SEQUENCE LISTING

<110> The Trustees of University of Pennsylvania
Powell, Daniel J.
Coukos, George
June, Carl H.

<120> Compositions and Methods for Treating Cancer

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35 40 45

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
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Phe Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
65 70 75 80

Gly Arg Ile His Pro Tyr Asp Gly Asp Thr Phe Tyr Asn Gln Asn Phe
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Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala His
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Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Phe Ala Val Tyr Tyr Cys
115 120 125

Thr Arg Tyr Asp Gly Ser Arg Ala Met Asp Tyr Trp Gly Gln Gly Thr
130 135 140

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

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Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ser Leu
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Ala Val Ser Leu Gly Gln Arg Ala Ile Ile Ser Cys Lys Ala Ser Gln
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Ser Val Ser Phe Ala Gly Thr Ser Leu Met His Trp Tyr His Gln Lys
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Pro Gly Gln Gln Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu
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Ala Gly Val Pro Thr Arg Phe Ser Gly Ser Gly Ser Lys Thr Asp Phe
225                 230                 235                 240

Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr
                245                 250                 255

Cys Gln Gln Ser Arg Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
            260                 265                 270

Leu Glu Ile Lys Arg Ala Ala Ala Ser Thr Thr Thr Pro Ala Pro Arg
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Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
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Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
            340                 345                 350

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
        355                 360                 365

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
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Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
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Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
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Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
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Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
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Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
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Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Met Asn Trp Val Lys Gln
35 40 45

Ser His Gly Lys Ser Leu Glu Trp Ile Gly Arg Ile His Pro Tyr Asp
50 55 60

Gly Asp Thr Phe Tyr Asn Gln Asn Phe Lys Asp Lys Ala Thr Leu Thr
65 70 75 80

Val Asp Lys Ser Ser Asn Thr Ala His Met Glu Leu Leu Ser Leu Thr
85 90 95

Ser Glu Asp Phe Ala Val Tyr Tyr Cys Thr Arg Tyr Asp Gly Ser Arg
100 105 110

Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
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Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
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Glu Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
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Ala Ile Ile Ser Cys Lys Ala Ser Gln Ser Val Ser Phe Ala Gly Thr
165 170 175

Ser Leu Met His Trp Tyr His Gln Lys Pro Gly Gln Gln Pro Lys Leu
180 185 190

Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ala Gly Val Pro Thr Arg Phe
195 200 205

Ser Gly Ser Gly Ser Lys Thr Asp Phe Thr Leu Asn Ile His Pro Val
210 215 220

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Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
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<400> 17

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Ser Leu Val Ile Thr Leu Tyr Cys
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Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
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Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
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Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
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Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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gggttggaag tgggtgggag agttcgaggc cttgcgctta aggagcccct tcgcctcgtg 8400

cttgagttga ggcctggcct gggcgctggg gccgccgcgt gcgaatctgg tggcaccttc 8460

gcgcctgtct cgctgctttc gataagtctc tagccattta aaatttttga tgacctgctg 8520

cgacgctttt tttctggcaa gatagtcttg taaatgcggg ccaagatctg cacactggta 8580

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cgaggcgggg cctgcgagcg cggccaccga gaatcggacg ggggtagtct caagctggcc 8700

ggcctgctct ggtgcctggc ctcgcgccgc cgtgtatcgc cccgccctgg gcggcaaggc 8760

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ggagctcaaa atggaggacg cggcgctcgg gagagcgggc gggtgagtca cccacacaaa 8880

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gctctagag 9189

<210> 21
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 21

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aaggggctgg agtgggtctc atccattagt agtagtagta gttacatata ctacgcagac 180

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atgaacagcc tgagagccga ggacacggct gtgtattact gtgcgagaga acgatacgat 300

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gttgggagtt ataaccttgt ctcctggtac caacagcacc caggcaaagc ccccaaactc 540

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tctggcaacg cggcctccct gacaatctct gggctccagg ctgaggacga ggctgattat 660

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gtcctaggt 729

<210> 22
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 22

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Phe
35 40 45

Thr Phe Gly Asp Tyr Ala Met Ile Trp Ala Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

```
Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Glu Arg Tyr Asp Phe Trp Ser Gly Met
        115                 120                 125

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser Ala Gln Ser Ala Leu Thr
145                 150                 155                 160

Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser
                165                 170                 175

Cys Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr Asn Leu Val Ser Trp
            180                 185                 190

Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Glu Gly
        195                 200                 205

Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser
    210                 215                 220

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

Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Val Val Phe
                245                 250                 255

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ser Thr Thr Thr Pro
            260                 265                 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
        275                 280                 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    290                 295                 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305                 310                 315                 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
                325                 330                 335

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
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            340                 345                 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
        355                 360                 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
    370                 375                 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385                 390                 395                 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
                405                 410                 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
            420                 425                 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
        435                 440                 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
    450                 455                 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465                 470                 475                 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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<210> 23
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 23

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Arg Leu Ser Cys Thr Thr Ser Gly Phe Thr Phe Gly Asp Tyr Ala Met
            20                  25                  30

Ile Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser
        35                  40                  45
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Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val Lys Gly
    50                  55                  60

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
65                  70                  75                  80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
                85                  90                  95

Glu Arg Tyr Asp Phe Trp Ser Gly Met Asp Val Trp Gly Lys Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Ser Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly
    130                 135                 140

Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp
145                 150                 155                 160

Val Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val
            180                 185                 190

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Ala Ala Ser Leu Thr
        195                 200                 205

Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser
    210                 215                 220

Tyr Asp Ser Ser Leu Ser Val Val Phe Gly Gly Gly Thr Lys Leu Thr
225                 230                 235                 240

Val Leu Gly
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<210> 24
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 24

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<210> 25
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 25
gcggctagcg gccgcccgtt ttatttccaa ctttgtcccc cc 42

<210> 26
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 26
gctgggacaa agttggaaat caaagctagc accacgacgc cagcgccgcg acc 53

<210> 27
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 27
tcgacagtcg acttagcgag ggggcagggc ct 32

<210> 28
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 28
atagcatcta gaatggcctt accagtgacc gccttgctcc tgccgctggc cttgctgctc 60

<210> 29
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 29
tcgacagtcg acttagcgag ggggcagggc ct 32