile Leu Ile Ala Ile Val Val Leu
225                 230                 235                 240

Val Ile Ile Ile Ile Val Leu Ile Tyr Leu Phe Ser Ser Arg Lys Lys
                245                 250                 255

Lys Ala Ala Ala Ile Glu Glu Glu Asp Ile Gln Phe Ile Asn Pro Tyr
            260                 265                 270

Gln Asp Gln Gln Trp Val Glu Val Thr Pro Gln Pro Gly Thr Ser Lys
        275                 280                 285

Pro Ala Gly Ala Thr Thr Ala Ser Val Gly Lys Pro Val Thr Gly Arg
    290                 295                 300

Pro Ala Thr Asn Arg Pro Ala Thr Asn Lys Pro Val Thr Asp Asn Pro
305                 310                 315                 320

Val Thr Asp Arg Leu Val Met Ala Thr Gly Gly Pro Ala Ala Ala Pro
                325                 330                 335
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Ala Ala Ala Ser Ala Pro Ala His Pro Ala Glu Pro Tyr Thr Thr Val
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Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu
355 360 365

Arg Gln Arg Asn Thr Tyr Thr His Lys Asp Leu Glu Asn Ser Leu
370 375 380

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

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<223> Chemically Synthesized, synthetic ASFV-p32 and p54 immunogen operably linked to IgE leader sequence

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ggccggatcg tgaccaccgc catcaagacc ctgctgagca ccgtgaagta cgacatcgtg 240

aagtccgcca ggatctacgc aggacaggga tacaccgagc accaggccca ggaggagtgg 300

aacatgatcc tgcacgtgct gttcgaggag gagacagagt ccagcgcctc cagcgagaac 360

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cacaacttca tccagaccat ctacggcacc ccactgaagg aggaggagaa ggaggtggtg 600

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cagccaggca ccagcaagcc agcaggagca accaccgcat ccgtgggcaa gccagtgacc 960

ggcaggcctg caaccaacag accagccacc aacaagcctg tgaccgacaa ccctgtgacc 1020

gacagactgg tcatggccac cggcggccca gcagcagcac cagcagcagc cagcgcccca 1080

gcacaccctg cagagccata caccaccgtg accacccaga acaccgcctc ccagaccatg 1140

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<212> PRT
<213> Artificial Sequence

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<223> Chemically Synthesized, synthetic ASFV-p32 and p54 immunogen operably linked to IgE leader sequence

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His Ser Asp Phe Ile Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe
20 25 30

Lys Thr Asp Leu Arg Ser Ser Ser Gln Val Val Phe His Ala Gly Ser
35 40 45

Leu Tyr Asn Trp Phe Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val
50 55 60

Thr Thr Ala Ile Lys Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val
65 70 75 80

Lys Ser Ala Arg Ile Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala
85 90 95

Gln Glu Glu Trp Asn Met Ile Leu His Val Leu Phe Glu Glu Glu Thr
100 105 110

Glu Ser Ser Ala Ser Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu
115 120 125

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Thr Asn Glu Cys Thr Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro
    130                 135                 140

Ser Ser Glu Val Pro Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys
145                 150                 155                 160

Thr Val Gln His Ile Glu Gln Tyr Gly Lys Ala Pro Asp Phe Asn Lys
                165                 170                 175

Val Ile Arg Ala His Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu
            180                 185                 190

Lys Glu Glu Glu Lys Glu Val Val Arg Leu Met Val Ile Lys Leu Leu
        195                 200                 205

Lys Lys Lys Arg Gly Arg Lys Arg Arg Ser Asp Ser Glu Phe Phe Gln
    210                 215                 220

Pro Val Tyr Pro Arg His Tyr Gly Glu Cys Leu Ser Pro Val Thr Thr
225                 230                 235                 240

Pro Ser Phe Phe Ser Thr His Met Tyr Thr Ile Leu Ile Ala Ile Val
                245                 250                 255

Val Leu Val Ile Ile Ile Ile Val Leu Ile Tyr Leu Phe Ser Ser Arg
            260                 265                 270

Lys Lys Lys Ala Ala Ala Ile Glu Glu Glu Asp Ile Gln Phe Ile Asn
        275                 280                 285

Pro Tyr Gln Asp Gln Gln Trp Val Glu Val Thr Pro Gln Pro Gly Thr
    290                 295                 300

Ser Lys Pro Ala Gly Ala Thr Thr Ala Ser Val Gly Lys Pro Val Thr
305                 310                 315                 320

Gly Arg Pro Ala Thr Asn Arg Pro Ala Thr Asn Lys Pro Val Thr Asp
                325                 330                 335

Asn Pro Val Thr Asp Arg Leu Val Met Ala Thr Gly Gly Pro Ala Ala
            340                 345                 350
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Ala Pro Ala Ala Ala Ser Ala Pro Ala His Pro Ala Glu Pro Tyr Thr
355 360 365

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

Leu

<210> 5
<211> 2910
<212> DNA
<213> Artificial Sequence

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<223> Chemically Synthesized, synthetic ASFV-ubi-CD2, p32 and p54 immunogen

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gacaccctgt acgagggcgg cctgttcaag gccaaggtgg cattccctcc cgagtaccca 180

tacgccccac ctaagctgac cttcaccagc gagatgtggc acccaaacat ctaccctgac 240

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atcgagtccc cacctcccga gagcaacgaa gaggagcagt gccagcacga cgacaccacc 1440

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acccagaaca ccgcctccca gaccatgagc gccattgaga acctgagaca gcggaatacc 2880

tacacccata aagacctgga aaacagcctg 2910

<210> 6
<211> 970
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-ubi-CD2, p32 and p54 immunogen

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Ser Glu Asn Phe Lys Ile Ser Val Asn Glu Asn Asn Ile Thr Glu Trp
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Asp Val Ile Leu Arg Gly Pro Pro Asp Thr Leu Tyr Glu Gly Gly Leu
35 40 45

Phe Lys Ala Lys Val Ala Phe Pro Pro Glu Tyr Pro Tyr Ala Pro Pro
50 55 60

Lys Leu Thr Phe Thr Ser Glu Met Trp His Pro Asn Ile Tyr Pro Asp
65 70 75 80

Gly Arg Leu Cys Ile Ser Ile Leu His Gly Asp Asn Ala Glu Glu Gln
85 90 95

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Gly Met Thr Trp Ser Pro Ala Gln Lys Ile Asp Thr Ile Leu Leu Ser
            100                 105                 110

Val Ile Ser Leu Leu Asn Glu Pro Asn Pro Asp Ser Pro Ala Asn Val
        115                 120                 125

Asp Ala Ala Lys Ser Tyr Arg Lys Tyr Val Tyr Lys Glu Asp Leu Glu
    130                 135                 140

Ser Tyr Pro Met Glu Val Lys Lys Thr Val Lys Lys Ser Leu Asp Glu
145                 150                 155                 160

Cys Ser Pro Glu Asp Ile Glu Tyr Phe Lys Asn Ala Ala Ser Asn Val
                165                 170                 175

Pro Pro Ile Pro Ser Asp Ala Tyr Glu Asp Glu Cys Glu Glu Met Glu
            180                 185                 190

Asp Asp Thr Tyr Ile Leu Thr Tyr Asp Asp Asp Glu Glu Glu Glu Asp
        195                 200                 205

Glu Glu Met Asp Asp Glu Arg Gly Arg Lys Arg Arg Ser Ile Ile Leu
    210                 215                 220

Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser Ile Asp Tyr Trp Val
225                 230                 235                 240

Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn Ile Thr Asn Asp Asn
                245                 250                 255

Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe Asn Asn Ser Phe Asn
            260                 265                 270

Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe Cys Glu Cys Ser Asn
        275                 280                 285

Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn Cys Ser Leu Thr Ile
    290                 295                 300

Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr Gln Val Val Trp Asn
305                 310                 315                 320
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Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr Pro Ala Thr Pro Pro
               325                 330                 335

Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile Thr Cys Lys Lys Asn
            340                 345                 350

Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile Asn Asp Thr Phe Val
        355                 360                 365

Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn Trp Asn Asn Ser Asn
    370                 375                 380

Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn Asn Thr Ile Ser Thr
385                 390                 395                 400

Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr Leu Thr Leu Ser Ser
               405                 410                 415

Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr Ile Pro Leu Ser Ile
            420                 425                 430

Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile Ser Ile Ile Thr Phe
        435                 440                 445

Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu Glu Ile Glu Ser Pro
    450                 455                 460

Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln His Asp Asp Thr Thr
465                 470                 475                 480

Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu Pro Lys Pro Tyr
               485                 490                 495

Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met Arg Pro Ser Thr
            500                 505                 510

Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys Pro Pro Pro Lys
        515                 520                 525
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Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Ser
    530                 535                 540

Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile Pro Leu Leu
545                 550                 555                 560

Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile His Val
                565                 570                 575

Asp Arg Ile Ile Arg Gly Arg Lys Arg Arg Ser Asp Phe Ile Leu Asn
            580                 585                 590

Ile Ser Met Lys Met Glu Val Ile Phe Lys Thr Asp Leu Arg Ser Ser
        595                 600                 605

Ser Gln Val Val Phe His Ala Gly Ser Leu Tyr Asn Trp Phe Ser Val
    610                 615                 620

Glu Ile Ile Asn Ser Gly Arg Ile Val Thr Thr Ala Ile Lys Thr Leu
625                 630                 635                 640

Leu Ser Thr Val Lys Tyr Asp Ile Val Lys Ser Ala Arg Ile Tyr Ala
                645                 650                 655

Gly Gln Gly Tyr Thr Glu His Gln Ala Gln Glu Glu Trp Asn Met Ile
            660                 665                 670

Leu His Val Leu Phe Glu Glu Glu Thr Glu Ser Ser Ala Ser Ser Glu
        675                 680                 685

Asn Ile His Glu Lys Asn Asp Asn Glu Thr Asn Glu Cys Thr Ser Ser
    690                 695                 700

Phe Glu Thr Leu Phe Glu Gln Glu Pro Ser Ser Glu Val Pro Lys Asp
705                 710                 715                 720

Ser Lys Leu Tyr Met Leu Ala Gln Lys Thr Val Gln His Ile Glu Gln
                725                 730                 735

Tyr Gly Lys Ala Pro Asp Phe Asn Lys Val Ile Arg Ala His Asn Phe
            740                 745                 750
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Ile Gln Thr Ile Tyr Gly Thr Pro Leu Lys Glu Glu Glu Lys Glu Val
        755                 760                 765

Val Arg Leu Met Val Ile Lys Leu Leu Lys Lys Lys Arg Gly Arg Lys
    770                 775                 780

Arg Arg Ser Asp Ser Glu Phe Phe Gln Pro Val Tyr Pro Arg His Tyr
785                 790                 795                 800

Gly Glu Cys Leu Ser Pro Val Thr Thr Pro Ser Phe Phe Ser Thr His
                805                 810                 815

Met Tyr Thr Ile Leu Ile Ala Ile Val Val Leu Val Ile Ile Ile Ile
            820                 825                 830

Val Leu Ile Tyr Leu Phe Ser Ser Arg Lys Lys Lys Ala Ala Ala Ile
        835                 840                 845

Glu Glu Glu Asp Ile Gln Phe Ile Asn Pro Tyr Gln Asp Gln Gln Trp
    850                 855                 860

Val Glu Val Thr Pro Gln Pro Gly Thr Ser Lys Pro Ala Gly Ala Thr
865                 870                 875                 880

Thr Ala Ser Val Gly Lys Pro Val Thr Gly Arg Pro Ala Thr Asn Arg
                885                 890                 895

Pro Ala Thr Asn Lys Pro Val Thr Asp Asn Pro Val Thr Asp Arg Leu
            900                 905                 910

Val Met Ala Thr Gly Gly Pro Ala Ala Ala Pro Ala Ala Ala Ser Ala
        915                 920                 925

Pro Ala His Pro Ala Glu Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr
    930                 935                 940

Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Arg Gln Arg Asn Thr
945                 950                 955                 960
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Tyr Thr His Lys Asp Leu Glu Asn Ser Leu
965 970

<210> 7
<211> 2964
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-ubi-CD2, p32 and p54 immunogen operably linked to IgE leader sequence

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agcgtgaacg agaacaacat caccgagtgg gacgtgatcc tgaggggccc acccgacacc 180

ctgtacgagg gcggcctgtt caaggccaag gtggcattcc ctcccgagta cccatacgcc 240

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aggaagcggc gcagcgactt catcctgaac atctccatga agatggaagt gatcttcaag 1860

accgacctgc gcagctccag ccaggtggtg ttccacgcag gctccctgta caactggttc 1920

agcgtggaga tcatcaactc cggccggatc gtgaccaccg ccatcaagac cctgctgagc 1980

accgtgaagt acgacatcgt gaagtccgcc aggatctacg caggacaggg atacaccgag 2040

caccaggccc aggaggagtg gaacatgatc ctgcacgtgc tgttcgagga ggagacagag 2100

tccagcgcct ccagcgagaa catccacgag aagaacgaca acgagacaaa cgagtgcacc 2160

agcagcttcg agacactgtt cgagcaggag ccctccagcg aggtgccaaa ggacagcaag 2220

ctgtacatgc tggcccagaa gaccgtgcag cacatcgagc agtacggcaa ggcccccgac 2280

ttcaacaaag tgatcagggc ccacaacttc atccagacca tctacggcac cccactgaag 2340

gaggaggaga aggaggtggt gagactgatg gtcatcaagc tgctgaagaa gaagaggggc 2400

agaaagagga gatccgacag cgagttcttc cagcccgtgt accccaggca ctacggcgag 2460

tgtctgtccc ctgtgaccac cccctccttc ttcagcaccc acatgtacac catcctgatc 2520

gccatcgtgg tgctggtcat catcatcatc gtgctgatct acctgttcag cagcaggaag 2580

aagaaggccg ccgccatcga ggaggaggac atccagttca tcaacccata ccaggaccag 2640

cagtgggtgg aggtgacccc acagcctggc accagcaagc ctgcaggagc aaccaccgca 2700

tccgtgggca agcctgtgac cggcaggccc gcaaccaaca ggccagccac caacaagcct 2760

gtgaccgaca accccgtgac cgacaggctg gtcatggcca ccggcggccc agcagcagca 2820

cctgcagcag cctccgcccc agcacaccct gcagagccat acaccaccgt gaccacccag 2880

aacaccgcct cccagaccat gagcgccatt gagaacctga gacagcggaa tacctacacc 2940

cataaagacc tggaaaacag cctg 2964

<210> 8
<211> 988
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-ubi-CD2, p32 and p54 immunogen operably linked to IgE leader sequence

<400> 8

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Val Ser Arg Phe Leu Ile Ala Glu Tyr Arg His Leu Ile Glu
20 25 30

Asn Pro Ser Glu Asn Phe Lys Ile Ser Val Asn Glu Asn Asn Ile Thr
35 40 45

Glu Trp Asp Val Ile Leu Arg Gly Pro Pro Asp Thr Leu Tyr Glu Gly
50 55 60

Gly Leu Phe Lys Ala Lys Val Ala Phe Pro Pro Glu Tyr Pro Tyr Ala
65 70 75 80

Pro Pro Lys Leu Thr Phe Thr Ser Glu Met Trp His Pro Asn Ile Tyr
85 90 95

Pro Asp Gly Arg Leu Cys Ile Ser Ile Leu His Gly Asp Asn Ala Glu
100 105 110

Glu Gln Gly Met Thr Trp Ser Pro Ala Gln Lys Ile Asp Thr Ile Leu
115 120 125

Leu Ser Val Ile Ser Leu Leu Asn Glu Pro Asn Pro Asp Ser Pro Ala
130 135 140

```
Asn Val Asp Ala Ala Lys Ser Tyr Arg Lys Tyr Val Tyr Lys Glu Asp
145                 150                 155                 160

Leu Glu Ser Tyr Pro Met Glu Val Lys Lys Thr Val Lys Lys Ser Leu
                165                 170                 175

Asp Glu Cys Ser Pro Glu Asp Ile Glu Tyr Phe Lys Asn Ala Ala Ser
            180                 185                 190

Asn Val Pro Pro Ile Pro Ser Asp Ala Tyr Glu Asp Glu Cys Glu Glu
        195                 200                 205

Met Glu Asp Asp Thr Tyr Ile Leu Thr Tyr Asp Asp Asp Glu Glu Glu
    210                 215                 220

Glu Asp Glu Glu Met Asp Asp Glu Arg Gly Arg Lys Arg Arg Ser Ile
225                 230                 235                 240

Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser Ile Asp Tyr
                245                 250                 255

Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn Ile Thr Asn
            260                 265                 270

Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe Asn Asn Ser
        275                 280                 285

Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe Cys Glu Cys
    290                 295                 300

Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn Cys Ser Leu
305                 310                 315                 320

Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr Gln Val Val
                325                 330                 335

Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr Pro Ala Thr
            340                 345                 350

Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile Thr Cys Lys
        355                 360                 365
```

```
Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile Asn Asp Thr
    370                 375                 380

Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn Trp Asn Asn
385                 390                 395                 400

Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn Asn Thr Ile
                405                 410                 415

Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr Leu Thr Leu
            420                 425                 430

Ser Ser Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr Ile Pro Leu
        435                 440                 445

Ser Ile Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile Ser Ile Ile
    450                 455                 460

Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu Glu Ile Glu
465                 470                 475                 480

Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln His Asp Asp
                485                 490                 495

Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu Pro Lys
            500                 505                 510

Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met Arg Pro
        515                 520                 525

Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys Pro Pro
    530                 535                 540

Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys
545                 550                 555                 560

Pro Ser Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile Pro
                565                 570                 575
```

```
Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile
            580                 585                 590

His Val Asp Arg Ile Ile Arg Gly Arg Lys Arg Arg Ser Asp Phe Ile
        595                 600                 605

Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe Lys Thr Asp Leu Arg
    610                 615                 620

Ser Ser Ser Gln Val Val Phe His Ala Gly Ser Leu Tyr Asn Trp Phe
625                 630                 635                 640

Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val Thr Thr Ala Ile Lys
                645                 650                 655

Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val Lys Ser Ala Arg Ile
            660                 665                 670

Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala Gln Glu Glu Trp Asn
        675                 680                 685

Met Ile Leu His Val Leu Phe Glu Glu Glu Thr Glu Ser Ser Ala Ser
    690                 695                 700

Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu Thr Asn Glu Cys Thr
705                 710                 715                 720

Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro Ser Ser Glu Val Pro
                725                 730                 735

Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys Thr Val Gln His Ile
            740                 745                 750

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

Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu Lys Glu Glu Glu Lys
    770                 775                 780

Glu Val Val Arg Leu Met Val Ile Lys Leu Leu Lys Lys Lys Arg Gly
785                 790                 795                 800
```

```
Arg Lys Arg Arg Ser Asp Ser Glu Phe Phe Gln Pro Val Tyr Pro Arg
                805                 810                 815

His Tyr Gly Glu Cys Leu Ser Pro Val Thr Thr Pro Ser Phe Phe Ser
            820                 825                 830

Thr His Met Tyr Thr Ile Leu Ile Ala Ile Val Val Leu Val Ile Ile
        835                 840                 845

Ile Ile Val Leu Ile Tyr Leu Phe Ser Ser Arg Lys Lys Lys Ala Ala
    850                 855                 860

Ala Ile Glu Glu Glu Asp Ile Gln Phe Ile Asn Pro Tyr Gln Asp Gln
865                 870                 875                 880

Gln Trp Val Glu Val Thr Pro Gln Pro Gly Thr Ser Lys Pro Ala Gly
                885                 890                 895

Ala Thr Thr Ala Ser Val Gly Lys Pro Val Thr Gly Arg Pro Ala Thr
            900                 905                 910

Asn Arg Pro Ala Thr Asn Lys Pro Val Thr Asp Asn Pro Val Thr Asp
        915                 920                 925

Arg Leu Val Met Ala Thr Gly Gly Pro Ala Ala Ala Pro Ala Ala Ala
    930                 935                 940

Ser Ala Pro Ala His Pro Ala Glu Pro Tyr Thr Thr Val Thr Thr Gln
945                 950                 955                 960

Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Arg Gln Arg
                965                 970                 975

Asn Thr Tyr Thr His Lys Asp Leu Glu Asn Ser Leu
            980                 985
```

<210> 9
<211> 2247
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV- CD2+p32+p54 immunogen

<400> 9
atcattctca tctttctcat cttttcaaac atcgtgctgt ccatcgacta ctgggtgagc 60

ttcaacaaga ccatcatcct ggacagcaac atcaccaacg acaacaacga catcaacggc 120

gtgagctgga acttcttcaa caactccttc aacaccctgg caacctgcgg caaggcaggc 180

aacttctgcg agtgtagcaa ctactccacc agcatctaca acatcaccaa caactgttcc 240

ctgaccatct tcccccacaa cgacgtgttc gacaccacct accaggtggt gtggaaccag 300

atcatcaact acaccatcaa gctgctgacc cccgccaccc cacccaacat cacctacaac 360

tgcaccaact tcctgatcac ctgtaagaag aacaacggca ccaacaccaa catctacctg 420

aacatcaacg acaccttcgt gaagtacacc aacgagagca tcctggagta caactggaac 480

aactccaaca tcaacaactt caccgccacc tgcatcatca acaacaccat ctccaccagc 540

aacgagacaa ccctgatcaa ctgtacctac ctgaccctga gctccaacta cttctacacc 600

ttcttcaagc tgtactacat ccccctgagc atcatcatcg gcatcaccat ctccatcctg 660

ctgatcagca tcatcacctt cctgtccctg aggaagagaa agaagcacgt ggaggagatc 720

gagtcccctc ccccagagag caacgaggag gagcagtgcc agcacgacga caccacctcc 780

atccacgagc caagcccaag ggagccactg ctgcctaagc cctacagcag ataccagtac 840

aacaccccaa tctactacat gaggccctcc acccagccac tgaacccatt ccctctgccc 900

aagccatgcc ctcccccaaa gccatgtcct cccccaaagc cttgccctcc cccaaagcct 960

tgtccaagcg ccgagtccta cagccctccc aagccactgc cttccatccc tctgctgccc 1020

aacatcccac ctctgtccac ccagaacatc agcctgatcc acgtggaccg gatcatccgg 1080

ggccgcaaga ggagaagcga cttcatcctg aacatctcca tgaagatgga agtgatcttc 1140

aagaccgacc tgcgcagctc cagccaggtg gtgttccacg caggctccct gtacaactgg 1200

ttcagcgtgg agatcatcaa ctccggccgg atcgtgacca ccgccatcaa gaccctgctg 1260

agcaccgtga agtacgacat cgtgaagtcc gccaggatct acgcaggaca gggatacacc 1320

gagcaccagg cccaggagga gtggaacatg atcctgcacg tgctgttcga ggaggagaca 1380

gagtccagcg cctccagcga gaacatccac gagaagaacg acaacgagac aaacgagtgc 1440

accagcagct tcgagacact gttcgagcag gagccctcca gcgaggtgcc aaaggacagc 1500

aagctgtaca tgctggccca gaagaccgtg cagcacatcg agcagtacgg caaggcccca 1560

gacttcaaca aagtgatcag ggcccacaac ttcatccaga ccatctacgg caccccactg 1620

aaggaggagg agaaggaggt ggtgagactg atggtcatca agctgctgaa gaagaagagg 1680

ggcagaaagc ggcgctccga cagcgagttc ttccagccag tgtaccctag gcactacggc 1740

gagtgtctgt cccctgtgac cacccctcc ttcttcagca cccacatgta caccatcctg 1800

atcgccatcg tggtgctggt catcatcatc atcgtgctga tctacctgtt cagcagcagg 1860

aagaagaagg ccgccgccat cgaggaggag gacatccagt tcatcaaccc ttaccaggac 1920

cagcagtggg tggaggtgac cccacagcca ggcaccagca agccagcagg agcaaccacc 1980

gcatccgtgg gcaagcctgt gaccggcagg cccgcaacca acaggccagc caccaacaag 2040

cctgtgaccg acaaccccgt gaccgaccgg ctggtcatgg ccaccggcgg cccagcagca 2100

gcacctgcag cagcctccgc ccccgcccac ccagccgagc cttacaccac cgtgaccacc 2160

cagaacaccg cctcccagac catgagcgcc attgaaaacc tcagacagcg aaatacttac 2220

actcacaaag acctggaaaa cagcctg 2247

<210> 10
<211> 749
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV- CD2+p32+p54 immunogen

<400> 10

Ile Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser Ile Asp
1 5 10 15

Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn Ile Thr
20 25 30

Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe Asn Asn
35 40 45

Ser Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe Cys Glu
50 55 60

```
Cys Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn Cys Ser
65                  70                  75                  80

Leu Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr Gln Val
                85                  90                  95

Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr Pro Ala
            100                 105                 110

Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile Thr Cys
        115                 120                 125

Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile Asn Asp
    130                 135                 140

Thr Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn Trp Asn
145                 150                 155                 160

Asn Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn Asn Thr
                165                 170                 175

Ile Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr Leu Thr
            180                 185                 190

Leu Ser Ser Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr Ile Pro
        195                 200                 205

Leu Ser Ile Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile Ser Ile
    210                 215                 220

Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu Glu Ile
225                 230                 235                 240

Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln His Asp
                245                 250                 255

Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu Pro
            260                 265                 270

Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met Arg
        275                 280                 285
```

```
Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys Pro
    290                 295                 300

Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro
305                 310                 315                 320

Cys Pro Ser Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile
                325                 330                 335

Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu
            340                 345                 350

Ile His Val Asp Arg Ile Ile Arg Gly Arg Lys Arg Arg Ser Asp Phe
        355                 360                 365

Ile Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe Lys Thr Asp Leu
    370                 375                 380

Arg Ser Ser Ser Gln Val Val Phe His Ala Gly Ser Leu Tyr Asn Trp
385                 390                 395                 400

Phe Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val Thr Thr Ala Ile
                405                 410                 415

Lys Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val Lys Ser Ala Arg
            420                 425                 430

Ile Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala Gln Glu Glu Trp
        435                 440                 445

Asn Met Ile Leu His Val Leu Phe Glu Glu Glu Thr Glu Ser Ser Ala
    450                 455                 460

Ser Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu Thr Asn Glu Cys
465                 470                 475                 480

Thr Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro Ser Ser Glu Val
                485                 490                 495
```

```
Pro Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys Thr Val Gln His
            500                 505                 510

Ile Glu Gln Tyr Gly Lys Ala Pro Asp Phe Asn Lys Val Ile Arg Ala
        515                 520                 525

His Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu Lys Glu Glu Glu
    530                 535                 540

Lys Glu Val Val Arg Leu Met Val Ile Lys Leu Leu Lys Lys Lys Arg
545                 550                 555                 560

Gly Arg Lys Arg Arg Ser Asp Ser Glu Phe Phe Gln Pro Val Tyr Pro
                565                 570                 575

Arg His Tyr Gly Glu Cys Leu Ser Pro Val Thr Thr Pro Ser Phe Phe
            580                 585                 590

Ser Thr His Met Tyr Thr Ile Leu Ile Ala Ile Val Val Leu Val Ile
        595                 600                 605

Ile Ile Ile Val Leu Ile Tyr Leu Phe Ser Ser Arg Lys Lys Lys Ala
    610                 615                 620

Ala Ala Ile Glu Glu Glu Asp Ile Gln Phe Ile Asn Pro Tyr Gln Asp
625                 630                 635                 640

Gln Gln Trp Val Glu Val Thr Pro Gln Pro Gly Thr Ser Lys Pro Ala
                645                 650                 655

Gly Ala Thr Thr Ala Ser Val Gly Lys Pro Val Thr Gly Arg Pro Ala
            660                 665                 670

Thr Asn Arg Pro Ala Thr Asn Lys Pro Val Thr Asp Asn Pro Val Thr
        675                 680                 685

Asp Arg Leu Val Met Ala Thr Gly Gly Pro Ala Ala Ala Pro Ala Ala
    690                 695                 700

Ala Ser Ala Pro Ala His Pro Ala Glu Pro Tyr Thr Thr Val Thr Thr
705                 710                 715                 720
```

Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Arg Gln
725 730 735

Arg Asn Thr Tyr Thr His Lys Asp Leu Glu Asn Ser Leu
740 745

<210> 11
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV- CD2+p32+p54 immunogen operably linked to IgE leader sequence

<400> 11
atggactgga cttggattct ctttctcgtc gccgcagcaa cacgggtgca tagcatcatt 60

ctcatctttc tcatcttttc aaacatcgtg ctgtccatcg actactgggt gagcttcaac 120

aagaccatca tcctggacag caacatcacc aacgacaaca acgacatcaa cggcgtgagc 180

tggaacttct tcaacaactc cttcaacacc ctggcaacct gcggcaaggc aggcaacttc 240

tgcgagtgta gcaactactc caccagcatc tacaacatca ccaacaactg ttccctgacc 300

atcttccccc acaacgacgt gttcgacacc acctaccagg tggtgtggaa ccagatcatc 360

aactacacca tcaagctgct gacccccgcc accccaccca acatcaccta caactgcacc 420

aacttcctga tcacctgtaa gaagaacaac ggcaccaaca ccaacatcta cctgaacatc 480

aacgacacct tcgtgaagta caccaacgag agcatcctgg agtacaactg gaacaactcc 540

aacatcaaca acttcaccgc cacctgcatc atcaacaaca ccatctccac cagcaacgag 600

acaaccctga tcaactgtac ctacctgacc ctgagctcca actacttcta caccttcttc 660

aagctgtact acatcccccc gagcatcatc atcggcatca ccatctccat cctgctgatc 720

agcatcatca ccttcctgtc cctgaggaag agaaagaagc acgtggagga gatcgagtcc 780

cctcccccag agagcaacga ggaggagcag tgccagcacg acgacaccac ctccatccac 840

gagccaagcc caagggagcc actgctgcct aagccctaca gcagatacca gtacaacacc 900

ccaatctact acatgaggcc ctccacccag ccactgaacc cattccctct gcccaagcca 960

tgccctcccc caaagccatg tcctccccca aagccttgcc ctcccccaaa gccttgtcca 1020

agcgccgagt cctacagccc tcccaagcca ctgccttcca tccctctgct gcccaacatc 1080

ccacctctgt ccacccagaa catcagcctg atccacgtgg accggatcat ccggggccgc 1140

aagaggagaa gcgacttcat cctgaacatc tccatgaaga tggaagtgat cttcaagacc 1200

gacctgcgca gctccagcca ggtggtgttc cacgcaggct ccctgtacaa ctggttcagc 1260

gtggagatca tcaactccgg ccggatcgtg accaccgcca tcaagaccct gctgagcacc 1320

gtgaagtacg acatcgtgaa gtccgccagg atctacgcag gacagggata caccgagcac 1380

caggcccagg aggagtggaa catgatcctg cacgtgctgt tcgaggagga gacagagtcc 1440

agcgcctcca gcgagaacat ccacgagaag aacgacaacg agacaaacga gtgcaccagc 1500

agcttcgaga cactgttcga gcaggagccc tccagcgagg tgccaaagga cagcaagctg 1560

tacatgctgg cccagaagac cgtgcagcac atcgagcagt acggcaaggc cccagacttc 1620

aacaaagtga tcagggccca caacttcatc cagaccatct acggcacccc actgaaggag 1680

gaggagaagg aggtggtgag actgatggtc atcaagctgc tgaagaagaa gaggggcaga 1740

aagcggcgct ccgacagcga gttcttccag ccagtgtacc ctaggcacta cggcgagtgt 1800

ctgtcccctg tgaccacccc ctccttcttc agcacccaca tgtacaccat cctgatcgcc 1860

atcgtggtgc tggtcatcat catcatcgtg ctgatctacc tgttcagcag caggaagaag 1920

aaggccgccg ccatcgagga ggaggacatc cagttcatca acccttacca ggaccagcag 1980

tgggtggagg tgaccccaca gccaggcacc agcaagccag caggagcaac caccgcatcc 2040

gtgggcaagc ctgtgaccgg caggcccgca accaacaggc cagccaccaa caagcctgtg 2100

accgacaacc ccgtgaccga ccggctggtc atggccaccg gcggcccagc agcagcacct 2160

gcagcagcct ccgcccccgc ccacccagcc gagccttaca ccaccgtgac cacccagaac 2220

accgcctccc agaccatgag cgccattgaa aacctcagac agcgaaatac ttacactcac 2280

aaagacctgg aaaacagcct g 2301

<210> 12
<211> 767
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV- CD2+p32+p54 immunogen operably linked to IgE leader sequence

<400> 12

```
Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1               5                  10                  15

His Ser Ile Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser
            20                  25                  30

Ile Asp Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn
        35                  40                  45

Ile Thr Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe
    50                  55                  60

Asn Asn Ser Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe
65                  70                  75                  80

Cys Glu Cys Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn
                85                  90                  95

Cys Ser Leu Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr
            100                 105                 110

Gln Val Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr
        115                 120                 125

Pro Ala Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile
    130                 135                 140

Thr Cys Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile
145                 150                 155                 160

Asn Asp Thr Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn
                165                 170                 175

Trp Asn Asn Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn
            180                 185                 190

Asn Thr Ile Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr
        195                 200                 205
```

```
Leu Thr Leu Ser Ser Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr
    210                 215                 220

Ile Pro Leu Ser Ile Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile
225                 230                 235                 240

Ser Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu
                245                 250                 255

Glu Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln
            260                 265                 270

His Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu
        275                 280                 285

Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr
    290                 295                 300

Met Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro
305                 310                 315                 320

Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro
                325                 330                 335

Lys Pro Cys Pro Ser Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro
            340                 345                 350

Ser Ile Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile
        355                 360                 365

Ser Leu Ile His Val Asp Arg Ile Ile Arg Gly Arg Lys Arg Arg Ser
    370                 375                 380

Asp Phe Ile Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe Lys Thr
385                 390                 395                 400

Asp Leu Arg Ser Ser Ser Gln Val Val Phe His Ala Gly Ser Leu Tyr
                405                 410                 415

Asn Trp Phe Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val Thr Thr
            420                 425                 430
```

```
Ala Ile Lys Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val Lys Ser
        435                 440                 445

Ala Arg Ile Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala Gln Glu
    450                 455                 460

Glu Trp Asn Met Ile Leu His Val Leu Phe Glu Glu Glu Thr Glu Ser
465                 470                 475                 480

Ser Ala Ser Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu Thr Asn
                485                 490                 495

Glu Cys Thr Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro Ser Ser
            500                 505                 510

Glu Val Pro Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys Thr Val
        515                 520                 525

Gln His Ile Glu Gln Tyr Gly Lys Ala Pro Asp Phe Asn Lys Val Ile
    530                 535                 540

Arg Ala His Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu Lys Glu
545                 550                 555                 560

Glu Glu Lys Glu Val Val Arg Leu Met Val Ile Lys Leu Leu Lys Lys
                565                 570                 575

Lys Arg Gly Arg Lys Arg Arg Ser Asp Ser Glu Phe Phe Gln Pro Val
            580                 585                 590

Tyr Pro Arg His Tyr Gly Glu Cys Leu Ser Pro Val Thr Thr Pro Ser
        595                 600                 605

Phe Phe Ser Thr His Met Tyr Thr Ile Leu Ile Ala Ile Val Val Leu
    610                 615                 620

Val Ile Ile Ile Ile Val Leu Ile Tyr Leu Phe Ser Ser Arg Lys Lys
625                 630                 635                 640
```

```
Lys Ala Ala Ala Ile Glu Glu Glu Asp Ile Gln Phe Ile Asn Pro Tyr
                645                 650                 655

Gln Asp Gln Gln Trp Val Glu Val Thr Pro Gln Pro Gly Thr Ser Lys
            660                 665                 670

Pro Ala Gly Ala Thr Thr Ala Ser Val Gly Lys Pro Val Thr Gly Arg
        675                 680                 685

Pro Ala Thr Asn Arg Pro Ala Thr Asn Lys Pro Val Thr Asp Asn Pro
    690                 695                 700

Val Thr Asp Arg Leu Val Met Ala Thr Gly Gly Pro Ala Ala Ala Pro
705                 710                 715                 720

Ala Ala Ala Ser Ala Pro Ala His Pro Ala Glu Pro Tyr Thr Thr Val
                725                 730                 735

Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu
            740                 745                 750

Arg Gln Arg Asn Thr Tyr Thr His Lys Asp Leu Glu Asn Ser Leu
        755                 760                 765
```

<210> 13
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV- p32, p12, p54 immunogen

<400> 13

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gactttattc tgaacattag catgaagatg gaagtgatct tcaagaccga cctgaggagc       60

tccagccagg tggtgttcca cgcaggctcc ctgtacaact ggttcagcgt ggagatcatc      120

aactccggcc ggatcgtgac caccgccatc aagaccctgc tgagcaccgt gaagtacgac      180

atcgtgaagt ccgccaggat ctacgcagga cagggataca ccgagcacca ggcccaggag      240

gagtggaaca tgatcctgca cgtgctgttc gaggaggaga cagagtccag cgcctccagc      300

gagaacatcc acgagaagaa cgacaacgag acaaacgagt gcaccagcag cttcgagaca      360

ctgttcgagc aggagccttc cagcgaggtg cccaaggaca gcaagctgta catgctggcc      420
```

cagaagaccg tgcagcacat cgagcagtac ggcaaggccc ctgacttcaa caaagtgatc 480

agggcccaca acttcatcca gaccatctac ggcaccccac tgaaggagga ggagaaggag 540

gtggtgagac tgatggtcat caagctgctg aagaagaaga ggggcagaaa gaggagaagc 600

gccctggacg gcagcagcgg cggcggcagc aacgtggaga cactgctgat cgtggccatc 660

atcgtggtca tcatggccat catgctgtac tacttctggt ggatgccacg gcagcagaag 720

aagtgcagca aggccgagga gtgcacctgt aacaacggct cctgtagcct gaagacctcc 780

cggggcagga agcggcgctc cgacagcgag ttcttccagc ccgtgtaccc aaggcactac 840

ggagagtgtc tgagcccagt gaccaccct tccttcttca gcacccacat gtacaccatc 900

ctgatcgcca tcgtggtgct ggtcatcatc atcatcgtgc tgatctacct gttcagcagc 960

aggaagaaga aggccgccgc catcgaggag gaggacatcc agttcatcaa cccctaccag 1020

gaccagcagt gggtggaggt gaccccacag ccaggcacca gcaagccagc aggagcaacc 1080

accgcatccg tgggcaagcc agtgaccggc aggcctgcaa ccaacagacc agccaccaac 1140

aagcctgtga ccgacaaccc tgtgaccgac cggctggtca tggccaccgg cggcccagca 1200

gcagcaccag cagcagcctc cgccccagca caccctgcag agccatacac caccgtgacc 1260

acccagaaca ccgcctccca gaccatgagc gccattgaaa atctgaggca gcggaataca 1320

tacacccata aggacctgga aaatagtctg 1350

<210> 14
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV- p32, p12, p54 immunogen

<400> 14

Asp Phe Ile Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe Lys Thr
1 5 10 15

Asp Leu Arg Ser Ser Ser Gln Val Val Phe His Ala Gly Ser Leu Tyr
20 25 30

Asn Trp Phe Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val Thr Thr
35 40 45

```
Ala Ile Lys Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val Lys Ser
    50                  55                  60

Ala Arg Ile Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala Gln Glu
65                  70                  75                  80

Glu Trp Asn Met Ile Leu His Val Leu Phe Glu Glu Glu Thr Glu Ser
                85                  90                  95

Ser Ala Ser Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu Thr Asn
            100                 105                 110

Glu Cys Thr Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro Ser Ser
        115                 120                 125

Glu Val Pro Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys Thr Val
    130                 135                 140

Gln His Ile Glu Gln Tyr Gly Lys Ala Pro Asp Phe Asn Lys Val Ile
145                 150                 155                 160

Arg Ala His Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu Lys Glu
                165                 170                 175

Glu Glu Lys Glu Val Val Arg Leu Met Val Ile Lys Leu Leu Lys Lys
            180                 185                 190

Lys Arg Gly Arg Lys Arg Arg Ser Ala Leu Asp Gly Ser Ser Gly Gly
        195                 200                 205

Gly Ser Asn Val Glu Thr Leu Leu Ile Val Ala Ile Ile Val Val Ile
    210                 215                 220

Met Ala Ile Met Leu Tyr Tyr Phe Trp Trp Met Pro Arg Gln Gln Lys
225                 230                 235                 240

Lys Cys Ser Lys Ala Glu Glu Cys Thr Cys Asn Asn Gly Ser Cys Ser
                245                 250                 255
```

```
Leu Lys Thr Ser Arg Gly Arg Lys Arg Arg Ser Asp Ser Glu Phe Phe
            260                 265                 270

Gln Pro Val Tyr Pro Arg His Tyr Gly Glu Cys Leu Ser Pro Val Thr
        275                 280                 285

Thr Pro Ser Phe Phe Ser Thr His Met Tyr Thr Ile Leu Ile Ala Ile
    290                 295                 300

Val Val Leu Val Ile Ile Ile Ile Val Leu Ile Tyr Leu Phe Ser Ser
305                 310                 315                 320

Arg Lys Lys Lys Ala Ala Ala Ile Glu Glu Glu Asp Ile Gln Phe Ile
                325                 330                 335

Asn Pro Tyr Gln Asp Gln Gln Trp Val Glu Val Thr Pro Gln Pro Gly
            340                 345                 350

Thr Ser Lys Pro Ala Gly Ala Thr Thr Ala Ser Val Gly Lys Pro Val
        355                 360                 365

Thr Gly Arg Pro Ala Thr Asn Arg Pro Ala Thr Asn Lys Pro Val Thr
    370                 375                 380

Asp Asn Pro Val Thr Asp Arg Leu Val Met Ala Thr Gly Gly Pro Ala
385                 390                 395                 400

Ala Ala Pro Ala Ala Ala Ser Ala Pro Ala His Pro Ala Glu Pro Tyr
                405                 410                 415

Thr Thr Val Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile
            420                 425                 430

Glu Asn Leu Arg Gln Arg Asn Thr Tyr Thr His Lys Asp Leu Glu Asn
        435                 440                 445

Ser Leu
    450
```

<210> 15
<211> 1404

<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV- p32, p12, p54 immunogen operably linked to IgE leader sequence

<400> 15
atggactgga cttggattct ctttctggtg gcagccgcaa ctcgggtgca tagcgacttt 60

attctgaaca ttagcatgaa gatggaagtg atcttcaaga ccgacctgag gagctccagc 120

caggtggtgt tccacgcagg ctccctgtac aactggttca gcgtggagat catcaactcc 180

ggccggatcg tgaccaccgc catcaagacc ctgctgagca ccgtgaagta cgacatcgtg 240

aagtccgcca ggatctacgc aggacaggga tacaccgagc accaggccca ggaggagtgg 300

aacatgatcc tgcacgtgct gttcgaggag gagacagagt ccagcgcctc cagcgagaac 360

atccacgaga agaacgacaa cgagacaaac gagtgcacca gcagcttcga gacactgttc 420

gagcaggagc cttccagcga ggtgcccaag gacagcaagc tgtacatgct ggcccagaag 480

accgtgcagc acatcgagca gtacggcaag gcccctgact tcaacaaagt gatcagggcc 540

cacaacttca tccagaccat ctacggcacc ccactgaagg aggaggagaa ggaggtggtg 600

agactgatgg tcatcaagct gctgaagaag aagaggggca gaaagaggag aagcgccctg 660

gacggcagca gcggcggcgg cagcaacgtg gagacactgc tgatcgtggc catcatcgtg 720

gtcatcatgg ccatcatgct gtactacttc tggtggatgc cacggcagca gaagaagtgc 780

agcaaggccg aggagtgcac ctgtaacaac ggctcctgta gcctgaagac ctcccggggc 840

aggaagcggc gctccgacag cgagttcttc cagcccgtgt acccaaggca ctacggagag 900

tgtctgagcc cagtgaccac cccttccttc ttcagcaccc acatgtacac catcctgatc 960

gccatcgtgg tgctggtcat catcatcatc gtgctgatct acctgttcag cagcaggaag 1020

aagaaggccg ccgccatcga ggaggaggac atccagttca tcaaccccta ccaggaccag 1080

cagtgggtgg aggtgacccc acagccaggc accagcaagc cagcaggagc aaccaccgca 1140

tccgtgggca agccagtgac cggcaggcct gcaaccaaca gaccagccac caacaagcct 1200

gtgaccgaca accctgtgac cgaccggctg gtcatggcca ccggcggccc agcagcagca 1260

ccagcagcag cctccgcccc agcacaccct gcagagccat acaccaccgt gaccacccag 1320

aacaccgcct cccagaccat gagcgccatt gaaaatctga ggcagcggaa tacatacacc 1380

cataaggacc tggaaaatag tctg 1404

<210> 16
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV- p32, p12, p54 immunogen operably linked to IgE leader sequence

<400> 16

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Asp Phe Ile Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe
20 25 30

Lys Thr Asp Leu Arg Ser Ser Ser Gln Val Val Phe His Ala Gly Ser
35 40 45

Leu Tyr Asn Trp Phe Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val
50 55 60

Thr Thr Ala Ile Lys Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val
65 70 75 80

Lys Ser Ala Arg Ile Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala
85 90 95

Gln Glu Glu Trp Asn Met Ile Leu His Val Leu Phe Glu Glu Glu Thr
100 105 110

Glu Ser Ser Ala Ser Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu
115 120 125

Thr Asn Glu Cys Thr Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro
130 135 140

Ser Ser Glu Val Pro Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys
145 150 155 160

```
Thr Val Gln His Ile Glu Gln Tyr Gly Lys Ala Pro Asp Phe Asn Lys
                165                 170                 175

Val Ile Arg Ala His Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu
            180                 185                 190

Lys Glu Glu Glu Lys Glu Val Val Arg Leu Met Val Ile Lys Leu Leu
        195                 200                 205

Lys Lys Lys Arg Gly Arg Lys Arg Arg Ser Ala Leu Asp Gly Ser Ser
    210                 215                 220

Gly Gly Gly Ser Asn Val Glu Thr Leu Leu Ile Val Ala Ile Ile Val
225                 230                 235                 240

Val Ile Met Ala Ile Met Leu Tyr Tyr Phe Trp Trp Met Pro Arg Gln
                245                 250                 255

Gln Lys Lys Cys Ser Lys Ala Glu Glu Cys Thr Cys Asn Asn Gly Ser
            260                 265                 270

Cys Ser Leu Lys Thr Ser Arg Gly Arg Lys Arg Arg Ser Asp Ser Glu
        275                 280                 285

Phe Phe Gln Pro Val Tyr Pro Arg His Tyr Gly Glu Cys Leu Ser Pro
    290                 295                 300

Val Thr Thr Pro Ser Phe Phe Ser Thr His Met Tyr Thr Ile Leu Ile
305                 310                 315                 320

Ala Ile Val Val Leu Val Ile Ile Ile Ile Val Leu Ile Tyr Leu Phe
                325                 330                 335

Ser Ser Arg Lys Lys Lys Ala Ala Ala Ile Glu Glu Glu Asp Ile Gln
            340                 345                 350

Phe Ile Asn Pro Tyr Gln Asp Gln Gln Trp Val Glu Val Thr Pro Gln
        355                 360                 365

Pro Gly Thr Ser Lys Pro Ala Gly Ala Thr Thr Ala Ser Val Gly Lys
    370                 375                 380
```

```
Pro Val Thr Gly Arg Pro Ala Thr Asn Arg Pro Ala Thr Asn Lys Pro
385                 390                 395                 400

Val Thr Asp Asn Pro Val Thr Asp Arg Leu Val Met Ala Thr Gly Gly
                405                 410                 415

Pro Ala Ala Ala Pro Ala Ala Ala Ser Ala Pro Ala His Pro Ala Glu
            420                 425                 430

Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser
        435                 440                 445

Ala Ile Glu Asn Leu Arg Gln Arg Asn Thr Tyr Thr His Lys Asp Leu
    450                 455                 460

Glu Asn Ser Leu
465
```

<210> 17
<211> 4203
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-CD2+p32+p54+p72

<400> 17

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atcatcctga tcttcctgat cttctccaac atcgtgctga gcatcgacta ctgggtgagc       60

ttcaacaaga ccatcatcct ggactccaac atcaccaacg acaacaacga catcaacggc      120

gtgagctgga acttcttcaa caactccttc aacaccctgg caacctgcgg caaggcaggc      180

aacttctgcg agtgtagcaa ctactccacc agcatctaca acatcaccaa caactgttcc      240

ctgaccatct tcccacacaa cgacgtgttc gacaccacct accaggtggt gtggaaccag      300

atcatcaact acaccatcaa gctgctgacc cccgccaccc ctcccaacat cacctacaac      360

tgcaccaact tcctgatcac ctgtaagaag aacaacggca ccaacaccaa catctacctg      420

aacatcaacg acaccttcgt gaagtacacc aacgagagca tcctggagta caactggaac      480

aactccaaca tcaacaactt caccgccacc tgcatcatca acaacaccat ctccaccagc      540

aacgagacaa ccctgatcaa ctgtacctac ctgaccctga gctccaacta cttctacacc      600
```

ttcttcaagc tgtactacat ccccctgagc atcatcatcg gcatcaccat ctccatcctg 660

ctgatcagca tcatcacctt cctgtccctg aggaagagaa agaagcacgt ggaggagatc 720

gagtccccac ctcccgagag caacgaagag gagcagtgcc agcacgacga caccacctcc 780

atccacgagc caagccctag ggagccactg ctgcccaagc catacagcag ataccagtac 840

aacaccccaa tctactacat gaggccctcc acccagccac tgaacccttt ccccctgcca 900

aagccttgcc cacctcccaa gccatgtcca cctcccaaac catgcccacc tcccaaacct 960

tgtccaagcg ccgagtccta cagcccacct aagcctctgc cctccatccc cctgctgcca 1020

aacatcccac ccctgtccac ccagaacatc agcctgatcc acgtggacag gatcatcagg 1080

ggaaggaagc ggcgcagcga cttcatcctg aacatctcca tgaagatgga agtgatcttc 1140

aagaccgacc tgcgcagctc cagccaggtg gtgttccacg caggctccct gtacaactgg 1200

ttcagcgtgg agatcatcaa ctccggccgg atcgtgacca ccgccatcaa gaccctgctg 1260

agcaccgtga agtacgacat cgtgaagtcc gccaggatct acgcaggaca gggatacacc 1320

gagcaccagg cccaggagga gtggaacatg atcctgcacg tgctgttcga ggaggagaca 1380

gagtccagcg cctccagcga gaacatccac gagaagaacg acaacgagac aaacgagtgc 1440

accagcagct tcgagacact gttcgagcag gagccctcca gcgaggtgcc aaaggacagc 1500

aagctgtaca tgctggccca gaagaccgtg cagcacatcg agcagtacgg caaggccccc 1560

gacttcaaca aagtgatcag ggcccacaac ttcatccaga ccatctacgg caccccactg 1620

aaggaggagg agaaggaggt ggtgagactg atggtcatca agctgctgaa gaagaagagg 1680

ggcagaaaga ggagatccga cagcgagttc ttccagcccg tgtaccccag gcactacggc 1740

gagtgtctgt cccctgtgac caccccctcc ttcttcagca cccacatgta caccatcctg 1800

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aagaagaagg ccgccgccat cgaggaggag gacatccagt tcatcaaccc ataccaggac 1920

cagcagtggg tggaggtgac cccacagcct ggcaccagca agcctgcagg agcaaccacc 1980

gcatccgtgg gcaagcctgt gaccggcagg cccgcaacca acaggccagc caccaacaag 2040

cctgtgaccg acaaccccgt gaccgacagg ctggtcatgg ccaccggcgg cccagcagca 2100

gcacctgcag cagcctccgc cccagcacac cctgcagagc catacaccac cgtgaccacc 2160

cagaacaccg cctcccagac catgagcgcc attgagaacc tgaggcagcg aaacacctac 2220

acccacaagg acctggagaa cagtctgcgg gggcggaaac gacggtcagc aagcggaggg 2280

gcattctgtc tcatcgcaaa cgacgggaag gccgacaaaa tcatcctggc tcaggacctg 2340

ctgaacagca ggatctccaa catcaagaac gtgaacaaga gctacggcaa gcctgacccc 2400

gagccaaccc tgtcccagat cgaggagaca cacctggtgc acttcaacgc ccacttcaag 2460

ccttacgtgc ccgtgggctt cgagtacaac aaggtgaggc cccacaccgg aaccccaacc 2520

ctgggcaaca agctgacctt cggcatccct cagtacggcg acttcttcca cgacatggtg 2580

ggacaccaca tcctgggagc atgccacagc tcctggcagg acgcaccaat ccagggcacc 2640

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gtgcctggca ccaagaacgc ctaccgcaac ctggtgtact actgcgagta cccaggagag 2820

cggctgtacg agaacgtgcg cttcgacgtg aacggcaact ccctggacga gtacagctcc 2880

gacgtgacca ccctggtgcg gaagttctgt atccccggcg acaagatgac cggctacaag 2940

cacctggtgg gacaggaggt gagcgtggag ggcacctccg gaccactgct gtgcaacatc 3000

cacgacctgc acaagcctca ccagagcaag cccatcctga ccgacgagaa cgacacccag 3060

cgcacctgtt cccacaccaa ccctaagttc ctgagccagc acttccccga gaactcccac 3120

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ccaagcgtgt ccatcccttt cggcgagaga ttcatcacca tcaagctggc ctcccagaag 3360

gacctggtga acgagttccc tggcctgttc gtgaggcaga gcagattcat cgcaggcagg 3420

ccctcccgga ggaacatcag attcaagcca tggttcatcc ctggcgtgat caacgagatc 3480

agcctgacca acaacgagct gtacatcaac aacctgttcg tgaccccaga gatccacaac 3540

ctgttcgtga agagggtgag attctccctg atcagggtgc acaagaccca ggtgacccac 3600

accaacaaca accaccacga cgagaagctg atgagcgccc tgaagtggcc catcgagtac 3660

atgttcatcg gcctgaagcc aacctggaac atctccgacc agaaccctca ccagcaccgg 3720

gactggcaca agttcggcca cgtggtgaac gccatcatgc agccaaccca ccacgccgag 3780

atcagcttcc aggacaggga caccgccctg cctgacgcct gcagctccat cagcgacatc 3840

tcccccgtga cctacccaat caccctgcct atcatcaaga acatcagcgt gaccgcccac 3900

ggcatcaacc tgatcgacaa gttcccctcc aagttctgta gctcctacat cccattccac 3960

tacggcggaa acgccatcaa gacccctgac gacccaggag ccatgatgat caccttcgcc 4020

ctgaagccca gagaggagta ccagccaagc ggacacatca acgtgtcccg ggcccgcgag 4080

ttctacatca gctgggacac cgactacgtg ggctccatca ccaccgccga cctggtggtg 4140

tccgcctcag caatcaactt cctcctcctc cagaatgggt ccgccgtcct ccgatactca 4200

aca 4203

<210> 18
<211> 1401
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-CD2+p32+p54+p72

<400> 18

Ile Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser Ile Asp
1 5 10 15

Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn Ile Thr
20 25 30

Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe Asn Asn
35 40 45

Ser Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe Cys Glu
50 55 60

Cys Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn Cys Ser
65 70 75 80

Leu Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr Gln Val
85 90 95

Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr Pro Ala
100 105 110

```
Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile Thr Cys
        115                 120                 125

Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile Asn Asp
    130                 135                 140

Thr Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn Trp Asn
145                 150                 155                 160

Asn Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn Asn Thr
                165                 170                 175

Ile Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr Leu Thr
            180                 185                 190

Leu Ser Ser Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr Ile Pro
        195                 200                 205

Leu Ser Ile Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile Ser Ile
    210                 215                 220

Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu Glu Ile
225                 230                 235                 240

Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln His Asp
                245                 250                 255

Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu Pro
            260                 265                 270

Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met Arg
        275                 280                 285

Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys Pro
    290                 295                 300

Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro
305                 310                 315                 320

Cys Pro Ser Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile
                325                 330                 335
```

```
Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu
            340                 345                 350

Ile His Val Asp Arg Ile Ile Arg Gly Arg Lys Arg Arg Ser Asp Phe
        355                 360                 365

Ile Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe Lys Thr Asp Leu
    370                 375                 380

Arg Ser Ser Ser Gln Val Val Phe His Ala Gly Ser Leu Tyr Asn Trp
385                 390                 395                 400

Phe Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val Thr Thr Ala Ile
                405                 410                 415

Lys Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val Lys Ser Ala Arg
            420                 425                 430

Ile Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala Gln Glu Glu Trp
        435                 440                 445

Asn Met Ile Leu His Val Leu Phe Glu Glu Glu Thr Glu Ser Ser Ala
    450                 455                 460

Ser Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu Thr Asn Glu Cys
465                 470                 475                 480

Thr Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro Ser Ser Glu Val
                485                 490                 495

Pro Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys Thr Val Gln His
            500                 505                 510

Ile Glu Gln Tyr Gly Lys Ala Pro Asp Phe Asn Lys Val Ile Arg Ala
        515                 520                 525

His Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu Lys Glu Glu Glu
    530                 535                 540
```

```
Lys Glu Val Val Arg Leu Met Val Ile Lys Leu Leu Lys Lys Lys Arg
545                 550                 555                 560

Gly Arg Lys Arg Arg Ser Asp Ser Glu Phe Phe Gln Pro Val Tyr Pro
                565                 570                 575

Arg His Tyr Gly Glu Cys Leu Ser Pro Val Thr Thr Pro Ser Phe Phe
            580                 585                 590

Ser Thr His Met Tyr Thr Ile Leu Ile Ala Ile Val Val Leu Val Ile
        595                 600                 605

Ile Ile Ile Val Leu Ile Tyr Leu Phe Ser Ser Arg Lys Lys Lys Ala
    610                 615                 620

Ala Ala Ile Glu Glu Glu Asp Ile Gln Phe Ile Asn Pro Tyr Gln Asp
625                 630                 635                 640

Gln Gln Trp Val Glu Val Thr Pro Gln Pro Gly Thr Ser Lys Pro Ala
                645                 650                 655

Gly Ala Thr Thr Ala Ser Val Gly Lys Pro Val Thr Gly Arg Pro Ala
            660                 665                 670

Thr Asn Arg Pro Ala Thr Asn Lys Pro Val Thr Asp Asn Pro Val Thr
        675                 680                 685

Asp Arg Leu Val Met Ala Thr Gly Gly Pro Ala Ala Ala Pro Ala Ala
    690                 695                 700

Ala Ser Ala Pro Ala His Pro Ala Glu Pro Tyr Thr Thr Val Thr Thr
705                 710                 715                 720

Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Arg Gln
                725                 730                 735

Arg Asn Thr Tyr Thr His Lys Asp Leu Glu Asn Ser Leu Arg Gly Arg
            740                 745                 750

Lys Arg Arg Ser Ala Ser Gly Gly Ala Phe Cys Leu Ile Ala Asn Asp
        755                 760                 765
```

```
Gly Lys Ala Asp Lys Ile Ile Leu Ala Gln Asp Leu Leu Asn Ser Arg
    770                 775                 780

Ile Ser Asn Ile Lys Asn Val Asn Lys Ser Tyr Gly Lys Pro Asp Pro
785                 790                 795                 800

Glu Pro Thr Leu Ser Gln Ile Glu Glu Thr His Leu Val His Phe Asn
                805                 810                 815

Ala His Phe Lys Pro Tyr Val Pro Val Gly Phe Glu Tyr Asn Lys Val
            820                 825                 830

Arg Pro His Thr Gly Thr Pro Thr Leu Gly Asn Lys Leu Thr Phe Gly
        835                 840                 845

Ile Pro Gln Tyr Gly Asp Phe Phe His Asp Met Val Gly His His Ile
    850                 855                 860

Leu Gly Ala Cys His Ser Ser Trp Gln Asp Ala Pro Ile Gln Gly Thr
865                 870                 875                 880

Ser Gln Met Gly Ala His Gly Gln Leu Gln Thr Phe Pro Arg Asn Gly
                885                 890                 895

Tyr Asp Trp Asp Asn Gln Thr Pro Leu Glu Gly Ala Val Tyr Thr Leu
            900                 905                 910

Val Asp Pro Phe Gly Arg Pro Ile Val Pro Gly Thr Lys Asn Ala Tyr
        915                 920                 925

Arg Asn Leu Val Tyr Tyr Cys Glu Tyr Pro Gly Glu Arg Leu Tyr Glu
    930                 935                 940

Asn Val Arg Phe Asp Val Asn Gly Asn Ser Leu Asp Glu Tyr Ser Ser
945                 950                 955                 960

Asp Val Thr Thr Leu Val Arg Lys Phe Cys Ile Pro Gly Asp Lys Met
                965                 970                 975
```

```
Thr Gly Tyr Lys His Leu Val Gly Gln Glu Val Ser Val Glu Gly Thr
            980                 985                 990


Ser Gly Pro Leu Leu Cys Asn Ile  His Asp Leu His Lys  Pro His Gln
        995                 1000                1005


Ser Lys  Pro Ile Leu Thr Asp  Glu Asn Asp Thr Gln  Arg Thr Cys
    1010                1015                1020


Ser His  Thr Asn Pro Lys Phe  Leu Ser Gln His Phe  Pro Glu Asn
    1025                1030                1035


Ser His  Asn Ile Gln Thr Ala  Gly Lys Gln Asp Ile  Thr Pro Ile
    1040                1045                1050


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


Cys Asn  Gly Pro Gln Thr Pro  Lys Tyr Tyr Gln Pro  Pro Leu Ala
    1070                1075                1080


Leu Trp  Ile Lys Leu Arg Phe  Trp Phe Asn Glu Asn  Val Asn Leu
    1085                1090                1095


Ala Ile  Pro Ser Val Ser Ile  Pro Phe Gly Glu Arg  Phe Ile Thr
    1100                1105                1110


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


Leu Phe  Val Arg Gln Ser Arg  Phe Ile Ala Gly Arg  Pro Ser Arg
    1130                1135                1140


Arg Asn  Ile Arg Phe Lys Pro  Trp Phe Ile Pro Gly  Val Ile Asn
    1145                1150                1155


Glu Ile  Ser Leu Thr Asn Asn  Glu Leu Tyr Ile Asn  Asn Leu Phe
    1160                1165                1170


Val Thr  Pro Glu Ile His Asn  Leu Phe Val Lys Arg  Val Arg Phe
    1175                1180                1185
```

```
Ser Leu  Ile Arg Val His Lys  Thr Gln Val Thr His  Thr Asn Asn
    1190                1195                1200

Asn His  His Asp Glu Lys Leu  Met Ser Ala Leu Lys  Trp Pro Ile
    1205                1210                1215

Glu Tyr  Met Phe Ile Gly Leu  Lys Pro Thr Trp Asn  Ile Ser Asp
    1220                1225                1230

Gln Asn  Pro His Gln His Arg  Asp Trp His Lys Phe  Gly His Val
    1235                1240                1245

Val Asn  Ala Ile Met Gln Pro  Thr His His Ala Glu  Ile Ser Phe
    1250                1255                1260

Gln Asp  Arg Asp Thr Ala Leu  Pro Asp Ala Cys Ser  Ser Ile Ser
    1265                1270                1275

Asp Ile  Ser Pro Val Thr Tyr  Pro Ile Thr Leu Pro  Ile Ile Lys
    1280                1285                1290

Asn Ile  Ser Val Thr Ala His  Gly Ile Asn Leu Ile  Asp Lys Phe
    1295                1300                1305

Pro Ser  Lys Phe Cys Ser Ser  Tyr Ile Pro Phe His  Tyr Gly Gly
    1310                1315                1320

Asn Ala  Ile Lys Thr Pro Asp  Asp Pro Gly Ala Met  Met Ile Thr
    1325                1330                1335

Phe Ala  Leu Lys Pro Arg Glu  Glu Tyr Gln Pro Ser  Gly His Ile
    1340                1345                1350

Asn Val  Ser Arg Ala Arg Glu  Phe Tyr Ile Ser Trp  Asp Thr Asp
    1355                1360                1365

Tyr Val  Gly Ser Ile Thr Thr  Ala Asp Leu Val Val  Ser Ala Ser
    1370                1375                1380
```

Ala Ile Asn Phe Leu Leu Leu Gln Asn Gly Ser Ala Val Leu Arg
    1385   1390   1395

Tyr Ser Thr
    1400

<210> 19
<211> 4257
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-IgE-CD2+p32+p54+p72

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ctgatcttcc tgatcttctc caacatcgtg ctgagcatcg actactgggt gagcttcaac 120

aagaccatca tcctggactc caacatcacc aacgacaaca acgacatcaa cggcgtgagc 180

tggaacttct tcaacaactc cttcaacacc ctggcaacct gcggcaaggc aggcaacttc 240

tgcgagtgta gcaactactc caccagcatc tacaacatca ccaacaactg ttccctgacc 300

atcttcccac acaacgacgt gttcgacacc acctaccagg tggtgtggaa ccagatcatc 360

aactacacca tcaagctgct gacccccgcc acccctccca acatcaccta caactgcacc 420

aacttcctga tcacctgtaa gaagaacaac ggcaccaaca ccaacatcta cctgaacatc 480

aacgacacct tcgtgaagta caccaacgag agcatcctgg agtacaactg gaacaactcc 540

aacatcaaca acttcaccgc cacctgcatc atcaacaaca ccatctccac cagcaacgag 600

acaaccctga tcaactgtac ctacctgacc ctgagctcca actacttcta caccttcttc 660

aagctgtact acatcccccc gagcatcatc atcggcatca ccatctccat cctgctgatc 720

agcatcatca ccttcctgtc cctgaggaag agaaagaagc acgtggagga gatcgagtcc 780

ccacctcccg agagcaacga agaggagcag tgccagcacg acgacaccac ctccatccac 840

gagccaagcc ctagggagcc actgctgccc aagccataca gcagatacca gtacaacacc 900

ccaatctact acatgaggcc ctccacccag ccactgaacc ctttcccccc gccaaagcct 960

tgcccacctc ccaagccatg tccacctccc aaaccatgcc cacctcccaa accttgtcca 1020

agcgccgagt cctacagccc acctaagcct ctgccctcca tccccctgct gccaaacatc 1080

ccacccctgt ccacccagaa catcagcctg atccacgtgg acaggatcat caggggaagg 1140

aagcggcgca gcgacttcat cctgaacatc tccatgaaga tggaagtgat cttcaagacc 1200

gacctgcgca gctccagcca ggtggtgttc cacgcaggct ccctgtacaa ctggttcagc 1260

gtggagatca tcaactccgg ccggatcgtg accaccgcca tcaagaccct gctgagcacc 1320

gtgaagtacg acatcgtgaa gtccgccagg atctacgcag gacagggata caccgagcac 1380

caggcccagg aggagtggaa catgatcctg cacgtgctgt tcgaggagga gacagagtcc 1440

agcgcctcca gcgagaacat ccacgagaag aacgacaacg agacaaacga gtgcaccagc 1500

agcttcgaga cactgttcga gcaggagccc tccagcgagg tgccaaagga cagcaagctg 1560

tacatgctgg cccagaagac cgtgcagcac atcgagcagt acggcaaggc ccccgacttc 1620

aacaaagtga tcagggccca caacttcatc cagaccatct acggcacccc actgaaggag 1680

gaggagaagg aggtggtgag actgatggtc atcaagctgc tgaagaagaa gaggggcaga 1740

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aaggccgccg ccatcgagga ggaggacatc cagttcatca acccatacca ggaccagcag 1980

tgggtggagg tgaccccaca gcctggcacc agcaagcctg caggagcaac caccgcatcc 2040

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accgcctccc agaccatgag cgccattgag aacctgaggc agcgaaacac ctacacccac 2280

aaggacctgg agaacagtct gcgggggcgg aaacgacggt cagcaagcgg aggggcattc 2340

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cacatcctgg gagcatgcca cagctcctgg caggacgcac caatccaggg caccagccag 2700

atgggagcac acggacagct gcagaccttc cctaggaacg gctacgactg ggacaaccag 2760

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ggcaccaaga acgcctaccg caacctggtg tactactgcg agtacccagg agagcggctg 2880

tacgagaacg tgcgcttcga cgtgaacggc aactccctgg acgagtacag ctccgacgtg 2940

accaccctgg tgcggaagtt ctgtatcccc ggcgacaaga tgaccggcta caagcacctg 3000

gtgggacagg aggtgagcgt ggagggcacc tccggaccac tgctgtgcaa catccacgac 3060

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cagaccgccg gcaagcagga catcaccccc atcaccgacg ccacctacct ggacatcagg 3240

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gccctgtgga tcaagctgag gttctggttc aacgagaacg tgaacctggc catcccaagc 3360

gtgtccatcc ctttcggcga gagattcatc accatcaagc tggcctccca gaaggacctg 3420

gtgaacgagt tccctggcct gttcgtgagg cagagcagat tcatcgcagg caggccctcc 3480

cggaggaaca tcagattcaa gccatggttc atccctggcg tgatcaacga gatcagcctg 3540

accaacaacg agctgtacat caacaacctg ttcgtgaccc cagagatcca caacctgttc 3600

gtgaagaggg tgagattctc cctgatcagg gtgcacaaga cccaggtgac ccacaccaac 3660

aacaaccacc acgacgagaa gctgatgagc gccctgaagt ggcccatcga gtacatgttc 3720

atcggcctga agccaacctg gaacatctcc gaccagaacc ctcaccagca ccgggactgg 3780

cacaagttcg gccacgtggt gaacgccatc atgcagccaa cccaccacgc cgagatcagc 3840

ttccaggaca gggacaccgc cctgcctgac gcctgcagct ccatcagcga catctccccc 3900

gtgacctacc caatcaccct gcctatcatc aagaacatca gcgtgaccgc ccacggcatc 3960

aacctgatcg acaagttccc ctccaagttc tgtagctcct acatcccatt ccactacggc 4020

ggaaacgcca tcaagacccc tgacgaccca ggagccatga tgatcacctt cgccctgaag 4080

cccagagagg agtaccagcc aagcggacac atcaacgtgt cccgggcccg cgagttctac 4140

atcagctggg acaccgacta cgtgggctcc atcaccaccg ccgacctggt ggtgtccgcc 4200

tcagcaatca acttcctcct cctccagaat gggtccgccg tcctccgata ctcaaca 4257

<210> 20
<211> 1419

<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-IgE-CD2+p32+p54+p72

<400> 20

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1   5   10   15

His Ser Ile Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser
            20   25   30

Ile Asp Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn
        35   40   45

Ile Thr Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe
    50   55   60

Asn Asn Ser Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe
65   70   75   80

Cys Glu Cys Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn
                85   90   95

Cys Ser Leu Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr
            100   105   110

Gln Val Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr
        115   120   125

Pro Ala Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile
    130   135   140

Thr Cys Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile
145   150   155   160

Asn Asp Thr Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn
                165   170   175

Trp Asn Asn Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn
            180   185   190

```
Asn Thr Ile Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr
        195                 200                 205

Leu Thr Leu Ser Ser Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr
    210                 215                 220

Ile Pro Leu Ser Ile Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile
225                 230                 235                 240

Ser Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu
                245                 250                 255

Glu Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln
            260                 265                 270

His Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu
        275                 280                 285

Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr
    290                 295                 300

Met Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro
305                 310                 315                 320

Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro
                325                 330                 335

Lys Pro Cys Pro Ser Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro
            340                 345                 350

Ser Ile Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile
        355                 360                 365

Ser Leu Ile His Val Asp Arg Ile Ile Arg Gly Arg Lys Arg Arg Ser
    370                 375                 380

Asp Phe Ile Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe Lys Thr
385                 390                 395                 400
```

```
Asp Leu Arg Ser Ser Ser Gln Val Val Phe His Ala Gly Ser Leu Tyr
                405                 410                 415

Asn Trp Phe Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val Thr Thr
            420                 425                 430

Ala Ile Lys Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val Lys Ser
        435                 440                 445

Ala Arg Ile Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala Gln Glu
    450                 455                 460

Glu Trp Asn Met Ile Leu His Val Leu Phe Glu Glu Glu Thr Glu Ser
465                 470                 475                 480

Ser Ala Ser Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu Thr Asn
                485                 490                 495

Glu Cys Thr Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro Ser Ser
            500                 505                 510

Glu Val Pro Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys Thr Val
        515                 520                 525

Gln His Ile Glu Gln Tyr Gly Lys Ala Pro Asp Phe Asn Lys Val Ile
    530                 535                 540

Arg Ala His Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu Lys Glu
545                 550                 555                 560

Glu Glu Lys Glu Val Val Arg Leu Met Val Ile Lys Leu Leu Lys Lys
                565                 570                 575

Lys Arg Gly Arg Lys Arg Arg Ser Asp Ser Glu Phe Phe Gln Pro Val
            580                 585                 590

Tyr Pro Arg His Tyr Gly Glu Cys Leu Ser Pro Val Thr Thr Pro Ser
        595                 600                 605

Phe Phe Ser Thr His Met Tyr Thr Ile Leu Ile Ala Ile Val Val Leu
    610                 615                 620
```

```
Val Ile Ile Ile Ile Val Leu Ile Tyr Leu Phe Ser Ser Arg Lys Lys
625                 630                 635                 640


Lys Ala Ala Ala Ile Glu Glu Glu Asp Ile Gln Phe Ile Asn Pro Tyr
                645                 650                 655


Gln Asp Gln Gln Trp Val Glu Val Thr Pro Gln Pro Gly Thr Ser Lys
            660                 665                 670


Pro Ala Gly Ala Thr Thr Ala Ser Val Gly Lys Pro Val Thr Gly Arg
        675                 680                 685


Pro Ala Thr Asn Arg Pro Ala Thr Asn Lys Pro Val Thr Asp Asn Pro
    690                 695                 700


Val Thr Asp Arg Leu Val Met Ala Thr Gly Gly Pro Ala Ala Ala Pro
705                 710                 715                 720


Ala Ala Ala Ser Ala Pro Ala His Pro Ala Glu Pro Tyr Thr Thr Val
                725                 730                 735


Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu
            740                 745                 750


Arg Gln Arg Asn Thr Tyr Thr His Lys Asp Leu Glu Asn Ser Leu Arg
        755                 760                 765


Gly Arg Lys Arg Arg Ser Ala Ser Gly Gly Ala Phe Cys Leu Ile Ala
    770                 775                 780


Asn Asp Gly Lys Ala Asp Lys Ile Ile Leu Ala Gln Asp Leu Leu Asn
785                 790                 795                 800


Ser Arg Ile Ser Asn Ile Lys Asn Val Asn Lys Ser Tyr Gly Lys Pro
                805                 810                 815


Asp Pro Glu Pro Thr Leu Ser Gln Ile Glu Glu Thr His Leu Val His
            820                 825                 830
```

```
Phe Asn Ala His Phe Lys Pro Tyr Val Pro Val Gly Phe Glu Tyr Asn
        835                 840                 845

Lys Val Arg Pro His Thr Gly Thr Pro Thr Leu Gly Asn Lys Leu Thr
    850                 855                 860

Phe Gly Ile Pro Gln Tyr Gly Asp Phe Phe His Asp Met Val Gly His
865                 870                 875                 880

His Ile Leu Gly Ala Cys His Ser Ser Trp Gln Asp Ala Pro Ile Gln
                885                 890                 895

Gly Thr Ser Gln Met Gly Ala His Gly Gln Leu Gln Thr Phe Pro Arg
            900                 905                 910

Asn Gly Tyr Asp Trp Asp Asn Gln Thr Pro Leu Glu Gly Ala Val Tyr
        915                 920                 925

Thr Leu Val Asp Pro Phe Gly Arg Pro Ile Val Pro Gly Thr Lys Asn
    930                 935                 940

Ala Tyr Arg Asn Leu Val Tyr Tyr Cys Glu Tyr Pro Gly Glu Arg Leu
945                 950                 955                 960

Tyr Glu Asn Val Arg Phe Asp Val Asn Gly Asn Ser Leu Asp Glu Tyr
                965                 970                 975

Ser Ser Asp Val Thr Thr Leu Val Arg Lys Phe Cys Ile Pro Gly Asp
            980                 985                 990

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

Gly Thr  Ser Gly Pro Leu Leu  Cys Asn Ile His Asp  Leu His Lys
    1010                1015                1020

Pro His  Gln Ser Lys Pro Ile  Leu Thr Asp Glu Asn  Asp Thr Gln
    1025                1030                1035

Arg Thr  Cys Ser His Thr Asn  Pro Lys Phe Leu Ser  Gln His Phe
    1040                1045                1050
```

```
Pro Glu  Asn Ser His Asn Ile  Gln Thr Ala Gly Lys  Gln Asp Ile
    1055                1060                1065

Thr Pro  Ile Thr Asp Ala Thr  Tyr Leu Asp Ile Arg  Arg Asn Val
    1070                1075                1080

His Tyr  Ser Cys Asn Gly Pro  Gln Thr Pro Lys Tyr  Tyr Gln Pro
    1085                1090                1095

Pro Leu  Ala Leu Trp Ile Lys  Leu Arg Phe Trp Phe  Asn Glu Asn
    1100                1105                1110

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

Phe Ile  Thr Ile Lys Leu Ala  Ser Gln Lys Asp Leu  Val Asn Glu
    1130                1135                1140

Phe Pro  Gly Leu Phe Val Arg  Gln Ser Arg Phe Ile  Ala Gly Arg
    1145                1150                1155

Pro Ser  Arg Arg Asn Ile Arg  Phe Lys Pro Trp Phe  Ile Pro Gly
    1160                1165                1170

Val Ile  Asn Glu Ile Ser Leu  Thr Asn Asn Glu Leu  Tyr Ile Asn
    1175                1180                1185

Asn Leu  Phe Val Thr Pro Glu  Ile His Asn Leu Phe  Val Lys Arg
    1190                1195                1200

Val Arg  Phe Ser Leu Ile Arg  Val His Lys Thr Gln  Val Thr His
    1205                1210                1215

Thr Asn  Asn Asn His His Asp  Glu Lys Leu Met Ser  Ala Leu Lys
    1220                1225                1230

Trp Pro  Ile Glu Tyr Met Phe  Ile Gly Leu Lys Pro  Thr Trp Asn
    1235                1240                1245
```

```
Ile Ser  Asp Gln Asn Pro His  Gln His Arg Asp Trp  His Lys Phe
    1250                1255                1260

Gly His  Val Val Asn Ala Ile  Met Gln Pro Thr His  His Ala Glu
    1265                1270                1275

Ile Ser  Phe Gln Asp Arg Asp  Thr Ala Leu Pro Asp  Ala Cys Ser
    1280                1285                1290

Ser Ile  Ser Asp Ile Ser Pro  Val Thr Tyr Pro Ile  Thr Leu Pro
    1295                1300                1305

Ile Ile  Lys Asn Ile Ser Val  Thr Ala His Gly Ile  Asn Leu Ile
    1310                1315                1320

Asp Lys  Phe Pro Ser Lys Phe  Cys Ser Ser Tyr Ile  Pro Phe His
    1325                1330                1335

Tyr Gly  Gly Asn Ala Ile Lys  Thr Pro Asp Asp Pro  Gly Ala Met
    1340                1345                1350

Met Ile  Thr Phe Ala Leu Lys  Pro Arg Glu Glu Tyr  Gln Pro Ser
    1355                1360                1365

Gly His  Ile Asn Val Ser Arg  Ala Arg Glu Phe Tyr  Ile Ser Trp
    1370                1375                1380

Asp Thr  Asp Tyr Val Gly Ser  Ile Thr Thr Ala Asp  Leu Val Val
    1385                1390                1395

Ser Ala  Ser Ala Ile Asn Phe  Leu Leu Leu Gln Asn  Gly Ser Ala
    1400                1405                1410

Val Leu  Arg Tyr Ser Thr
    1415
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<210> 21
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Chemically Synthesized, synthetic ASFV-CD2 immunogen

<400> 21
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tttaacaaaa ccattattct ggatagcaac atcaccaacg acaacaacga catcaacggc 120

gtgagctgga acttcttcaa caactccttc aacaccctgg caacctgcgg caaggcaggc 180

aacttctgcg agtgttccaa ctacagcacc tccatctaca atatcaccaa caactgttcc 240

ctgaccatct tcccacacaa cgacgtgttc gacaccacct accaggtggt gtggaaccag 300

atcatcaact acaccatcaa gctgctgacc cccgccaccc cacccaacat cacctacaac 360

tgcaccaact tcctgatcac ctgtaagaag aacaacggca ccaacaccaa catctacctg 420

aacatcaacg acaccttcgt gaagtacacc aacgagagca tcctggagta caactggaac 480

aactccaaca tcaacaactt caccgccacc tgcatcatca acaacaccat cagcacctcc 540

aacgagacaa ccctgatcaa ctgtacctac ctgaccctga gctccaacta cttctacacc 600

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aacaccccca tctactacat gaggccatcc acccagcctc tgaacccttt ccccctgcca 900

aagccttgcc ctcccccaaa gccctgtcct cccccaaagc catgccctcc cccaaagcca 960

tgtccaagcg ccgagagcta ctcccctccc aagcctctgc catccatccc actgctgcca 1020

aacatccctc ctctcagcac tcagaacatt agcctcattc acgtggaccg catcatc 1077

<210> 22
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-CD2 immunogen

<400> 22

Ile Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser Ile Asp
1 5 10 15

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Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn Ile Thr
            20                  25                  30

Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe Asn Asn
        35                  40                  45

Ser Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe Cys Glu
    50                  55                  60

Cys Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn Cys Ser
65                  70                  75                  80

Leu Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr Gln Val
                85                  90                  95

Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr Pro Ala
            100                 105                 110

Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile Thr Cys
        115                 120                 125

Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile Asn Asp
    130                 135                 140

Thr Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn Trp Asn
145                 150                 155                 160

Asn Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn Asn Thr
                165                 170                 175

Ile Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr Leu Thr
            180                 185                 190

Leu Ser Ser Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr Ile Pro
        195                 200                 205

Leu Ser Ile Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile Ser Ile
    210                 215                 220

Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu Glu Ile
225                 230                 235                 240
```

```
Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln His Asp
                245                 250                 255

Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu Pro
            260                 265                 270

Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met Arg
        275                 280                 285

Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys Pro
    290                 295                 300

Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro
305                 310                 315                 320

Cys Pro Ser Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile
                325                 330                 335

Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu
            340                 345                 350

Ile His Val Asp Arg Ile Ile
        355
```

<210> 23
<211> 180
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-p12 immunogen

<400> 23
gccctggatg gctcaagcgg cggcggatct aacgtggaga ccctgctgat tgtggctatt 60

attgtcgtga ttatggctat tatgctctac tacttctggt ggatgcccag gcagcagaag 120

aaatgctcaa aagccgaaga gtgtacctgt aataacggga gttgtagcct gaaaaccagc 180

<210> 24
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-p12 immunogen

<400> 24

Ala Leu Asp Gly Ser Ser Gly Gly Gly Ser Asn Val Glu Thr Leu Leu
1 5 10 15

Ile Val Ala Ile Ile Val Val Ile Met Ala Ile Met Leu Tyr Tyr Phe
20 25 30

Trp Trp Met Pro Arg Gln Gln Lys Lys Cys Ser Lys Ala Glu Glu Cys
35 40 45

Thr Cys Asn Asn Gly Ser Cys Ser Leu Lys Thr Ser
50 55 60

<210> 25
<211> 579
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-p32 immunogen

<400> 25
gactttattc tcaacatcag tatgaaaatg gaggtcatct tcaaaaccga tctcaggagt 60

tcttcccagg tcgtcttcca cgcaggaagc ctgtacaact ggttctccgt ggagatcatc 120

aacagcggca ggatcgtgac caccgccatc aagaccctgc tgtccaccgt gaagtacgac 180

atcgtgaaga gcgccagaat ctacgcagga cagggataca ccgagcacca ggcccaggag 240

gagtggaaca tgatcctgca cgtgctgttc gaggaggaga cagagagctc cgccagctcc 300

gagaacatcc acgagaagaa cgacaacgag acaaacgagt gcaccagcag cttcgagaca 360

ctgttcgagc aggagcccag ctccgaggtg ccaaaggact ccaagctgta catgctggcc 420

cagaagaccg tgcagcacat cgagcagtac ggcaaggccc ctgacttcaa caaagtgatc 480

agggcccaca acttcatcca gaccatctac ggcacccccc tgaaggaaga agagaaagaa 540

gtggtccgac tcatggtcat caaactgctg aaaaagaaa 579

<210> 26
<211> 193

<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-p32 immunogen

<400> 26

```
Asp Phe Ile Leu Asn Ile Ser Met Lys Met Glu Val Ile Phe Lys Thr
1               5                   10                  15


Asp Leu Arg Ser Ser Ser Gln Val Val Phe His Ala Gly Ser Leu Tyr
            20                  25                  30


Asn Trp Phe Ser Val Glu Ile Ile Asn Ser Gly Arg Ile Val Thr Thr
        35                  40                  45


Ala Ile Lys Thr Leu Leu Ser Thr Val Lys Tyr Asp Ile Val Lys Ser
    50                  55                  60


Ala Arg Ile Tyr Ala Gly Gln Gly Tyr Thr Glu His Gln Ala Gln Glu
65                  70                  75                  80


Glu Trp Asn Met Ile Leu His Val Leu Phe Glu Glu Glu Thr Glu Ser
                85                  90                  95


Ser Ala Ser Ser Glu Asn Ile His Glu Lys Asn Asp Asn Glu Thr Asn
            100                 105                 110


Glu Cys Thr Ser Ser Phe Glu Thr Leu Phe Glu Gln Glu Pro Ser Ser
        115                 120                 125


Glu Val Pro Lys Asp Ser Lys Leu Tyr Met Leu Ala Gln Lys Thr Val
    130                 135                 140


Gln His Ile Glu Gln Tyr Gly Lys Ala Pro Asp Phe Asn Lys Val Ile
145                 150                 155                 160


Arg Ala His Asn Phe Ile Gln Thr Ile Tyr Gly Thr Pro Leu Lys Glu
                165                 170                 175


Glu Glu Lys Glu Val Val Arg Leu Met Val Ile Lys Leu Leu Lys Lys
            180                 185                 190
```

Lys

<210> 27
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-p54 immunogen

<400> 27
gatagcgagt tcttccagcc tgtctaccca cggcactacg gcgaatgtct ctcacctgtc 60

actaccccat ctttctttag cacccacatg tacaccatcc tgatcgccat cgtggtgctg 120

gtcatcatca tcatcgtgct gatctacctg ttcagcagca ggaagaagaa ggccgccgcc 180

atcgaggagg aggacatcca gttcatcaac ccctaccagg accagcagtg ggtggaggtg 240

accccacagc caggcaccag caagccagca ggagcaacca ccgcatccgt gggcaagcca 300

gtgaccggca ggcctgcaac caacagacca gccaccaaca agcctgtgac cgacaaccct 360

gtgaccgaca ggctggtcat ggccaccggc ggccctgcag cagcaccagc agcagccagc 420

gcccctgcac acccagcaga gccatacacc accgtgacca cccagaacac cgccagccag 480

accatgtccg ccattgaaaa cctgcgacag agaaatacct acacccacaa ggacctggag 540

aactcactc 549

<210> 28
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-p54 immunogen

<400> 28

Asp Ser Glu Phe Phe Gln Pro Val Tyr Pro Arg His Tyr Gly Glu Cys
1 5 10 15

Leu Ser Pro Val Thr Thr Pro Ser Phe Phe Ser Thr His Met Tyr Thr
20 25 30

```
Ile Leu Ile Ala Ile Val Val Leu Val Ile Ile Ile Ile Val Leu Ile
        35                  40                  45

Tyr Leu Phe Ser Ser Arg Lys Lys Lys Ala Ala Ala Ile Glu Glu Glu
    50                  55                  60

Asp Ile Gln Phe Ile Asn Pro Tyr Gln Asp Gln Gln Trp Val Glu Val
65                  70                  75                  80

Thr Pro Gln Pro Gly Thr Ser Lys Pro Ala Gly Ala Thr Thr Ala Ser
                85                  90                  95

Val Gly Lys Pro Val Thr Gly Arg Pro Ala Thr Asn Arg Pro Ala Thr
            100                 105                 110

Asn Lys Pro Val Thr Asp Asn Pro Val Thr Asp Arg Leu Val Met Ala
        115                 120                 125

Thr Gly Gly Pro Ala Ala Ala Pro Ala Ala Ala Ser Ala Pro Ala His
    130                 135                 140

Pro Ala Glu Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr Ala Ser Gln
145                 150                 155                 160

Thr Met Ser Ala Ile Glu Asn Leu Arg Gln Arg Asn Thr Tyr Thr His
                165                 170                 175

Lys Asp Leu Glu Asn Ser Leu
            180
```

<210> 29
<211> 1938
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-p72 immunogen

<400> 29

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atggcaagcg gaggggcatt ctgtctcatc gcaaacgacg ggaaggccga caaaatcatc       60

ctggctcagg acctgctgaa cagcaggatc tccaacatca agaacgtgaa caagagctac      120

ggcaagcctg accccgagcc aaccctgtcc cagatcgagg agacacacct ggtgcacttc      180
```

aacgcccact tcaagcctta cgtgcccgtg ggcttcgagt acaacaaggt gaggccccac 240

accggaaccc caaccctggg caacaagctg accttcggca tccctcagta cggcgacttc 300

ttccacgaca tggtgggaca ccacatcctg ggagcatgcc acagctcctg gcaggacgca 360

ccaatccagg gcaccagcca gatgggagca cacggacagc tgcagacctt ccctaggaac 420

ggctacgact gggacaacca gaccccactg gagggagccg tgtacaccct ggtggaccca 480

ttcggccggc caatcgtgcc tggcaccaag aacgcctacc gcaacctggt gtactactgc 540

gagtacccag gagagcggct gtacgagaac gtgcgcttcg acgtgaacgg caactccctg 600

gacgagtaca gctccgacgt gaccaccctg gtgcggaagt tctgtatccc cggcgacaag 660

atgaccggct acaagcacct ggtgggacag gaggtgagcg tggagggcac ctccggacca 720

ctgctgtgca acatccacga cctgcacaag cctcaccaga gcaagcccat cctgaccgac 780

gagaacgaca cccagcgcac ctgttcccac accaacccta agttcctgag ccagcacttc 840

cccgagaact cccacaacat ccagaccgcc ggcaagcagg acatcacccc catcaccgac 900

gccacctacc tggacatcag gagaaacgtg cactacagct gtaacggccc ccagacccca 960

aagtactacc agcccccact ggccctgtgg atcaagctga ggttctggtt caacgagaac 1020

gtgaacctgg ccatcccaag cgtgtccatc cctttcggcg agagattcat caccatcaag 1080

ctggcctccc agaaggacct ggtgaacgag ttccctggcc tgttcgtgag gcagagcaga 1140

ttcatcgcag gcaggccctc ccggaggaac atcagattca agccatggtt catccctggc 1200

gtgatcaacg agatcagcct gaccaacaac gagctgtaca tcaacaacct gttcgtgacc 1260

ccagagatcc acaacctgtt cgtgaagagg gtgagattct ccctgatcag ggtgcacaag 1320

acccaggtga cccacaccaa caacaaccac cacgacgaga agctgatgag cgccctgaag 1380

tggcccatcg agtacatgtt catcggcctg aagccaacct ggaacatctc cgaccagaac 1440

cctcaccagc accgggactg gcacaagttc ggccacgtgg tgaacgccat catgcagcca 1500

acccaccacg ccgagatcag cttccaggac agggacaccg ccctgcctga cgcctgcagc 1560

tccatcagcg acatctcccc cgtgacctac ccaatcaccc tgcctatcat caagaacatc 1620

agcgtgaccg cccacggcat caacctgatc gacaagttcc cctccaagtt ctgtagctcc 1680

tacatcccat tccactacgg cggaaacgcc atcaagaccc ctgacgaccc aggagccatg 1740

atgatcacct tcgccctgaa gcccagagag gagtaccagc caagcggaca catcaacgtg 1800

tcccgggccc gcgagttcta catcagctgg gacaccgact acgtgggctc catcaccacc 1860

gccgacctgg tggtgtccgc ctcagcaatc aacttcctcc tcctccagaa tgggtccgcc 1920

gtcctccgat actcaaca 1938

<210> 30
<211> 646
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, synthetic ASFV-p72 immunogen

<400> 30

Met Ala Ser Gly Gly Ala Phe Cys Leu Ile Ala Asn Asp Gly Lys Ala
1 5 10 15

Asp Lys Ile Ile Leu Ala Gln Asp Leu Leu Asn Ser Arg Ile Ser Asn
20 25 30

Ile Lys Asn Val Asn Lys Ser Tyr Gly Lys Pro Asp Pro Glu Pro Thr
35 40 45

Leu Ser Gln Ile Glu Glu Thr His Leu Val His Phe Asn Ala His Phe
50 55 60

Lys Pro Tyr Val Pro Val Gly Phe Glu Tyr Asn Lys Val Arg Pro His
65 70 75 80

Thr Gly Thr Pro Thr Leu Gly Asn Lys Leu Thr Phe Gly Ile Pro Gln
85 90 95

Tyr Gly Asp Phe Phe His Asp Met Val Gly His His Ile Leu Gly Ala
100 105 110

Cys His Ser Ser Trp Gln Asp Ala Pro Ile Gln Gly Thr Ser Gln Met
115 120 125

Gly Ala His Gly Gln Leu Gln Thr Phe Pro Arg Asn Gly Tyr Asp Trp
130 135 140

```
Asp Asn Gln Thr Pro Leu Glu Gly Ala Val Tyr Thr Leu Val Asp Pro
145                 150                 155                 160

Phe Gly Arg Pro Ile Val Pro Gly Thr Lys Asn Ala Tyr Arg Asn Leu
                165                 170                 175

Val Tyr Tyr Cys Glu Tyr Pro Gly Glu Arg Leu Tyr Glu Asn Val Arg
            180                 185                 190

Phe Asp Val Asn Gly Asn Ser Leu Asp Glu Tyr Ser Ser Asp Val Thr
        195                 200                 205

Thr Leu Val Arg Lys Phe Cys Ile Pro Gly Asp Lys Met Thr Gly Tyr
    210                 215                 220

Lys His Leu Val Gly Gln Glu Val Ser Val Glu Gly Thr Ser Gly Pro
225                 230                 235                 240

Leu Leu Cys Asn Ile His Asp Leu His Lys Pro His Gln Ser Lys Pro
                245                 250                 255

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

Pro Lys Phe Leu Ser Gln His Phe Pro Glu Asn Ser His Asn Ile Gln
        275                 280                 285

Thr Ala Gly Lys Gln Asp Ile Thr Pro Ile Thr Asp Ala Thr Tyr Leu
    290                 295                 300

Asp Ile Arg Arg Asn Val His Tyr Ser Cys Asn Gly Pro Gln Thr Pro
305                 310                 315                 320

Lys Tyr Tyr Gln Pro Pro Leu Ala Leu Trp Ile Lys Leu Arg Phe Trp
                325                 330                 335

Phe Asn Glu Asn Val Asn Leu Ala Ile Pro Ser Val Ser Ile Pro Phe
            340                 345                 350

Gly Glu Arg Phe Ile Thr Ile Lys Leu Ala Ser Gln Lys Asp Leu Val
        355                 360                 365
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Asn Glu Phe Pro Gly Leu Phe Val Arg Gln Ser Arg Phe Ile Ala Gly
    370                 375                 380

Arg Pro Ser Arg Arg Asn Ile Arg Phe Lys Pro Trp Phe Ile Pro Gly
385                 390                 395                 400

Val Ile Asn Glu Ile Ser Leu Thr Asn Asn Glu Leu Tyr Ile Asn Asn
                405                 410                 415

Leu Phe Val Thr Pro Glu Ile His Asn Leu Phe Val Lys Arg Val Arg
            420                 425                 430

Phe Ser Leu Ile Arg Val His Lys Thr Gln Val Thr His Thr Asn Asn
        435                 440                 445

Asn His His Asp Glu Lys Leu Met Ser Ala Leu Lys Trp Pro Ile Glu
    450                 455                 460

Tyr Met Phe Ile Gly Leu Lys Pro Thr Trp Asn Ile Ser Asp Gln Asn
465                 470                 475                 480

Pro His Gln His Arg Asp Trp His Lys Phe Gly His Val Val Asn Ala
                485                 490                 495

Ile Met Gln Pro Thr His His Ala Glu Ile Ser Phe Gln Asp Arg Asp
            500                 505                 510

Thr Ala Leu Pro Asp Ala Cys Ser Ser Ile Ser Asp Ile Ser Pro Val
        515                 520                 525

Thr Tyr Pro Ile Thr Leu Pro Ile Ile Lys Asn Ile Ser Val Thr Ala
    530                 535                 540

His Gly Ile Asn Leu Ile Asp Lys Phe Pro Ser Lys Phe Cys Ser Ser
545                 550                 555                 560

Tyr Ile Pro Phe His Tyr Gly Gly Asn Ala Ile Lys Thr Pro Asp Asp
                565                 570                 575
```

Pro Gly Ala Met Met Ile Thr Phe Ala Leu Lys Pro Arg Glu Glu Tyr
580 585 590

Gln Pro Ser Gly His Ile Asn Val Ser Arg Ala Arg Glu Phe Tyr Ile
595 600 605

Ser Trp Asp Thr Asp Tyr Val Gly Ser Ile Thr Thr Ala Asp Leu Val
610 615 620

Val Ser Ala Ser Ala Ile Asn Phe Leu Leu Leu Gln Asn Gly Ser Ala
625 630 635 640

Val Leu Arg Tyr Ser Thr
645

<210> 31
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, Synthetic ubiquitin

<400> 31
gtcagtcgct tcctcatcgc agaatacaga cacctcatcg aaaacccatc cgaaaacttc 60

aaaatctccg tcaacgaaaa caacatcacc gagtgggacg tgatcctgag gggcccaccc 120

gacaccctgt acgagggcgg cctgttcaag gccaaggtgg ccttccctcc cgagtaccca 180

tacgccccac ctaagctgac cttcaccagc gagatgtggc acccaaacat ctaccctgac 240

ggcagactgt gcatcagcat cctgcacggc gacaacgcag aggagcaggg aatgacctgg 300

tcccctgccc agaagatcga caccatcctg ctgagcgtga tctccctgct gaacgagcct 360

aacccagaca gcccagcaaa cgtggacgca gcaaagtcct acaggaagta cgtgtacaag 420

gaggacctgg agtcctaccc catggaggtg aagaagaccg tgaagaagag cctggacgag 480

tgctccccag aggacatcga gtacttcaag aacgcagcaa gcaacgtgcc cccaatccca 540

tccgacgcct acgaggacga gtgtgaggag atggaggacg acacatacat tctgacatac 600

gacgatgatg aagaggaaga ggatgaagag atggatgatg aa 642

<210> 32
<211> 214

<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, Synthetic ubiquitin

<400> 32

Val Ser Arg Phe Leu Ile Ala Glu Tyr Arg His Leu Ile Glu Asn Pro
1 5 10 15

Ser Glu Asn Phe Lys Ile Ser Val Asn Glu Asn Asn Ile Thr Glu Trp
20 25 30

Asp Val Ile Leu Arg Gly Pro Pro Asp Thr Leu Tyr Glu Gly Gly Leu
35 40 45

Phe Lys Ala Lys Val Ala Phe Pro Pro Glu Tyr Pro Tyr Ala Pro Pro
50 55 60

Lys Leu Thr Phe Thr Ser Glu Met Trp His Pro Asn Ile Tyr Pro Asp
65 70 75 80

Gly Arg Leu Cys Ile Ser Ile Leu His Gly Asp Asn Ala Glu Glu Gln
85 90 95

Gly Met Thr Trp Ser Pro Ala Gln Lys Ile Asp Thr Ile Leu Leu Ser
100 105 110

Val Ile Ser Leu Leu Asn Glu Pro Asn Pro Asp Ser Pro Ala Asn Val
115 120 125

Asp Ala Ala Lys Ser Tyr Arg Lys Tyr Val Tyr Lys Glu Asp Leu Glu
130 135 140

Ser Tyr Pro Met Glu Val Lys Lys Thr Val Lys Lys Ser Leu Asp Glu
145 150 155 160

Cys Ser Pro Glu Asp Ile Glu Tyr Phe Lys Asn Ala Ala Ser Asn Val
165 170 175

Pro Pro Ile Pro Ser Asp Ala Tyr Glu Asp Glu Cys Glu Glu Met Glu
180 185 190

Asp Asp Thr Tyr Ile Leu Thr Tyr Asp Asp Asp Glu Glu Glu Glu Asp
195 200 205

Glu Glu Met Asp Asp Glu
210

<210> 33
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, IgE leader sequence

<400> 33

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser