SEQUENCE LISTING

<110> CytomX Therapeutics, Inc.

<120> Activatable Antibodies That Bind Epidermal Growth Factor Receptor And Methods Of Use Thereof

<130> 42652-517001WO

<140> PCT/US2013/038540
<141> 2013-04-26

<150> US 61/639796
<151> 2012-04-27

<150> US 61/662204
<151> 2012-06-20

<150> US 61/749220
<151> 2013-01-04

<150> US 61/749529
<151> 2013-01-07

<150> US 61/763237
<151> 2013-02-11

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<170> PatentIn version 3.5

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acctgcaccg tgagcggctt tagcctgacc aactatggcg tgcattgggt gcgccagagc 180

ccgggcaaag gcctggaatg gctgggcgtg atttggagcg gcggcaacac cgattataac 240

accccgttta ccagccgcct gagcattaac aaagataaca gcaaaagcca ggtgtttttt 300

aaaatgaaca gcctgcaaag ccaggatacc gcgatttatt attgcgcgcg cgcgctgacc 360

tattatgatt atgaatttgc gtattggggc cagggcaccc tggtgaccgt gagcgcggct 420

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 480

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 540

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 660

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tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 780

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 840

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 900

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 960

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1020

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

Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly
50 55 60

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

Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser
85 90 95

Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile
100 105 110

Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
115 120 125

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

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
210 215 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305 310 315 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
355 360 365

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
450 455 460

Leu Ser Pro Gly Lys
465

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aatcatggca gtagcggtac ccagatcttg ctgacccaga gcccggtgat tctgagcgtg 240

agcccgggcg aacgtgtgag ctttagctgc cgcgcgagcc agagcattgg caccaacatt 300

cattggtatc agcagcgcac caacggcagc ccgcgcctgc tgattaaata tgcgagcgaa 360

agcattagcg gcattccgag ccgctttagc ggcagcggca gcggcaccga ttttaccctg 420

agcattaaca gcgtggaaag cgaagatatt gcggattatt attgccagca gaacaacaac 480

tggccgacca cctttggcgc gggcaccaaa ctggaactga aacgtacggt ggctgcacca 540

tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 600

tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 660

ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 720

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<212> PRT
<213> Artificial Sequence

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Val Thr Asn Ser Gln Gly Gln Ser Gly Gln Cys Ile Ser Pro Arg Gly
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Cys Pro Asp Gly Pro Tyr Val Met Tyr Gly Ser Ser Gly Gly Ser Gly
35 40 45

Gly Ser Gly Gly Ser Gly Leu Ser Gly Arg Ser Asp Asn His Gly Ser
50 55 60

Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val
65 70 75 80

Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile
85 90 95

Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg
100 105 110

Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg
115 120 125

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser
130 135 140

Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn
145 150 155 160

Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr
165 170 175

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
180 185 190

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
195 200 205

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
210 215 220

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
225 230 235 240

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
245 250 255

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
260 265 270

Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<212> DNA
<213> Artificial Sequence

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acctgcaccg tgagcggctt tagcctgacc aactatggcg tgcattgggt gcgccagagc 180

ccgggcaaag gcctggaatg gctgggcgtg atttggagcg gcggcaacac cgattataac 240

accccgttta ccagccgcct gagcattaac aaagataaca gcaaaagcca ggtgtttttt 300

aaaatgaaca gcctgcaaag caacgatacc gcgatttatt attgcgcgcg cgcgctgacc 360

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agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 480

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 540

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 660

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 720

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 780

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 840

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acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1020

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1080

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgaactg 1140

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1200

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1260

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1320

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1380

aagagcctct ccctgtctcc gggtaaatga 1410

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<400> 6

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Val Thr Asn Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val
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Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
35 40 45

Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly
50 55 60

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

Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser
85 90 95

Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile
100 105 110

Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
115 120 125

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

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
210 215 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305 310 315 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
355 360 365

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
450 455 460

Leu Ser Pro Gly Lys
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Pro Arg Phe Lys Ile Ile Gly Gly
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<210> 8
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<212> PRT
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Pro Arg Phe Arg Ile Ile Gly Gly
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ccgggcaaag gcctggaatg gctgggcgtg atttggagcg gcggcaacac cgattataac 240

accccgttta ccagccgcct gagcattaac aaagataaca gcaaaagcca ggtgtttttt 300

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aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 660

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tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 840

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gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgaactg 1140

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1200

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

Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly
50 55 60

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

Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser
85 90 95

Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile
100 105 110

Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
115 120 125

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

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
210 215 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser
305 310 315 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
355 360 365

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
450 455 460

Leu Ser Pro Gly Lys
465

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<400> 11

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<400> 12

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<210> 13
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<400> 13

Leu Ser Gly Arg Ser Asp Asn His
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<210> 14
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<400> 14

Cys Ile Ser Pro Arg Gly Cys Pro Asp Gly Pro Tyr Val Met Tyr
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<210> 15
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<400> 15

Gly Ser Gly Gly Ser
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<400> 16

Gly Gly Gly Ser
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<400> 17

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<400> 18

Gly Gly Ser Gly Gly

1 5

<210> 19
<211> 5
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<400> 19

Gly Ser Gly Ser Gly
1 5

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Gly Ser Gly Gly Gly
1 5

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<400> 21

Gly Gly Gly Ser Gly
1 5

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<400> 22

Gly Ser Ser Ser Gly
1 5

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<212> PRT
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<400> 23

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<210> 24
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<400> 24

Gly Ser Ser Gly Thr
1 5

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ccgggcaaag gcctggaatg gctgggcgtg atttggagcg gcggcaacac cgattataac 180

accccgttta ccagccgcct gagcattaac aaagataaca gcaaaagcca ggtgtttttt 240

aaaatgaaca gcctgcaaag ccaggatacc gcgatttatt attgcgcgcg cgcgctgacc 300

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acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

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tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

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accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaatga 1350

<210> 26
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 26

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

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

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

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

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 27
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 27
caaggccagt ctggccagtg catctcacct cgtggttgtc cggacggccc atacgtcatg 60

tacggctcga gcggtggcag cggtggctct ggtggatccg gtctgagcgg ccgttccgat 120

aatcatggca gtagcggtac ccagatcttg ctgacccaga gcccggtgat tctgagcgtg 180

agcccgggcg aacgtgtgag ctttagctgc cgcgcgagcc agagcattgg caccaacatt 240

cattggtatc agcagcgcac caacggcagc ccgcgcctgc tgattaaata tgcgagcgaa 300

agcattagcg gcattccgag ccgctttagc ggcagcggca gcggcaccga ttttaccctg 360

agcattaaca gcgtggaaag cgaagatatt gcggattatt attgccagca gaacaacaac 420

tggccgacca cctttggcgc gggcaccaaa ctggaactga aacgtacggt ggctgcacca 480

tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 540

tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 600

ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 660

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 720

tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 780

tgttag 786

<210> 28
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 28

Gln Gly Gln Ser Gly Gln Cys Ile Ser Pro Arg Gly Cys Pro Asp Gly
1 5 10 15

Pro Tyr Val Met Tyr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Leu Ser Gly Arg Ser Asp Asn His Gly Ser Ser Gly Thr Gln
35 40 45

Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly Glu
50 55 60

Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile
65 70 75 80

His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys
85 90 95

Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser
100 105 110

Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser Glu
115 120 125

Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr
130 135 140

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala Pro
145 150 155 160

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
165 170 175

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
180 185 190

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu

195 200 205

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
210 215 220

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
225 230 235 240

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
245 250 255

Asn Arg Gly Glu Cys
260

<210> 29
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 29
caggtgcagc tgaaacagag cggcccgggc ctggtgcagc cgagccagag cctgagcatt 60

acctgcaccg tgagcggctt tagcctgacc aactatggcg tgcattgggt gcgccagagc 120

ccgggcaaag gcctggaatg gctgggcgtg atttggagcg gcggcaacac cgattataac 180

accccgttta ccagccgcct gagcattaac aaagataaca gcaaaagcca ggtgtttttt 240

aaaatgaaca gcctgcaaag caacgatacc gcgatttatt attgcgcgcg cgcgctgacc 300

tattatgatt atgaatttgc gtattggggc cagggcaccc tggtgaccgt gagcgcggct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgaactg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaatga 1350

<210> 30
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 30

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

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

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp

145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

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

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 31
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 31

Ser Ser Ser Phe Asp Lys Gly Lys Tyr Lys Lys Gly Asp Asp Ala
1 5 10 15

<210> 32
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 32

Ser Ser Ser Phe Asp Lys Gly Lys Tyr Lys Arg Gly Asp Asp Ala
1 5 10 15

<210> 33
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 33
caggtgcagc tgaaacagag cggcccgggc ctggtgcagc cgagccagag cctgagcatt 60

acctgcaccg tgagcggctt tagcctgacc aactatggcg tgcattgggt gcgccagagc 120

ccgggcaaag gcctggaatg gctgggcgtg atttggagcg gcggcaacac cgattataac 180

accccgttta ccagccgcct gagcattaac aaagataaca gcaaaagcca ggtgtttttt 240

aaaatgaaca gcctgcaaag ccaggatacc gcgatttatt attgcgcgcg cgcgctgacc 300

tattatgatt atgaatttgc gtattggggc cagggcaccc tggtgaccgt gagcgcggct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacgccagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgaactg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaatga 1350

<210> 34
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 34

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

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

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

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

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 35
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 35

Ile Glu Gly Arg
1

<210> 36
<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 36

Ile Asp Gly Arg
1

<210> 37
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 37

Gly Ser Ser Gly
1

<210> 38
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 38

Gln Gly Gln Ser Gly Gln
1 5

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 39

Gly Gly Ser Ile Asp Gly Arg
1 5

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 40

Pro Leu Gly Leu Trp Ala
1 5

<210> 41
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 41

Gly Pro Gln Gly Ile Ala Gly Gln
1 5

<210> 42
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 42

Gly Pro Gln Gly Leu Leu Gly Ala
1 5

<210> 43
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 43

Gly Ile Ala Gly Gln
1 5

<210> 44
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 44

Gly Pro Leu Gly Ile Ala Gly Ile
1 5

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 45

Gly Pro Glu Gly Leu Arg Val Gly
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 46

Tyr Gly Ala Gly Leu Gly Val Val
1 5

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 47

Ala Gly Leu Gly Val Val Glu Arg
1 5

<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 48

Ala Gly Leu Gly Ile Ser Ser Thr
1 5

<210> 49
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 49

Glu Pro Gln Ala Leu Ala Met Ser
1 5

<210> 50
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 50

Gln Ala Leu Ala Met Ser Ala Ile
1 5

<210> 51
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 51

Ala Ala Tyr His Leu Val Ser Gln
1 5

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 52

Met Asp Ala Phe Leu Glu Ser Ser
1 5

<210> 53
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 53

Glu Ser Leu Pro Val Val Ala Val
1 5

<210> 54
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 54

Ser Ala Pro Ala Val Glu Ser Glu
1 5

<210> 55
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 55

Asp Val Ala Gln Phe Val Leu Thr
1 5

<210> 56
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 56

Val Ala Gln Phe Val Leu Thr Glu
1 5

<210> 57
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 57

Ala Gln Phe Val Leu Thr Glu Gly
1 5

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 58

Pro Val Gln Pro Ile Gly Pro Gln
1 5

<210> 59
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 59

Gln Gly Gln Ser Gly Gln Cys Ile Ser Pro Arg Gly Cys Pro Asp Gly
1 5 10 15

Pro Tyr Val Met Tyr
20

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

<220>
<223> chemically synthesized

<400> 60
atgtacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacgaattcg 60

<210> 61
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 61

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 62
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 62
caaggccagt ctggccag 18

<210> 63
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 63
tgcatctcac ctcgtggttg tccggacggc ccatacgtca tgtac 45

<210> 64
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 64
ggctcgagcg gtggcagcgg tggctctggt ggatccggt 39

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 65
ctgagcggcc gttccgataa tcat 24

<210> 66
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 66
ggcagtagcg gtacc 15

<210> 67
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 67
cagatcttgc tgacccagag cccggtgatt ctgagcgtga gcccgggcga acgtgtgagc 60

tttagctgcc gcgcgagcca gagcattggc accaacattc attggtatca gcagcgcacc 120

aacggcagcc cgcgcctgct gattaaatat gcgagcgaaa gcattagcgg cattccgagc 180

cgctttagcg gcagcggcag cggcaccgat tttaccctga gcattaacag cgtggaaagc 240

gaagatattg cggattatta ttgccagcag aacaacaact ggccgaccac ctttggcgcg 300

ggcaccaaac tggaactgaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 68
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 68

Gln Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 69
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<400> 69

Ser Asp Asn His Gly Ser Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser
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Pro Val Ile Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys
20 25 30

Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg
35 40 45

Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile

50 55 60

Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
65 70 75 80

Thr Leu Ser Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr
85 90 95

Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys
100 105 110

Leu Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
115 120 125

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155 160

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
165 170 175

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
180 185 190

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
195 200 205

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 70
<211> 220
<212> PRT
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<400> 70

His Gly Ser Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser Pro Val Ile
1 5 10 15

Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser
20 25 30

Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly
35 40 45

Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser
65 70 75 80

Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln
85 90 95

Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220