

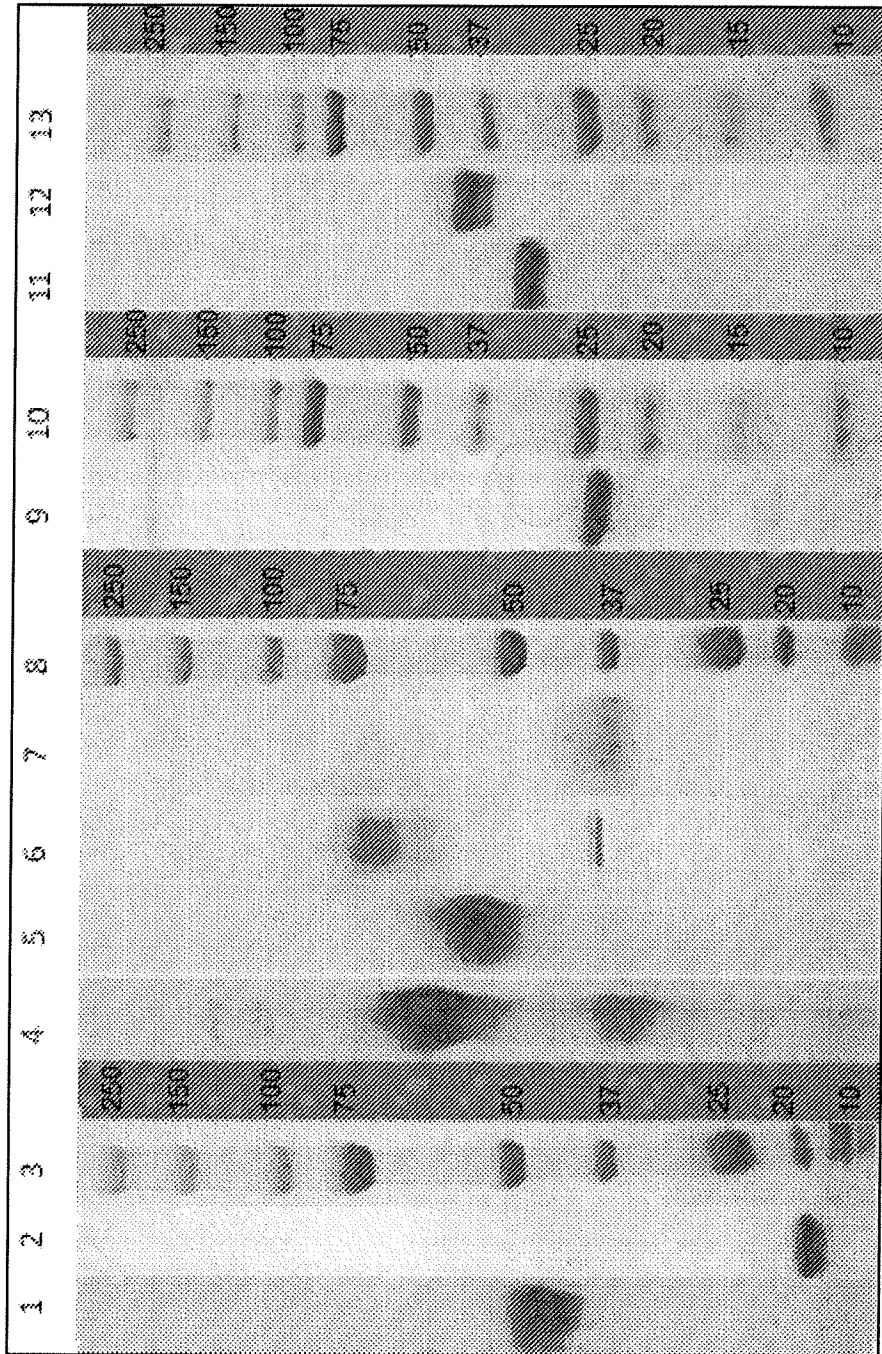


FIGURE 1

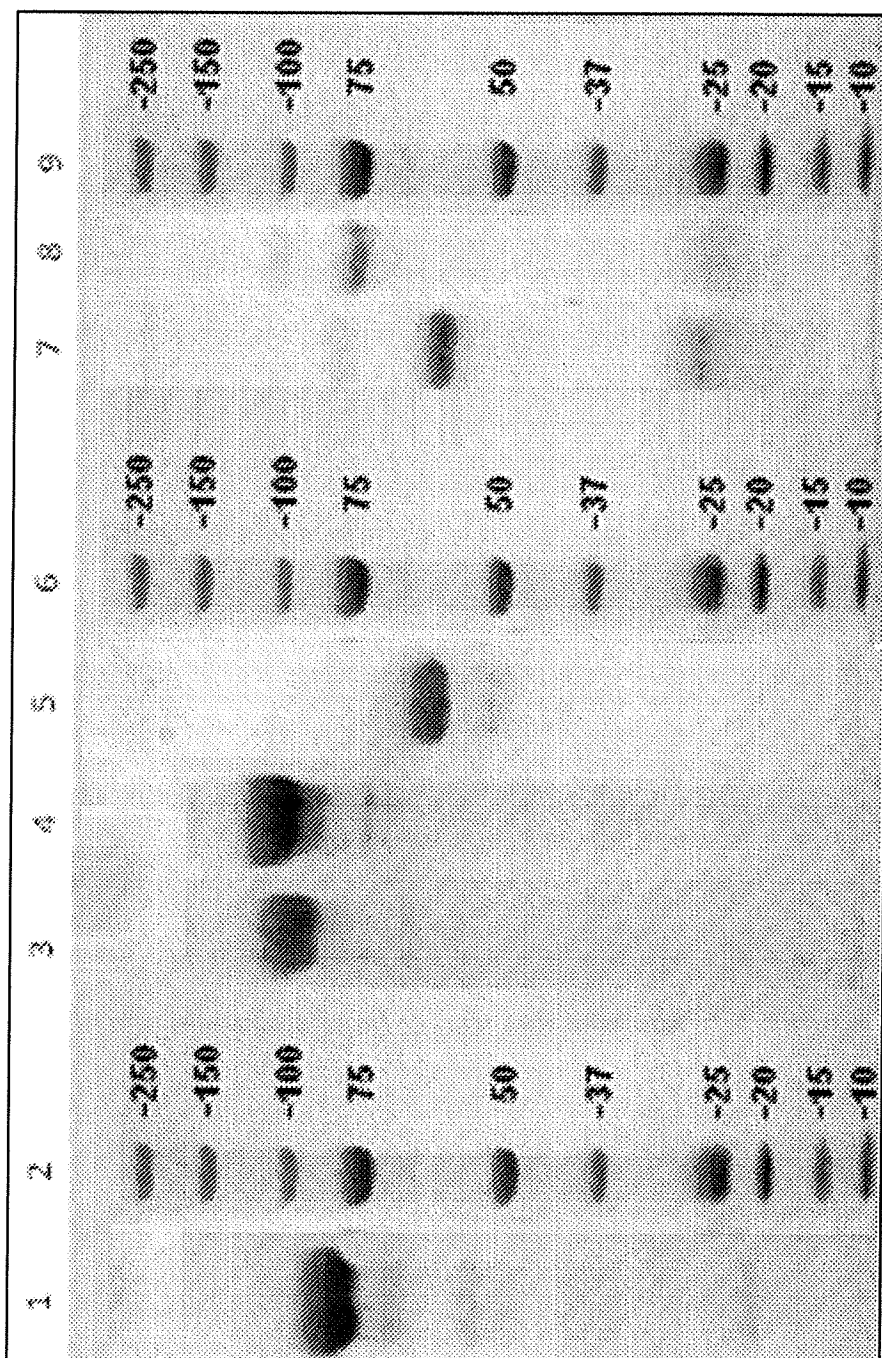


FIGURE 2

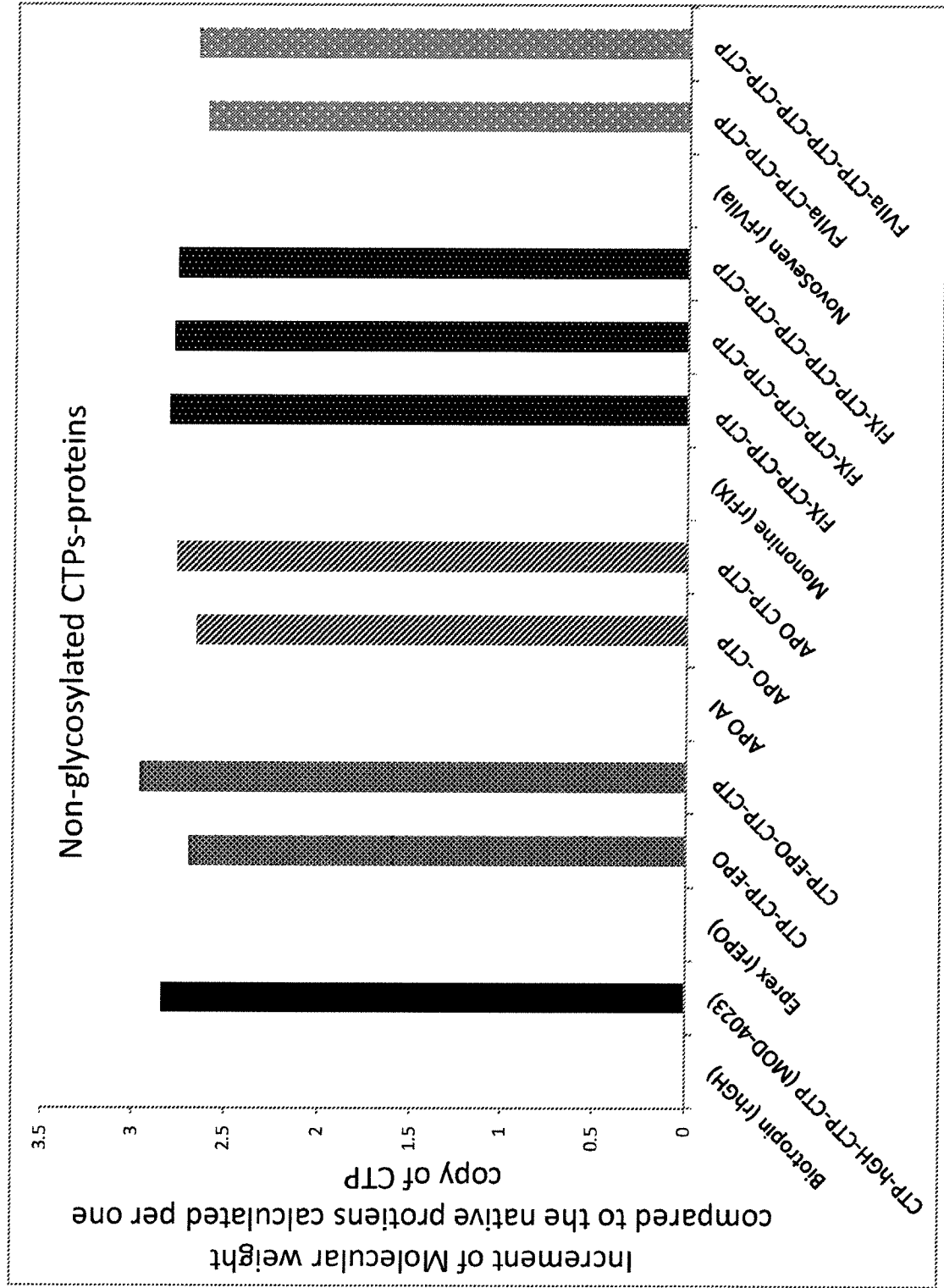


FIGURE 3A

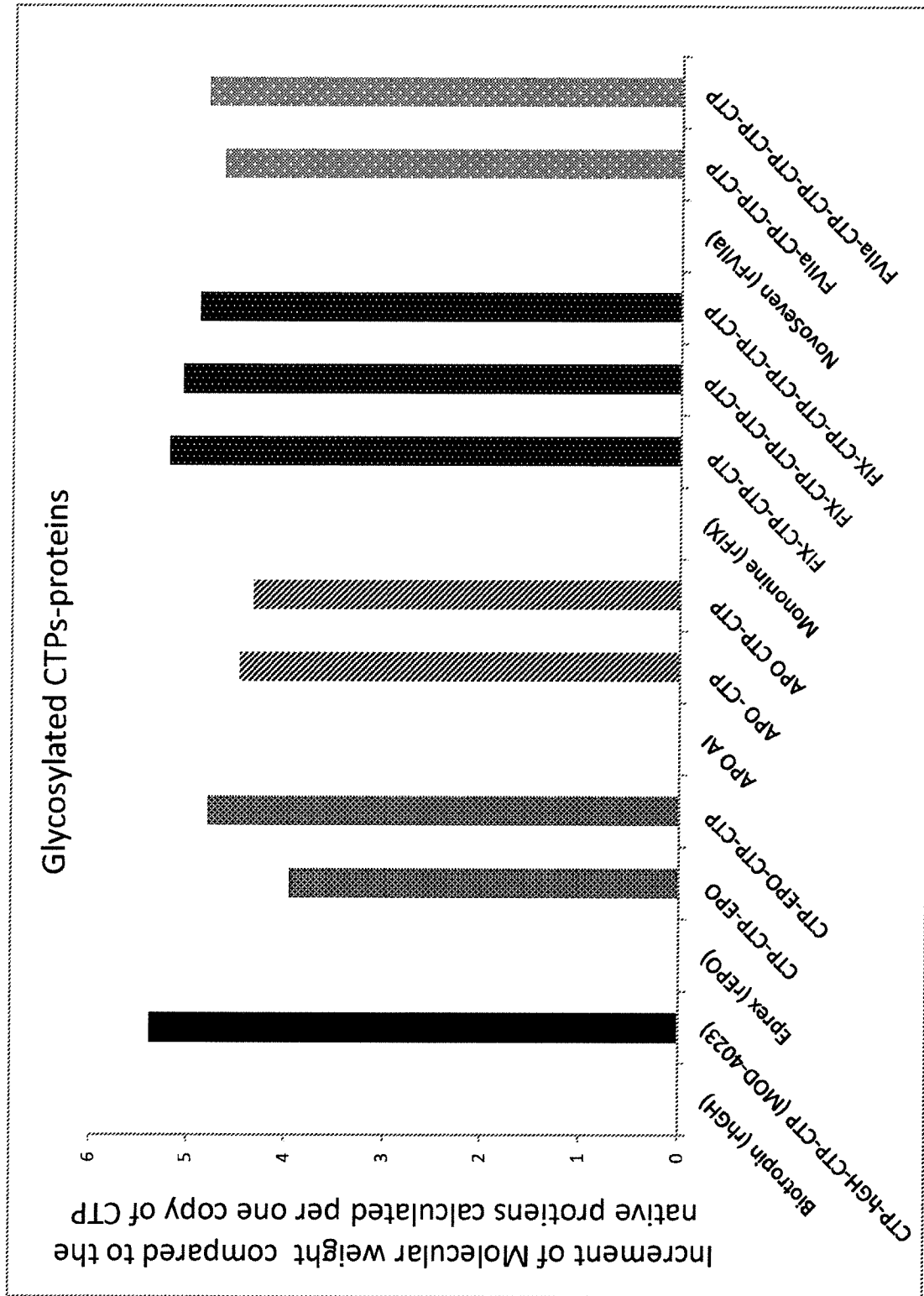


FIGURE 3B

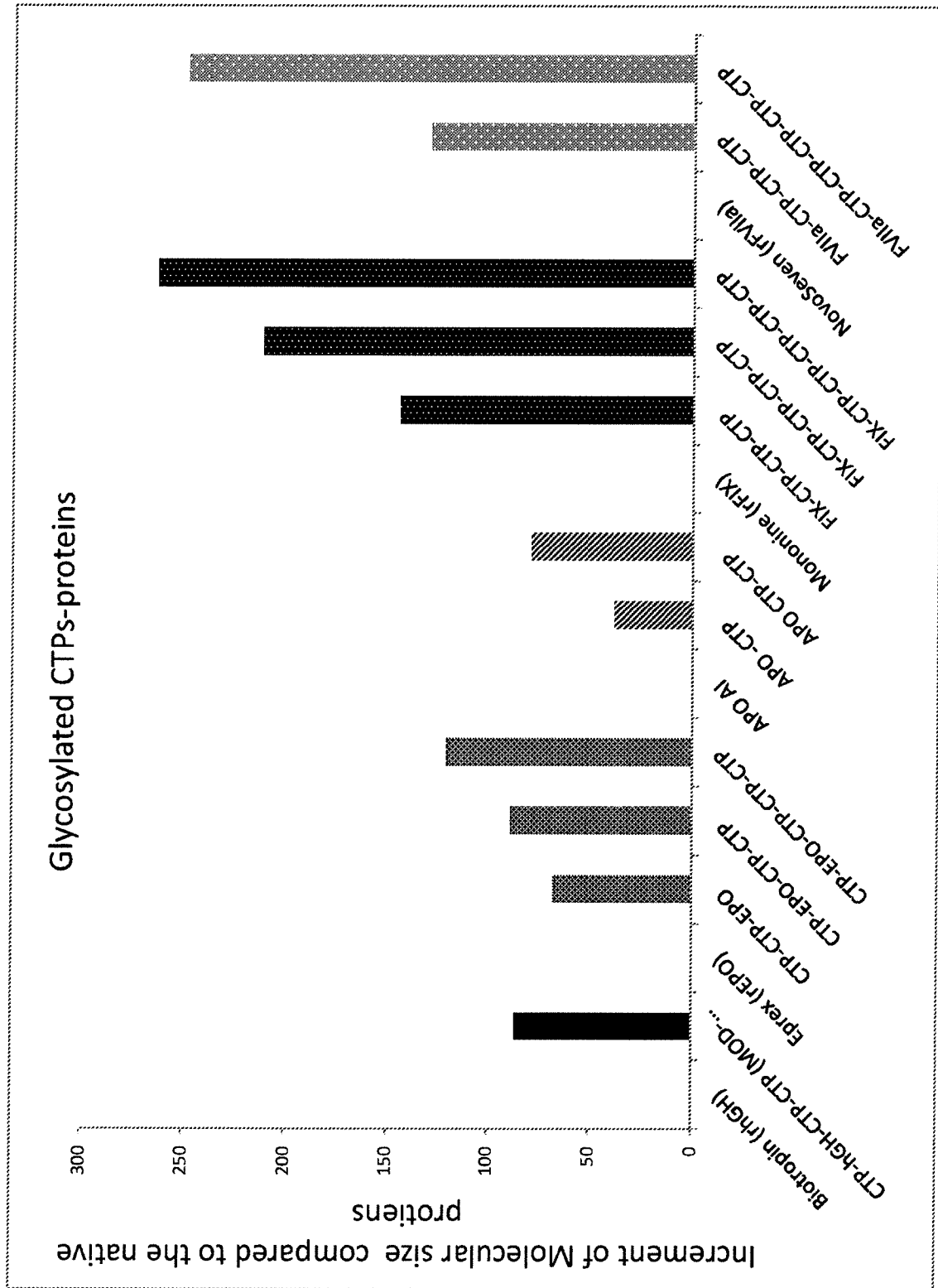


FIGURE 4A

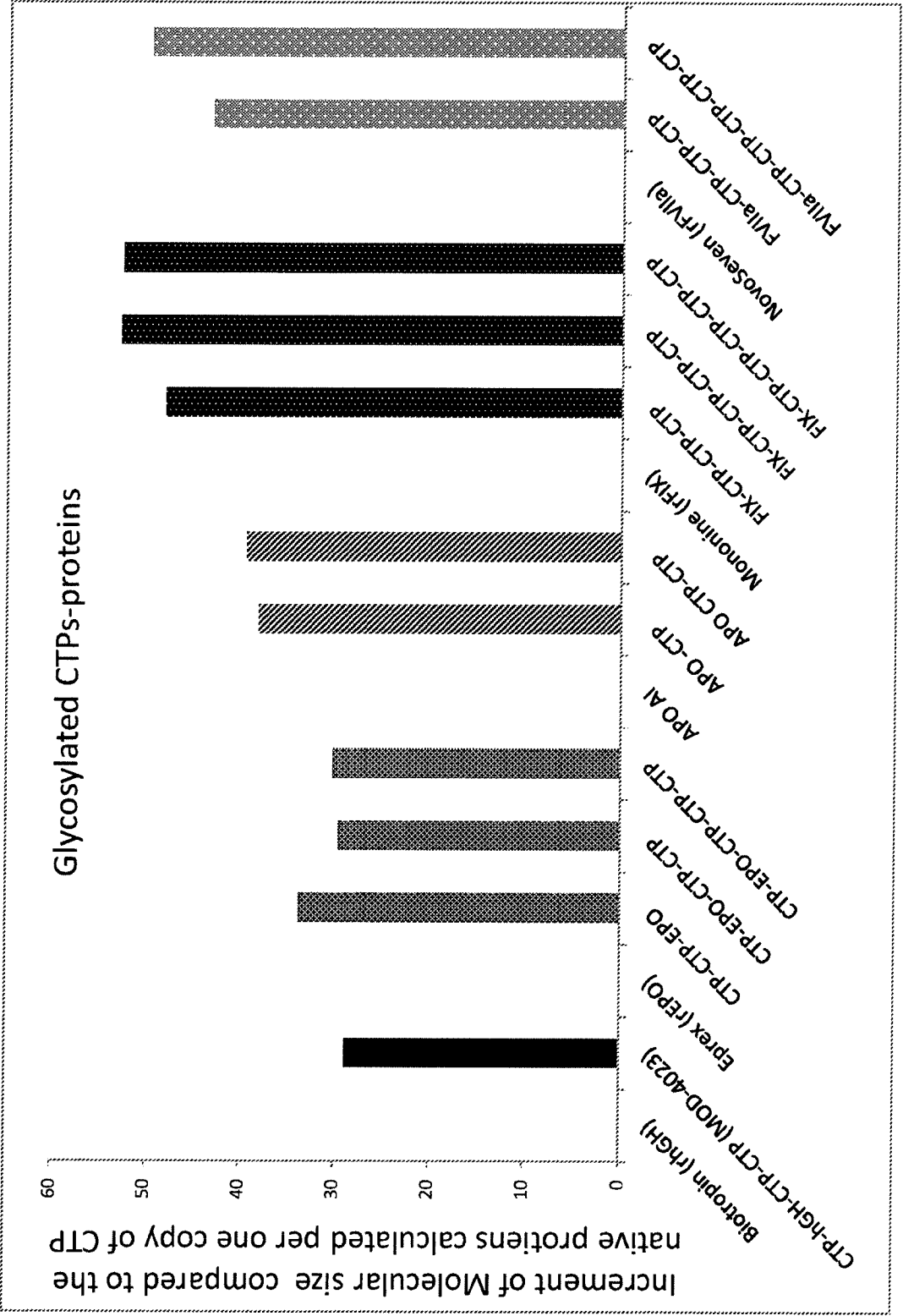


FIGURE 4B

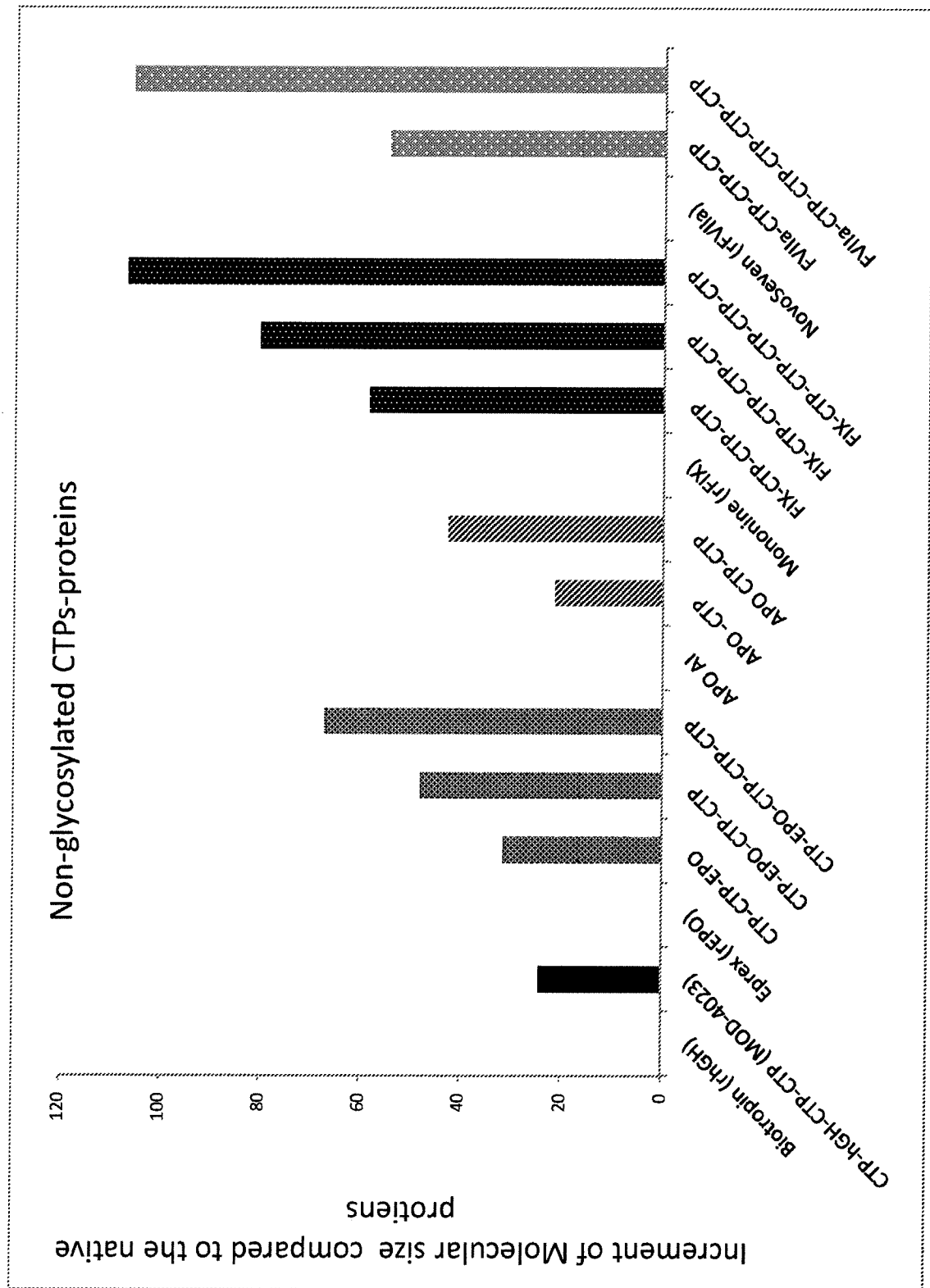


FIGURE 5A

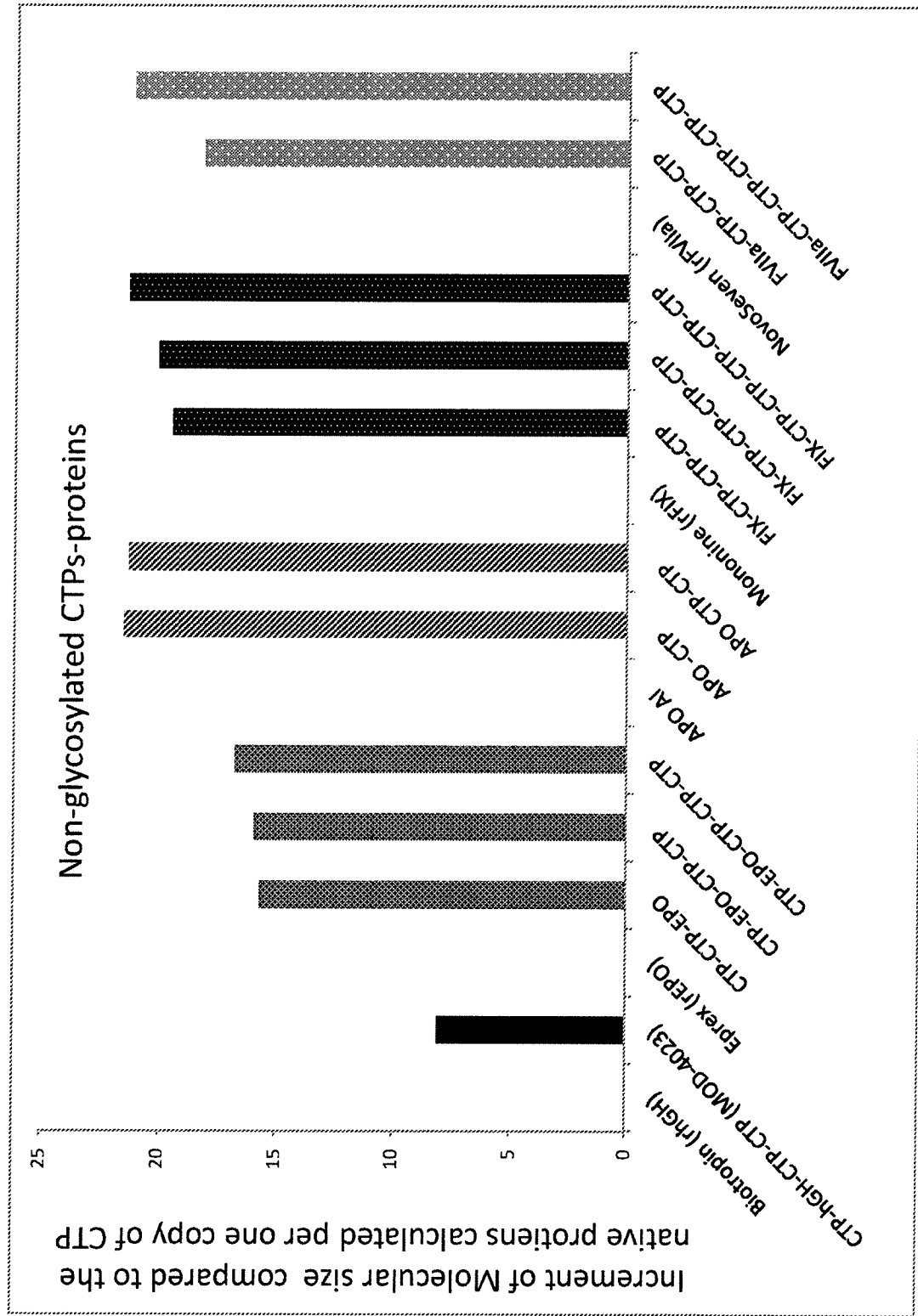


FIGURE 5B

SEQUENCE LISTING

<110> Opko Biologics Ltd.

<120> METHOD OF INCREASING THE HYDRODYNAMIC VOLUME OF POLYPEPTIDES BY ATTACHING TO GONADOTROPHIN CARBOXY TERMINAL PEPTIDES

<130> SG5495A

<150> 61/728,662

<151> 2012-11-20

<160> 73

<170> PatentIn version 3.5

<210> 1

<211> 32

<212> PRT

<213> Artificial

<220>

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<212> PRT

<213> artificial

<220>

<223> Truncated CTP sequence

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<213> artificial

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<223> hGH signal peptide

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<213> Homo sapiens

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1 5 10 15

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20 25 30

Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
35 40 45

Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
50 55 60

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65 70 75 80

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
85 90 95

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
100 105 110

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

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
130 135 140

Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
145 150 155 160

Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
195 200 205

Arg Ser Val Glu Gly Ser Cys Gly Phe
210 215

<210> 6
<211> 192
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<213> Artificial

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Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

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165 170 175

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20 25 30

Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
35 40 45

Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
50 55 60

Val Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65 70 75 80

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
85 90 95

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
100 105 110

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

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
130 135 140

Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
145 150 155 160

Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
180 185 190

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Arg Ser Val Glu Gly Ser Cys Gly Phe
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20 25 30

Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
35 40 45

Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
50 55 60

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65 70 75 80

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
85 90 95

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
100 105 110

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

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
130 135 140

Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
145 150 155 160

Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
195 200 205

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

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
225 230 235 240

Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu
245 250 255

Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
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Gln

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<400> 11

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20 25 30

Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp
35 40 45

Thr Pro Ile Leu Pro Gln Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe
50 55 60

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp
65 70 75 80

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr
85 90 95

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile
100 105 110

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu
115 120 125

Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val
130 135 140

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser
145 150 155 160

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln
165 170 175

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile
180 185 190

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp
195 200 205

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met
210 215 220

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu
225 230 235 240

Gly Ser Cys Gly Phe Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu
245 250 255

Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
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Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser
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Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
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Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Ser Ser Ser Ser Lys Ala
20 25 30

Pro Pro Pro Ser Leu Pro Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe
35 40 45

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp
50 55 60

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr
65 70 75 80

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile
85 90 95

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu
100 105 110

Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val
115 120 125

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser
130 135 140

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

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile
165 170 175

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp
180 185 190

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met
195 200 205

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu
210 215 220

Gly Ser Cys Gly Phe Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu
225 230 235 240

Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
245 250 255

Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser
260 265 270

Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
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Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Ser Ser Ser Ser Lys Ala
20 25 30

Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp
35 40 45

Thr Pro Ile Leu Pro Gln Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe
50 55 60

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp
65 70 75 80

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr
85 90 95

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile
100 105 110

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu
115 120 125

Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val
130 135 140

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser
145 150 155 160

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln
165 170 175

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile
180 185 190

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp
195 200 205

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met
210 215 220

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu
Page 11

225

230

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gcccagcccc agcagactgc cgggccccag cgacacaccc attctgcccc agttccccac 180
catccccctg agcaggctgt tcgacaacgc catgctgagg gctcacaggc tgcaccagct 240
ggcctttgac acctaccagg agttcgagga agcctacatc cccaaggagc agaagtacag 300
cttcctgcag aacccccaga cctccctgtg cttcagcgag agcatcccca cccccagcaa 360
cagagaggag acccagcaga agagcaacct ggagctgctg aggatctccc tgctgctgat 420
ccagagctgg ctggagcccc tgcagttcct gagaagcgtg ttcgccaaca gcctggtgta 480
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aagcgtggag ggcagctgcg gcttcagctc cagcagcaag gcccctcccc cgagcctgcc 780
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cctgatgggc cggctggagg acggcagccc caggaccggc cagatcttca agcagaccta	600
cagcaagttc gacaccaaca gccacaacga cgacgccctg ctgaagaact acgggctgct	660
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caagcagacc tacagcaagt tcgacaccaa cagccacaac gacgacgccc tgctgaagaa	600
ctacgggctg ctgtactgct tcagaaagga catggacaag gtggagacct tcctgaggat	660
cgtgcagtgc agaagcgtgg agggcagctg cggcttcagc tccagcagca agggccctcc	720
cccgagcctg ccctcccaa gcaggctgcc tgggccctcc gacacaccaa tcctgccaca	780
gagcagctcc tctaaggccc ctctccatc cctgccatcc ccctcccggc tgcttgcccc	840
ctctgacacc cctatcctgc ctactgatg aaggtctgga tgcggccgc	889

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20 25 30

Arg Asn Asn Ile Ala
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<210> 19
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1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser
195 200 205

Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
210 215 220

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20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser
Page 15

195 200 205
 Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser
 210 215 220
 Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly
 225 230 235 240
 Pro Ser Asp Thr Pro Ile Leu Pro Gln
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 20 25 30
 Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
 35 40 45
 Asp Thr Pro Ile Leu Pro Gln Ala Pro Pro Arg Leu Ile Cys Asp Ser
 50 55 60
 Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
 65 70 75 80
 Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
 85 90 95
 Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
 100 105 110
 Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
 115 120 125
 Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
 130 135 140
 Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
 145 150 155 160
 Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
 165 170 175

Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr
180 185 190

Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
195 200 205

Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Ser Ser Ser
210 215 220

Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly
225 230 235 240

Pro Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro
245 250 255

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
260 265 270

Pro Ile Leu Pro Gln
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<213> Artificial

<220>
<223> EPO-CTP

<400> 22

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 130 135 140
 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160
 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175
 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190
 Arg Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser
 195 200 205
 Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Ala Pro Pro
 210 215 220
 Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
 225 230 235 240
 Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu
 245 250 255
 Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp
 260 265 270
 Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu
 275 280 285
 Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn
 290 295 300
 Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val
 305 310 315 320
 Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln
 325 330 335
 Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg
 340 345 350
 Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn
 355 360 365
 Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr
 370 375 380
 Gly Asp Arg
 385

<210> 23
<211> 221
<212> PRT
<213> Artificial

<220>
<223> CTP-EPO

<400> 23

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ser Ser Ser Ser Lys
20 25 30

Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
35 40 45

Asp Thr Pro Ile Leu Pro Gln Ala Pro Pro Arg Leu Ile Cys Asp Ser
50 55 60

Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
65 70 75 80

Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
85 90 95

Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
100 105 110

Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
115 120 125

Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
130 135 140

Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
145 150 155 160

Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
165 170 175

Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr
180 185 190

Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
195 200 205

Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
210 215 220

<210> 24
<211> 249
<212> PRT

<213> Artificial

<220>

<223> CTP-EPO-CTP

<400> 24

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ser Ser Ser Ser Lys
20 25 30

Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
35 40 45

Asp Thr Pro Ile Leu Pro Gln Ala Pro Pro Arg Leu Ile Cys Asp Ser
50 55 60

Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
65 70 75 80

Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
85 90 95

Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
100 105 110

Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
115 120 125

Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
130 135 140

Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
145 150 155 160

Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
165 170 175

Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr
180 185 190

Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
195 200 205

Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Ser Ser Ser
210 215 220

Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly
225 230 235 240

Pro Ser Asp Thr Pro Ile Leu Pro Gln
245

<210> 25
<211> 193
<212> PRT
<213> Artificial

<220>
<223> EPO

<400> 25

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg

<210> 26
<211> 873
<212> DNA
<213> Artificial

<220>

<223> EPO-CTP-CTP

<400> 26

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tctgtcgctc cctctggggc tcccagtcct gggctcctct tcctcaaagg cccctcccc      120
gagccttcca agtccatccc gactcccggg gccctcggac accccaatat taccacaagc      180
cccaccacgc ctcatctgtg acagccgagt cctggagagg tacctcttgg aggccaagga      240
ggccgagaat atcacgacgg gctgtgctga aactgcagc ttgaatgaga atatcactgt      300
cccagacacc aaagttaatt tctatgcctg gaagaggatg gaggtcgggc agcaggccgt      360
agaagtctgg cagggcctgg ccctgctgtc ggaagctgtc ctgcggggcc aggccctgtt      420
ggtcaactct tcccagccgt gggagccctt gcagctgcat gtggataaag ccgtcagtgg      480
ccttcgcagc ctccactc tgcttcgggc tctgggagcc cagaaggaag ccatctcccc      540
tccagatgcg gcctcagctg ctccactccg aacaatcact gctgacactt tccgcaaact      600
cttccgagtc tactccaatt tcctccgggg aaagctgaag ctgtacacag gggaggcctg      660
caggacaggg gacagatcct ctctctcaaa ggccctccc ccgagccttc caagtccatc      720
ccgactcccg gggccctccg acacaccaat cctgccacag agcagctcct ctaaggcccc      780
tcctccatcc ctgccatccc cctcccggct gcctggcccc tctgacaccc ctatcctgcc      840
tcagtgatga aggtcttctg gatccgcggc cgc      873
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<210> 27

<211> 187

<212> PRT

<213> Homo sapiens

<400> 27

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Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1          5          10          15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
          20          25          30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
          35          40          45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
          50          55          60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65          70          75          80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
          85          90          95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
          100          105          110
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Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
180 185

<210> 28
<211> 589
<212> DNA
<213> Homo sapiens

<400> 28
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caccgccctg agcatgagct acaacctgct gggcttcctg cagaggtcca gcaacttcca 120
gtgccagaag ctgctgtggc agctgaacgg caggctggaa tactgcctga aggacaggat 180
gaacttcgac atccagagg aaatcaagca gctgcagcag ttccagaagg aggacgccgc 240
cctgaccatc tacgagatgc tgcagaacat cttcgccatc ttcaggcagg acagcagcag 300
caccggctgg aacgagacca tcgtggagaa cctgctggcc aacgtgtacc accagatcaa 360
ccacctgaaa accgtgctgg aagagaagct ggaaaaggag gacttcacca ggggcaagct 420
gatgagcagc ctgcacctga agaggtacta cggcagaatc ctgcactacc tgaaggccaa 480
ggagtacagc cactgcgcct ggaccatcgt gaggtggag atcctgagga acttctactt 540
catcaacagg ctgaccggct acctgaggaa ctgatgagtc cgcgccgc 589

<210> 29
<211> 211
<212> PRT
<213> Artificial

<220>
<223> Interferon

<400> 29

Thr Phe Leu Gln Pro Phe Glu Ala Phe Ala Leu Ala Gln Gln Val Val
1 5 10 15

Gly Asp Thr Val Arg Val Val Asn Met Thr Asn Lys Cys Leu Leu Gln
20 25 30

Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr
35 40 45

Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys
50 55 60

Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg
65 70 75 80

Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln
85 90 95

Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe
100 105 110

Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile
115 120 125

Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys
130 135 140

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

Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His
165 170 175

Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg
180 185 190

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

Leu Arg Asn
210

<210> 30
<211> 639
<212> DNA
<213> Artificial

<220>
<223> Interferon

<400> 30
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gttcgtgttg tcaacatgac caacaagtgt ctctccaaa ttgctctcct gttgtgcttc 120
tccactacag ctctttccat gagctacaac ttgcttggat tcctacaaag aagcagcaat 180
tttcagtgtc agaagctcct gtggcaattg aatgggaggc ttgaatactg cctcaaggac 240
aggatgaact ttgacatccc tgaggagatt aagcagctgc agcagttcca gaaggaggac 300
gccgcattga ccatctatga gatgctccag aacatctttg ctattttcag acaagattca 360
tctagcactg gctggaatga gactattgtt gagaacctcc tggctaattg ctatcatcag 420
ataaaccatc tgaagacagt cctggaagaa aaactggaga aagaagattt caccagggga 480

aaactcatga gcagtctgca cctgaaaaga tattatggga ggattctgca ttacctgaag 540
 gccaaaggagt acagtcactg tgcctggacc atagtcagag tggaaatcct aaggaacttt 600
 tacttcatta acagacttac aggttacctc cgaaactga 639

<210> 31
 <211> 215
 <212> PRT
 <213> Artificial

<220>
 <223> IFN-CTP

<400> 31

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
 1 5 10 15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
 20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
 145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
 165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn Ser Ser Ser Ser Lys
 180 185 190

Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
 195 200 205

Asp Thr Pro Ile Leu Pro Gln
210 215

<210> 32
<211> 661
<212> DNA
<213> Artificial

<220>
<223> IFN-CTP

<400> 32
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caccgccctg agcatgagct acaacctgct gggcttcctg cagaggtcca gcaacttcca 120
gtgccagaag ctgctgtggc agctgaacgg caggctggaa tactgcctga aggacaggat 180
gaacttcgac atccagagg aaatcaagca gctgcagcag ttccagaagg aggacgccgc 240
cctgaccatc tacgagatgc tgcagaacat cttcgccatc ttcaggcagg acagcagcag 300
caccggctgg aacgagacca tcgtggagaa cctgctggcc aacgtgtacc accagatcaa 360
ccacctgaaa accgtgctgg aagagaagct ggaaaaggag gacttcacca ggggcaagct 420
gatgagcagc ctgcacctga agaggtacta cggcagaatc ctgcactacc tgaaggccaa 480
ggagtacagc cactgcgctt ggaccatcgt gaggggtggag atcctgagga acttctactt 540
catcaacagg ctgaccggct acctgaggaa cagctccagc agcaaggccc ctccaccttc 600
cctgcccagt ccaagccgac tccctgggcc ctccgataca ccaattctgc cacagtgatg 660
a 661

<210> 33
<211> 243
<212> PRT
<213> Artificial

<220>
<223> IFN-CTP-CTP

<400> 33

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1 5 10 15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95
 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125
 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140
 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
 145 150 155 160
 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
 165 170 175
 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn Ser Ser Ser Ser Lys
 180 185 190
 Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
 195 200 205
 Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro
 210 215 220
 Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile
 225 230 235 240
 Leu Pro Gln

<210> 34
 <211> 765
 <212> DNA
 <213> Artificial

<220>
 <223> IFN-CTP-CTP

<400> 34
 tctagaggac atgaccaaca agtgcctgct gcagatcgcc ctgctgctgt gcttcagcac 60
 caccgccctg agcatgagct acaacctgct gggcttcctg cagaggtcca gcaacttcca 120
 gtgccagaag ctgctgtggc agctgaacgg caggctggaa tactgcctga aggacaggat 180
 gaacttcgac atcccagagg aaatcaagca gctgcagcag ttccagaagg aggacgccgc 240
 cctgaccatc tacgagatgc tgcagaacat cttcgccatc ttcaggcagg acagcagcag 300
 caccggctgg aacgagacca tcgtggagaa cctgctggcc aacgtgtacc accagatcaa 360
 ccacctgaaa accgtgctgg aagagaagct ggaaaaggag gacttcacca ggggcaagct 420
 gatgagcagc ctgcacctga agaggtacta cggcagaatc ctgcactacc tgaaggccaa 480

ggagtacagc cactgcgctt ggaccatcgt gaggggtggag atcctgagga acttctactt 540
 catcaacagg ctgaccggct acctgaggaa cagctccagc agcaaggccc ctccaccttc 600
 cctgcccagt ccaagccgac tccctggggc ctccgacaca ccaatcctgc cacagagcag 660
 ctctcttaag gccctctctc catccctgcc atccccctcc cggctgcctg gccctctga 720
 caccctatc ctgcctcagt gatgaagggtc tggatccgcg gccgc 765

<210> 35
 <211> 271
 <212> PRT
 <213> CTP-IFN-CTP-CTP

<400> 35

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1 5 10 15

Thr Thr Ala Leu Ser Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu
20 25 30

Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
35 40 45

Gln Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe
50 55 60

Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys
65 70 75 80

Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu
85 90 95

Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu
100 105 110

Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp
115 120 125

Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile
130 135 140

Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe
145 150 155 160

Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly
165 170 175

Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp
180 185 190

Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg
195 200 205

Leu Thr Gly Tyr Leu Arg Asn Ser Ser Ser Ser Lys Ala Pro Pro Pro
210 215 220

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

Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser
245 250 255

Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
260 265 270

<210> 36
<211> 849
<212> DNA
<213> Artificial

<220>
<223> CTP-IFN-CTP-CTP

<400> 36
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caccgccctg agcagcagca gctccaaggc cccaccccc agcctgcca gccccagcag 120
actgccaggc cccagcgaca cccccatcct gccccagatg agctacaacc tgctgggctt 180
cctgcagagg tccagcaact tccagtgcc gaagctgctg tggcagctga acggcaggct 240
ggaatactgc ctgaaggaca ggatgaactt cgacatccca gaggaaatca agcagctgca 300
gcagttccag aaggaggacg ccgccctgac catctacgag atgctgcaga acatcttcgc 360
catcttcagg caggacagca gcagcaccgg ctggaacgag accatcgtgg agaacctgct 420
ggccaacgtg taccaccaga tcaaccacct gaaaaccgtg ctggaagaga agctggaaaa 480
ggaggacttc accaggggca agctgatgag cagcctgcac ctgaagaggt actacggcag 540
aatcctgcac tacctgaagg ccaaggagta cagccactgc gcctggacca tcgtgagggt 600
ggagatcctg aggaacttct acttcatcaa caggctgacc ggctacctga ggaacagctc 660
cagcagcaag gcccctccac cttccctgcc cagtccaagc cgactccctg ggccctccga 720
cacaccaatc ctgccacaga gcagctcctc taaggcccct cctccatccc tgccatcccc 780
ctcccggtg cctggcccct ctgacacccc taccctgcct cagtgatgaa ggtctggatc 840
cgcgccgc 849

<210> 37
<211> 409
<212> PRT
<213> Artificial

<220>
<223> CTP-IFN(CTP)

<400> 37

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1 5 10 15

Thr Thr Ala Leu Ser Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu
 20 25 30
 Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
 35 40 45
 Gln Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe
 50 55 60
 Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys
 65 70 75 80
 Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu
 85 90 95
 Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu
 100 105 110
 Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp
 115 120 125
 Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile
 130 135 140
 Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe
 145 150 155 160
 Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly
 165 170 175
 Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp
 180 185 190
 Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg
 195 200 205
 Leu Thr Gly Tyr Leu Arg Asn Ser Ser Ser Ser Lys Ala Pro Pro Pro
 210 215 220
 Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile
 225 230 235 240
 Leu Pro Gln Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser
 245 250 255
 Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu
 260 265 270
 Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys
 275 280 285

Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu
290 295 300

Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr
305 310 315 320

Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His
325 330 335

Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu
340 345 350

Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr
355 360 365

Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys
370 375 380

Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile
385 390 395 400

Asn Arg Leu Thr Gly Tyr Leu Arg Asn
405

<210> 38
<211> 1261
<212> DNA
<213> Artificial

<220>
<223> CTP-IFN(CTP)

<400> 38
tctagaggac atgaccaaca agtgcctgct gcagatcgcc ctgctgctgt gcttcagcac 60
caccgccctg agcagcagca gctccaaggc cccaccccc agcctgcca gccccagcag 120
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cctgcagagg tccagcaact tccagtgcc aaaactgctg tggcagctga acggcaggct 240
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Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
35 40 45

Gln Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe
50 55 60

Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys
65 70 75 80

Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu
85 90 95

Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu
100 105 110

Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp
115 120 125

Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile
130 135 140

Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe
145 150 155 160

Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly

165

170

175

Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp
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Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg
 195 200 205

Leu Thr Gly Tyr Leu Arg Asn
 210 215

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<400> 41

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Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
 35 40 45

Gln Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe
50 55 60

Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys
65 70 75 80

Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu
85 90 95

Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu
100 105 110

Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp
115 120 125

Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile
130 135 140

Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe
145 150 155 160

Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly
165 170 175

Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp
180 185 190

Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg
195 200 205

Leu Thr Gly Tyr Leu Arg Asn Ser Ser Ser Ser Lys Ala Pro Pro Pro
210 215 220

Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile
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Leu Pro Gln

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Lys	Asp	Arg	Met	Asn	Phe	Asp	Ile	Pro	Glu	Glu	Ile	Lys	Gln	Leu	Gln
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Gln	Phe	Gln	Lys	Glu	Asp	Ala	Ala	Leu	Thr	Ile	Tyr	Glu	Met	Leu	Gln
	50					55					60				

Asn	Ile	Phe	Ala	Ile	Phe	Arg	Gln	Asp	Ser	Ser	Ser	Thr	Gly	Trp	Asn
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Glu	Thr	Ile	Val	Glu	Asn	Leu	Leu	Ala	Asn	Val	Tyr	His	Gln	Ile	Asn
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His	Leu	Lys	Thr	Val	Leu	Glu	Glu	Lys	Leu	Glu	Lys	Glu	Asp	Phe	Thr
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Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg
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Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr
	130					135					140				

Ile	Val	Arg	Val	Glu	Ile	Leu	Arg	Asn	Phe	Tyr	Phe	Ile	Asn	Arg	Leu
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Thr Gly Tyr Leu Arg Asn
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<220>
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<400> 44

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Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln
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Phe Glu Gly Ser Ala Gly Lys Gly Leu Asn Leu Lys Leu Leu Asp Asn
35 40 45

Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly
50 55 60

Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly
65 70 75 80

Leu Arg Gly Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val
85 90 95

Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu
100 105 110

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

Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly
130 135 140

Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr
145 150 155 160

His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg
165 170 175

Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His
180 185 190

Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro
195 200 205

Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe
Page 36

210 215 220
 Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn
 225 230 235 240

Thr Gln

<210> 45
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 45

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 35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
 50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
 85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
 100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
 115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
 130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
 145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
 165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
 180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
 195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225 230 235 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
260 265 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
290 295 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305 310 315 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
325 330 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
340 345 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
355 360 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
370 375 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385 390 395 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
405 410 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
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Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
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<212> PRT
<213> Homo sapiens
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Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
Page 38

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Thr	Gln	Glu	Glu	Ala	His	Gly	Val
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Leu	His	Arg	Arg	Arg	Arg	Ala	Asn
		35				40	
Ala	Phe	Leu	Glu	Glu	Leu	Arg	Pro
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Gly	Ser	Leu	Glu	Arg	Glu	Cys	Lys
	50					55	
Glu	Gln	Cys	Ser	Phe	Glu	Glu	
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Ala	Arg	Glu	Ile	Phe	Lys	Asp	Ala
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Glu	Arg	Thr	Lys	Leu	Phe	Trp	Ile
		75					80
Ser	Tyr	Ser	Asp	Gly	Asp	Gln	Cys
			85				
Ala	Ser	Pro	Cys	Gln	Asn	Gly	
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Gly	Ser	Cys	Lys	Asp	Gln	Leu	Gln
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Ser	Tyr	Ile	Cys	Phe	Cys	Leu	Pro
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Ala	Phe	Glu	Gly	Arg	Asn	Cys	Glu
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Thr	His	Lys	Asp	Asp	Gln	Leu	Ile
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Cys	Val	Asn	Glu	Asn	Gly	Gly	Cys
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Gly	Thr	Lys	Arg	Ser	Cys	Arg	Cys
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His	Glu	Gly	Tyr	Ser	Leu	Leu	Ala
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Asp	Gly	Val	Ser	Cys	Thr	Pro	Thr
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Val	Glu	Tyr	Pro	Cys	Gly	Lys	Ile
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Pro	Ile	Leu	Glu	Lys	Arg	Asn	Ala
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Ser	Lys	Pro	Gln	Gly	Arg	Ile	Val
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Leu	Val	Asn	Gly	Ala	Gln	Leu	Cys
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Trp	Val	Val	Ser	Ala	Ala	His	Cys
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Phe	Asp	Lys	Ile	Lys	Asn	Trp	Arg
		235				240	
Asn	Leu	Ile	Ala	Val	Leu	Gly	Glu
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His	Asp	Leu	Ser	Glu	His	Asp	Gly
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Asp	Glu	Gln	Ser	Arg	Arg	Val	Ala
		260					
Gln	Val	Ile	Ile	Pro	Ser	Thr	Tyr
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Val	Pro	Gly	Thr	Thr	Asn	His	Asp
		275					280
Ile	Ala	Leu	Leu	Arg	Leu	His	Gln
				285			

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
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 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
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 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
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 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
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 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
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 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
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 <213> Homo sapiens

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Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
 180 185 190
 Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
 195 200 205
 Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
 210 215 220
 Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
 225 230 235 240
 Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
 245 250 255
 Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
 260 265 270
 Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 275 280 285
 Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300
 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415
 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
 420 425 430
 Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ser Ser Ser Ser
 435 440 445

Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro
 450 455 460

Ser Asp Thr Pro Ile Leu Pro Gln
 465 470

<210> 50
 <211> 1535
 <212> DNA
 <213> Artificial

<220>
 <223> Factor VII-CTP-CTP

<400> 50
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 tgcctggctg cagtcttcgt aaccaggag gaagccacg gcgtcctgca ccggcgccgg 120
 cgcgccaacg cgctcctgga ggagctgcgg ccgggctccc tggagagggg gtgcaaggag 180
 gagcagtgtc ctttcgagga ggcccgggag atcttcaagg acgcggagag gacgaagctg 240
 ttctggattt cttacagtga tggggaccag tgtgcctcaa gtccatgcca gaatgggggc 300
 tcctgcaagg accagctcca gtcctatata tgcttctgcc tccctgcctt cgagggccgg 360
 aactgtgaga cgcacaagga tgaccagctg atctgtgtga acgagaacgg cggctgtgag 420
 cagtactgca gtgaccacac gggcaccaag cgctcctgtc ggtgccacga ggggtactct 480
 ctgctggcag acgggggtgc ctgcacaccc acagtgaat atccatgtgg aaaaatacct 540
 attctagaaa aaagaaatgc cagcaaacc caaggccgaa ttgtgggggg caagggtgtgc 600
 cccaaagggg agtgtccatg gcaggtcctg ttgttggtga atggagctca gttgtgtggg 660
 gggaccctga tcaacaccat ctgggtggtc tccgcggccc actgtttcga caaaatcaag 720
 aactggagga acctgatcgc ggtgctgggc gagcacgacc tcagcgagca cgacggggat 780
 gagcagagcc ggcgggtggc gcaggtcatc atccccagca cgtacgtccc gggcaccacc 840
 aaccacgaca tcgcgtgtc ccgcctgcac cagcccgtgg tcctcactga ccatgtgggtg 900
 cccctctgcc tgcccgaacg gacgttctct gagaggacgc tggccttcgt gcgcttctca 960
 ttggtcagcg gctggggcca gctgctggac cgtggcgcca cggccctgga gctcatggtc 1020
 ctcaacgtgc cccggctgat gaccaggac tgctgcagc agtcacggaa ggtgggagac 1080
 tccccaaata tcacggagta catgttctgt gccggctact cggatggcag caaggactcc 1140
 tgcaaggggg acagtggagg ccacatgcc acccactacc ggggcacgtg gtacctgacc 1200
 ggcatcgtga gctggggcca gggctgcgcc accgtgggcc acttcggcgt gtacaccagg 1260
 gtgtcccagt acatcgagtg gctgcagaaa ctgatgagaa gcgagcccag acccggcgtg 1320
 ctgctgagag ccccttccc cagcagcagc tccaaggccc ctccccctag cctgcccagc 1380
 cctagcagac tgctggggc ctccgacaca ccaatcctgc cacagagcag ctctctaag 1440
 gccctctct catcctgcc atccccctcc cggctgccag gccctctga caccctatc 1500
 ctgcctcagt gatgaaggtc tggatccgcg gccgc 1535

<210> 51
<211> 500
<212> PRT
<213> artificial

<220>
<223> factor VII-CTP-CTP

<400> 51

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
1 5 10 15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20 25 30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
Page 45

225 230 235 240
 Asn Leu Ile Ala Val₂₄₅ Leu Gly Glu His Asp₂₅₀ Leu Ser Glu His Asp₂₅₅ Gly
 Asp Glu Gln Ser₂₆₀ Arg Arg Val Ala Gln Val Ile Ile Pro Ser₂₇₀ Thr Tyr
 Val Pro Gly₂₇₅ Thr Thr Asn His Asp₂₈₀ Ile Ala Leu Leu Arg₂₈₅ Leu His Gln
 Pro Val₂₉₀ Val Leu Thr Asp His₂₉₅ Val Val Pro Leu Cys₃₀₀ Leu Pro Glu Arg
 Thr Phe Ser Glu Arg Thr₃₁₀ Leu Ala Phe Val Arg₃₁₅ Phe Ser Leu Val Ser₃₂₀
 Gly Trp Gly Gln Leu₃₂₅ Leu Asp Arg Gly Ala₃₃₀ Thr Ala Leu Glu Leu₃₃₅ Met
 Val Leu Asn Val₃₄₀ Pro Arg Leu Met Thr₃₄₅ Gln Asp Cys Leu Gln Gln Ser
 Arg Lys Val₃₅₅ Gly Asp Ser Pro Asn₃₆₀ Ile Thr Glu Tyr Met₃₆₅ Phe Cys Ala
 Gly Tyr Ser Asp Gly Ser Lys₃₇₅ Asp Ser Cys Lys Gly₃₈₀ Asp Ser Gly Gly
 Pro His Ala Thr His Tyr₃₉₀ Arg Gly Thr Trp Tyr₃₉₅ Leu Thr Gly Ile Val₄₀₀
 Ser Trp Gly Gln Gly₄₀₅ Cys Ala Thr Val Gly₄₁₀ His Phe Gly Val Tyr₄₁₅ Thr
 Arg Val Ser Gln Tyr Ile Glu Trp Leu₄₂₅ Gln Lys Leu Met Arg₄₃₀ Ser Glu
 Pro Arg Pro Gly Val Leu Leu Arg₄₄₀ Ala Pro Phe Pro Ser₄₄₅ Ser Ser Ser
 Lys Ala₄₅₀ Pro Pro Pro Ser Leu₄₅₅ Pro Ser Pro Ser Arg₄₆₀ Leu Pro Gly Pro
 Ser Asp Thr Pro Ile Leu₄₇₀ Pro Gln Ser Ser Ser₄₇₅ Ser Lys Ala Pro Pro₄₈₀
 Pro Ser Leu Pro Ser₄₈₅ Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr₄₉₅ Pro
 Ile Leu Pro Gln₅₀₀

<210> 52
<211> 528
<212> PRT
<213> artificial

<220>
<223> factor VII-CTP-CTP-CTP

<400> 52

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
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Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20 25 30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
Page 47

225 230 235 240
 Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
 245 250 255
 Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
 260 265 270
 Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 275 280 285
 Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300
 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415
 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
 420 425 430
 Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ser Ser Ser Ser
 435 440 445
 Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro
 450 455 460
 Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro
 465 470 475 480
 Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro
 485 490 495
 Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro
 500 505 510

Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
515 520 525

<210> 53
<211> 556
<212> PRT
<213> artificial

<220>
<223> factor VII-CTP-CTP-CTP-CTP
<400> 53

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
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Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20 25 30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile

210	215	220
Trp Val Val Ser Ala	Ala His Cys Phe Asp	Lys Ile Lys Asn Trp Arg
225	230	235 240
Asn Leu Ile Ala Val	Leu Gly Glu His Asp	Leu Ser Glu His Asp Gly
	245	250 255
Asp Glu Gln Ser Arg Arg Val Ala	Gln Val Ile Ile Pro Ser Thr Tyr	
	260 265	270
Val Pro Gly Thr Thr Asn His Asp	Ile Ala Leu Leu Arg Leu His Gln	
	275 280	285
Pro Val Val Leu Thr Asp His Val Val Pro	Leu Cys Leu Pro Glu Arg	
	290 295	300
Thr Phe Ser Glu Arg Thr Leu Ala Phe Val	Arg Phe Ser Leu Val Ser	
	310 315	320
Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met		
	325 330	335
Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser		
	340 345	350
Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala		
	355 360	365
Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly		
	370 375	380
Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val		
	385 390	395 400
Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr		
	405 410	415
Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu		
	420 425	430
Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ser Ser Ser		
	435 440	445
Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro		
	450 455	460
Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro		
	465 470	475 480
Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro		
	485 490	495

Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro
500 505 510

Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
515 520 525

Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg
530 535 540

Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
545 550 555

<210> 54
<211> 584
<212> PRT
<213> artificial

<220>
<223> factor VII-CTP-CTP-CTP-CTP

<400> 54

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
1 5 10 15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20 25 30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile

				165						170						175
Pro	Ile	Leu	Glu	Lys	Arg	Asn	Ala	Ser	Lys	Pro	Gln	Gly	Arg	Ile	Val	
			180					185					190			
Gly	Gly	Lys	Val	Cys	Pro	Lys	Gly	Glu	Cys	Pro	Trp	Gln	Val	Leu	Leu	
		195					200					205				
Leu	Val	Asn	Gly	Ala	Gln	Leu	Cys	Gly	Gly	Thr	Leu	Ile	Asn	Thr	Ile	
	210					215					220					
Trp	Val	Val	Ser	Ala	Ala	His	Cys	Phe	Asp	Lys	Ile	Lys	Asn	Trp	Arg	
225					230					235					240	
Asn	Leu	Ile	Ala	Val	Leu	Gly	Glu	His	Asp	Leu	Ser	Glu	His	Asp	Gly	
				245					250					255		
Asp	Glu	Gln	Ser	Arg	Arg	Val	Ala	Gln	Val	Ile	Ile	Pro	Ser	Thr	Tyr	
			260					265					270			
Val	Pro	Gly	Thr	Thr	Asn	His	Asp	Ile	Ala	Leu	Leu	Arg	Leu	His	Gln	
		275					280					285				
Pro	Val	Val	Leu	Thr	Asp	His	Val	Val	Pro	Leu	Cys	Leu	Pro	Glu	Arg	
	290					295					300					
Thr	Phe	Ser	Glu	Arg	Thr	Leu	Ala	Phe	Val	Arg	Phe	Ser	Leu	Val	Ser	
305					310					315					320	
Gly	Trp	Gly	Gln	Leu	Leu	Asp	Arg	Gly	Ala	Thr	Ala	Leu	Glu	Leu	Met	
				325					330					335		
Val	Leu	Asn	Val	Pro	Arg	Leu	Met	Thr	Gln	Asp	Cys	Leu	Gln	Gln	Ser	
			340					345					350			
Arg	Lys	Val	Gly	Asp	Ser	Pro	Asn	Ile	Thr	Glu	Tyr	Met	Phe	Cys	Ala	
		355					360					365				
Gly	Tyr	Ser	Asp	Gly	Ser	Lys	Asp	Ser	Cys	Lys	Gly	Asp	Ser	Gly	Gly	
	370					375					380					
Pro	His	Ala	Thr	His	Tyr	Arg	Gly	Thr	Trp	Tyr	Leu	Thr	Gly	Ile	Val	
385					390					395					400	
Ser	Trp	Gly	Gln	Gly	Cys	Ala	Thr	Val	Gly	His	Phe	Gly	Val	Tyr	Thr	
				405					410					415		
Arg	Val	Ser	Gln	Tyr	Ile	Glu	Trp	Leu	Gln	Lys	Leu	Met	Arg	Ser	Glu	
			420				425						430			
Pro	Arg	Pro	Gly	Val	Leu	Leu	Arg	Ala	Pro	Phe	Pro	Ser	Ser	Ser	Ser	
		435					440					445				

Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro
450 455 460

Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro
465 470 475 480

Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro
485 490 495

Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro
500 505 510

Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
515 520 525

Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg
530 535 540

Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser
545 550 555 560

Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro
565 570 575

Ser Asp Thr Pro Ile Leu Pro Gln
580

<210> 55
<211> 1404
<212> DNA
<213> Homo sapiens

<400> 55
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acaaaattct gaatcggcca aagaggtata attcaggtaa attggaagag tttgttcaag 180
ggaaccttga gagagaatgt atggaagaaa agtgtagttt tgaagaagca cgagaagttt 240
ttgaaaacac tgaaagaaca actgaatttt ggaagcagta tgttgatgga gatcagtgtg 300
agtccaatcc atgttttaaat ggcggcagtt gcaaggatga cattaattcc tatgaatgtt 360
ggtgtccctt tggatttgaa ggaagaact gtgaattaga tgtaacatgt aacattaaga 420
atggcagatg cgagcagttt tgtaaaaata gtgctgataa caagggtggtt tgctcctgta 480
ctgaggggata tcgacttgca gaaaaccaga agtcctgtga accagcagtg ccatttccat 540
gtggaagagt ttctgtttca caaacttcta agctcaccgc tgctgagact gtttttcctg 600
atgtggacta tgtaaatctt actgaagctg aaaccatttt ggataacatc actcaaagca 660
cccaatcatt taatgacttc actcgagttg ttggtggaga agatgccaaa ccagggtcaat 720
tcccttggca ggttgttttg aatggttaaag ttgatgcatt ctgtggaggc tctatcgta 780

atgaaaaatg gattgtaact gctgcccact gtgttgaaac tgggtgttaa attacagttg 840
 tcgcaggtga acataatatt gaggagacag aacatacaga gcaaaagcga aatgtgattc 900
 gaattattcc tcaccacaac tacaatgcag ctattaataa gtacaaccat gacattgccc 960
 ttctggaact ggacgaaccc ttagtgctaa acagctacgt tacacctatt tgcattgctg 1020
 acaaggaata cacgaacatc ttcctcaa at ttggatctgg ctatgtaagt ggctggggaa 1080
 gagtctttcca caaagggaga tcagcttttag ttctccagta ccttagagtt ccacttggtg 1140
 accgagccac atgtcttcga tctacaaagt tcaccatcta taacaacatg ttctgtgctg 1200
 gcttccatga aggaggtaga gattcatgtc aaggagatag tgggggaccc catgttactg 1260
 aagtggaagg gaccagtttc ttaactggaa ttattagctg ggggtgaagag tgtgcaatga 1320
 aaggcaaata tggaatatat accaaggat cccggatatg caactggatt aaggaaaaaa 1380
 caaagctcac ttgaacgcgg ccgc 1404

<210> 56
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 56

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

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

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
145 150 155 160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
 165 170 175
 Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
 180 185 190
 Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu
 195 200 205
 Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
 210 215 220
 Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
 225 230 235 240
 Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
 245 250 255
 Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270
 Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285
 His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn
 290 295 300
 Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu
 305 310 315 320
 Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile
 325 330 335
 Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr
 340 345 350
 Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val
 355 360 365
 Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg
 370 375 380
 Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His
 385 390 395 400
 Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val
 405 410 415
 Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
 420 425 430

Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
435 440 445

Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
450 455 460

<210> 57
<211> 1502
<212> DNA
<213> artificial

<220>
<223> factor IX-CTP

<400> 57
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aacaaaattc tgaatcggcc aaagaggtat aattcaggtta aattggaaga gtttggtcaa 180
gggaaccttg agagagaatg tatggaagaa aagtgtagtt ttgaagaagc acgagaagtt 240
tttggaaaaca ctgaaagaac aactgaattt tgggaagcagt atgttgatgg agatcagttg 300
gagtccaatc catgttttaa tggcggcagt tgcaaggatg acattaattc ctatgaatgt 360
tgggtgtccct ttggatttga aggaaagaac tgtgaattag atgtaacatg taacattaag 420
aatggcagat gcgagcagtt ttgtaaaaat agtgctgata acaagggtgg ttgctcctgt 480
actgagggat atcgacttgc agaaaaccag aagtcctgtg aaccagcagt gccatttcca 540
tgtggaagag tttctgtttc acaaacttct aagctcaccg gtgctgagac tgtttttcct 600
gatgtggact atgtaaattc tactgaagct gaaaccattt tggataacat cactcaaagc 660
acccaatcat ttaatgactt cactcgagtt gttggtggag aagatgccaa accaggtcaa 720
ttcccttggc aggttggttt gaattgtaaa gttgatgcat tctgtggagg ctctatcgtt 780
aatgaaaaat ggattgtaac tgctgccac tgtgttgaaa ctggtgttaa aattacagtt 840
gtcgcagggtg aacataatat tgaggagaca gaacatacag agcaaaagcg aaatgtgatt 900
cgaattattc ctaccacaa ctacaatgca gctattaata agtacaacca tgacattgcc 960
cttctggaac tggacgaacc cttagtgtta aacagctacg ttacacctat ttgcattgct 1020
gacaaggaat acacgaacat cttcctcaa tttggatctg gctatgtaag tggctgggga 1080
agagtcttcc acaaaggag atcagcttta gttcttcagt accttagagt tccacttgtt 1140
gaccgagcca catgtcttcg atctacaaag ttcaccatct ataacaacat gttctgtgct 1200
ggcttccatg aaggaggtag agattcatgt caaggagata gtgggggacc ccatgttact 1260
gaagtggaag ggaccagttt cttaactgga attattagct ggggtgaaga gtgtgcaatg 1320
aaaggcaaat atggaatata taccaaggtat tcccgggtat tcaactggat taaggaaaaa 1380
acaaagctca ctagctccag cagcaaggcc cttccccga gcctgccctc cccaagcagg 1440
ctgcctgggc cttccgacac accaatcctg ccacagtgat gaaggctctg atccgcggcc 1500
gc 1502

<210> 58
 <211> 489
 <212> PRT
 <213> artificial

<220>
 <223> factor IX-CTP

<400> 58

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
 1 5 10 15

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

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
 35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
 50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
 65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
 85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
 100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
 115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
 130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
 145 150 155 160

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

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
 180 185 190

Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu
 195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
 210 215 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp

<212> DNA
<213> artificial

<220>
<223> factor IX-CTP-CTP

<400> 59
gcgatcgcca tgcagcgcg tgaacatgac atggcagaat caccaggcct catcaccatc 60
tgccttttag gatattact cagtgtgaa tgtacagttt ttcttgatca tgaaaacgcc 120
aacaaaattc tgaatcggcc aaagaggat aattcaggta aattggaaga gtttgttcaa 180
gggaaccttg agagagaatg tatggaagaa aagtgtagtt ttgaagaagc acgagaagtt 240
tttgaaaaca ctgaaagaac aactgaattt tggaagcagt atgttgatgg agatcagtgt 300
gagtccaatc catgttttaa tggcggcagt tgcaaggatg acattaattc ctatgaatgt 360
tgggtgtccct ttggatttga aggaaagaac tgtgaattag atgtaacatg taacattaag 420
aatggcagat gcgagcagtt ttgtaaaaat agtgtgata acaagggtgt ttgtctctgt 480
actgagggat atcgacttgc agaaaaccag aagtcctgtg aaccagcagt gccatttcca 540
tgtggaagag ttctgtttc acaacttct aagctcacc gtgtgagac tgtttttctt 600
gatgtggact atgtaaattc tactgaagct gaaaccattt tggataacat cactcaaagc 660
acccaatcat ttaatgactt cactcgagtt gttggtggag aagatgcca accaggtcaa 720
ttcccttggc aggttgtttt gaattgtaaa gttgatgcat tctgtggagg ctctatcgtt 780
aatgaaaaat ggattgtaac tgctgccac tgtgttgaac ctggtgttaa aattacagtt 840
gtcgcagggtg aacataatat tgaggagaca gaacatacag agcaaaagcg aaatgtgatt 900
cgaattattc ctaccacaa ctacaatga gctattaata agtacaacca tgacattgcc 960
cttctggaac tggacgaacc cttagtgtc aacagctacg ttacacctat ttgcattgct 1020
acaaggaata cacgaacatc ttctcaaat ttggatctgg ctatgtaagt ggctggggaa 1080
gagctttcca caaagggaga tcagcttttag ttcttcagta ccttagagtt ccacttgttg 1140
accgagccac atgtcttcga tctacaaagt tcaccatcta taacaacatg ttctgtgctg 1200
gcttccatga aggaggtaga gattcatgtc aaggagatag tgggggaccc catgttactg 1260
aagtggaagg gaccagtttc ttaactggaa ttattagctg ggggtgaagag tgtgcaatga 1320
aaggcaaata tggaatatat accaaggat cccggtatgt caactggatt aaggaaaaaa 1380
caaagctcac tagctccagc agcaaggccc ctccccgag cctgccctcc ccaagcaggc 1440
tgcctgggcc ctccgacaca ccaatcctgc cacagagcag ctctctaaag gccctcctc 1500
catccctgcc atccccctcc cggctgcctg gccctctga cccccctatc ctgcctcagt 1560
gatgaagggtc tggatccgcg gccgc 1585

<210> 60
<211> 517
<212> PRT
<213> artificial

<220>
<223> factor IX-CTP-CTP

<400> 60

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

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

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
145 150 155 160

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

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
180 185 190

Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu
195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
210 215 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
225 230 235 240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
245 250 255

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn
290 295 300

Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu
305 310 315 320

Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile
325 330 335

Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr
340 345 350

Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val
355 360 365

Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg
370 375 380

Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His
385 390 395 400

Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val
405 410 415

Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
420 425 430

Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
435 440 445

Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Ser Ser Ser
450 455 460

Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly
465 470 475 480

Pro Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro
485 490 495

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
500 505 510

Pro Ile Leu Pro Gln
515

<210> 61
<211> 545
<212> PRT

<213> artificial

<220>

<223> factor IX-CTP-CTP-CTP

<400> 61

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

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

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
145 150 155 160

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

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
180 185 190

Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu
195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
210 215 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
225 230 235 240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
245 250 255

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn
 290 295 300

Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu
 305 310 315 320

Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile
 325 330 335

Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr
 340 345 350

Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val
 355 360 365

Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg
 370 375 380

Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His
 385 390 395 400

Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val
 405 410 415

Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
 420 425 430

Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
 435 440 445

Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Ser Ser Ser
 450 455 460

Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly
 465 470 475 480

Pro Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro
 485 490 495

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
 500 505 510

Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu
 515 520 525

Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
 530 535 540

Gln
 545

<210> 62
 <211> 573
 <212> PRT
 <213> artificial

<220>
 <223> factor IX-CTP-CTP-CTP-CTP

<400> 62

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
 1 5 10 15

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

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
 35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
 50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
 65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
 85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
 100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
 115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
 130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
 145 150 155 160

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

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
 180 185 190

Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu
 195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
 210 215 220
 Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
 225 230 235 240
 Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
 245 250 255
 Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270
 Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285
 His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn
 290 295 300
 Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu
 305 310 315 320
 Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile
 325 330 335
 Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr
 340 345 350
 Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val
 355 360 365
 Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg
 370 375 380
 Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His
 385 390 395 400
 Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val
 405 410 415
 Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
 420 425 430
 Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
 435 440 445
 Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Ser Ser Ser
 450 455 460
 Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly
 465 470 475 480

Pro Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro
485 490 495

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
500 505 510

Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu
515 520 525

Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
530 535 540

Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser
545 550 555 560

Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
565 570

<210> 63
<211> 601
<212> PRT
<213> artificial

<220>
<223> factor IX-CTP-CTP-CTP-CTP

<400> 63

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

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

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
 145 150 155 160
 Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
 165 170 175
 Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
 180 185 190
 Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu
 195 200 205
 Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
 210 215 220
 Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
 225 230 235 240
 Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
 245 250 255
 Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270
 Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285
 His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn
 290 295 300
 Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu
 305 310 315 320
 Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile
 325 330 335
 Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr
 340 345 350
 Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val
 355 360 365
 Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg
 370 375 380
 Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His
 385 390 395 400
 Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val
 405 410 415

Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
 420 425 430
 Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
 435 440 445
 Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Ser Ser Ser
 450 455 460
 Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly
 465 470 475 480
 Pro Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro
 485 490 495
 Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
 500 505 510
 Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu
 515 520 525
 Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
 530 535 540
 Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser
 545 550 555 560
 Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser
 565 570 575
 Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly
 580 585 590
 Pro Ser Asp Thr Pro Ile Leu Pro Gln
 595 600

<210> 64
 <211> 2413
 <212> DNA
 <213> Homo sapiens

<400> 64
 tctagagtcg accccgccat ggagctgagg ccctggttgc tatgggtggt agcagcaaca 60
 ggaaccttgg tcctgctagc agctgatgct cagggccaga aggtcttcac caacacgtgg 120
 gctgtgcgca tccctggagg ccagcggtg gccaacagtg tggcacggaa gcatgggttc 180
 ctcaacctgg gccagatctt cggggactat taccatttct ggcacgagg agtgacgaag 240
 cgggccctgt cgctcaccg cccgcggcac agccggctgc agagggagcc tcaagtacag 300
 tggctggaac agcaggtggc aaagcgacgg actaaacggg acgtgtacca ggagcccaca 360
 gacccaagt ttctcagca gtggtacctg tctggtgtca ctacgcggga cctgaatgtg 420

aaggcggcct gggcgaggg ctacacaggg cacggcattg tggctctccat tctggacgat	480
ggcatcgaga agaaccaccc ggacttggca ggcaattatg atcctggggc cagttttgat	540
gtcaatgacc aggaccctga cccccagcct cggtacacac agatgaatga caacaggcac	600
ggcacacggg gtgcggggga agtggctgcg gtggccaaca acggtgtctg tgggtgtagg	660
gtggcctaca acgcccgcac tggaggggtg cgcagtctgg atggcgagg gacagatgca	720
gtggaggcac gctcgctggg cctgaacccc aaccacatcc acatctacag tgccagctgg	780
ggccccgagg atgacggcaa gacagtggat gggccagccc gcctcgccga ggaggccttc	840
ttcctgtggg ttagccaggg ccgagggggg ctgggctcca tctttgtctg ggcctcgggg	900
aacggggggc gggaacatga cagctgcaac tgcgacggct acaccaacag tatctacacg	960
ctgtccatca gcagcgccac gcagtttggc aacgtgccgt ggtacagcga ggcctgctcg	1020
tccacactgg ccacgaccta cagcagtggc aaccagaatg agaagcagat cgtgacgact	1080
gacttgccggc agaagtgcac ggagtctcac acgggcacct cagcctctgc ccccttagca	1140
gccggcatca ttgctctcac cctggaggcc aataagaacc tcacatggcg ggacatgcaa	1200
cacctgggtg tacagacctc gaagccagcc cacctcaatg ccaacgactg ggccaccaat	1260
ggtgtggggc ggaaagtgag ccactcatat ggctacgggc ttttggacgc aggcgccatg	1320
gtggccctgg ccagaattg gaccacagtg gcccccagc ggaagtgcac catcgacatc	1380
ctcaccgagc ccaaagacat cgggaaacgg ctcgaggtgc ggaagaccgt gaccgcgtgc	1440
ctgggcgagc ccaaccacat cactcggctg gagcacgctc aggcgcggct caccctgtcc	1500
tataatcgcc gtggcgacct ggccatccac ctggtcagcc ccatgggcac ccgctccacc	1560
ctgctggcag ccaggccaca tgactactcc gcagatgggt ttaatgactg ggccttcatg	1620
acaactcatt cctgggatga ggatccctct ggcgagtggg tcctagagat tgaaaacacc	1680
agcgaagcca acaactatgg gacgtgacc aagttcacc tcgtactcta tggcaccgcc	1740
cctgaggggc tgcccgtacc tccagaaagc agtggctgca agaccctcac gtccagtcag	1800
gcctgtgtgg tgtgcgagga aggtctctcc ctgcaccaga agagctgtgt ccagcactgc	1860
cctccaggct tcgccccca agtcctcgat acgcactata gcaccgagaa tgacgtggag	1920
accatccggg ccagcgtctg cgccccctgc cacgcctcat gtgccacatg ccagggggccg	1980
gccctgacag actgcctcag ctgccccagc cacgcctcct tggaccctgt ggagcagact	2040
tgctcccggc aaagccagag cagccgagag tccccgccac agcagcagcc acctcggctg	2100
cccccgagg tggaggcggg gcaacggctg cgggcagggc tgctgccctc acacctgcct	2160
gaggtggtgg ccggcctcag ctgcgccttc atcgtgctgg tcttcgtcac tgtcttcctg	2220
gtcctgcagc tgcgctctgg ctttagtttt cgggggggtga aggtgtacac catggaccgt	2280
ggcctcatct cctacaagg gctgccccct gaagcctggc aggaggagtg cccgtctgac	2340
tcagaagagg acgagggccg gggcgagagg accgccttta tcaaagacca gagcgccctc	2400
tgaacgcggc cgc	2413

<210> 65
 <211> 794
 <212> PRT
 <213> Homo sapiens

<400> 65

Met Glu Leu Arg Pro Trp Leu Leu Trp Val Val Ala Ala Thr Gly Thr
 1 5 10 15

Leu Val Leu Leu Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn
 20 25 30

Thr Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn Ser Val
 35 40 45

Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln Ile Phe Gly Asp Tyr
 50 55 60

Tyr His Phe Trp His Arg Gly Val Thr Lys Arg Ser Leu Ser Pro His
 65 70 75 80

Arg Pro Arg His Ser Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu
 85 90 95

Glu Gln Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln Glu
 100 105 110

Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu Ser Gly Val Thr
 115 120 125

Gln Arg Asp Leu Asn Val Lys Ala Ala Trp Ala Gln Gly Tyr Thr Gly
 130 135 140

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

Pro Asp Leu Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn
 165 170 175

Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met Asn Asp Asn
 180 185 190

Arg His Gly Thr Arg Cys Ala Gly Glu Val Ala Ala Val Ala Asn Asn
 195 200 205

Gly Val Cys Gly Val Gly Val Ala Tyr Asn Ala Arg Ile Gly Gly Val
 210 215 220

Arg Met Leu Asp Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu
 225 230 235 240

Gly Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp Gly Pro
 245 250 255

Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala Arg Leu Ala Glu Glu
 260 265 270

Ala Phe Phe Arg Gly Val Ser Gln Gly Arg Gly Gly Leu Gly Ser Ile
 275 280 285

Phe Val Trp Ala Ser Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn
 290 295 300

Cys Asp Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser Ala
 305 310 315 320

Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala Cys Ser Ser Thr
 325 330 335

Leu Ala Thr Thr Tyr Ser Ser Gly Asn Gln Asn Glu Lys Gln Ile Val
 340 345 350

Thr Thr Asp Leu Arg Gln Lys Cys Thr Glu Ser His Thr Gly Thr Ser
 355 360 365

Ala Ser Ala Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
 370 375 380

Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val Val Gln Thr
 385 390 395 400

Ser Lys Pro Ala His Leu Asn Ala Asn Asp Trp Ala Thr Asn Gly Val
 405 410 415

Gly Arg Lys Val Ser His Ser Tyr Gly Tyr Gly Leu Leu Asp Ala Gly
 420 425 430

Ala Met Val Ala Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg
 435 440 445

Lys Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly Lys Arg
 450 455 460

Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu Gly Glu Pro Asn His
 465 470 475 480

Ile Thr Arg Leu Glu His Ala Gln Ala Arg Leu Thr Leu Ser Tyr Asn
 485 490 495

Arg Arg Gly Asp Leu Ala Ile His Leu Val Ser Pro Met Gly Thr Arg
 500 505 510

Ser Thr Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly Phe
 515 520 525

Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp Glu Asp Pro Ser
 530 535 540

Gly Glu Trp Val Leu Glu Ile Glu Asn Thr Ser Glu Ala Asn Asn Tyr
 545 550 555 560

Gly Thr Leu Thr Lys Phe Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu
 565 570 575

Gly Leu Pro Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
 580 585 590

Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu His Gln Lys
 595 600 605

Ser Cys Val Gln His Cys Pro Pro Gly Phe Ala Pro Gln Val Leu Asp
 610 615 620

Thr His Tyr Ser Thr Glu Asn Asp Val Glu Thr Ile Arg Ala Ser Val
 625 630 635 640

Cys Ala Pro Cys His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu
 645 650 655

Thr Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro Val Glu
 660 665 670

Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg Glu Ser Pro Pro Gln
 675 680 685

Gln Gln Pro Pro Arg Leu Pro Pro Glu Val Glu Ala Gly Gln Arg Leu
 690 695 700

Arg Ala Gly Leu Leu Pro Ser His Leu Pro Glu Val Val Ala Gly Leu
 705 710 715 720

Ser Cys Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val Leu
 725 730 735

Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys Val Tyr Thr Met
 740 745 750

Asp Arg Gly Leu Ile Ser Tyr Lys Gly Leu Pro Pro Glu Ala Trp Gln
 755 760 765

Glu Glu Cys Pro Ser Asp Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg
 770 775 780

Thr Ala Phe Ile Lys Asp Gln Ser Ala Leu
 785 790

<210> 66
 <211> 249
 <212> PRT
 <213> Artificial

<220>
 <223> CTP-CTP-EPO

<400> 66

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ser Ser Ser Ser Lys
 20 25 30

Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
 35 40 45

Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro
 50 55 60

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

Leu Pro Gln Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
 85 90 95

Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
 100 105 110

Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
 115 120 125

Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val
 130 135 140

Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
 145 150 155 160

Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu
 165 170 175

His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
 180 185 190

Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
 195 200 205

Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
 210 215 220

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

Gly Glu Ala Cys Arg Thr Gly Asp Arg
245

<210> 67
<211> 762
<212> DNA
<213> Artificial

<220>
<223> CTP-CTP-EPO

<400> 67
atgggcgtgc acgagtgtcc tgcttggctg tggctgctgc tgagcctgct gtccctgcct 60
ctgggcctgc ctgtgctggg cagcagcagc tctaaggccc ctccaccag cctgcccagc 120
ccttctagac tgcttggccc cagcgacacc cccatcctgc ctgagagcag cagcagcaag 180
gccccaccac catccctgcc tagccccagc agactgccag gcccttccga taccccaatc 240
ctgccccagg cccctcccag actgatctgc gacagccggg tgctggaaag atacctgctg 300
gaagccaaag aggccgagaa catcaccacc ggctgcgccg agcactgcag cctgaacgag 360
aatatcaccg tgcccgacac caaagtgaac ttctacgcct ggaagcggat ggaagtgggc 420
cagcaggccg tggaagtgtg gcagggactg gccctgctga gcgagggcgt gctgagagga 480
caggccctgc tggatgaacag cagccagccc tgggagcccc tgcagctgca tgtggataag 540
gccgtgtccg gcctgaggag cctgaccaca ctgctgagag ccctgggagc tcagaaagag 600
gccatctctc cccctgatgc cgctctctgc gccctctga gaaccatcac cgccgacacc 660
ttccggaagc tgttccgggt gtacagcaac ttctgaggg gcaagctgaa gctgtacacc 720
ggcgaggcct gccggaccgg cgatagataa gcttggcgcg cc 762

<210> 68
<211> 305
<212> PRT
<213> Artificial

<220>
<223> CTP-CTP-EPO-CTP-CTP

<400> 68

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15
Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ser Ser Ser Ser Lys
20 25 30
Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
35 40 45
Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro
50 55 60
Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile
65 70 75 80

Leu Pro Gln Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
85 90 95

Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
100 105 110

Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
115 120 125

Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val
130 135 140

Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
145 150 155 160

Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu
165 170 175

His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
180 185 190

Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
195 200 205

Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
210 215 220

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

Gly Glu Ala Cys Arg Thr Gly Asp Arg Ser Ser Ser Ser Lys Ala Pro
245 250 255

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
260 265 270

Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu
275 280 285

Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro
290 295 300

Gln
305

<210> 69
<211> 930
<212> DNA
<213> Artificial

<220>
<223> CTP-CTP-EPO-CTP-CTP

<400> 69
atgggcgtgc acgagtgtcc tgcttggtg tggtgctgc tgagcctgct gtccctgcct 60
ctgggcctgc ctgtgctggg cagcagcagc tctaaggccc ctccaccag cctgcccagc 120
ccttctagac tgcctggccc cagcgacacc cccatcctgc ctgagagcag cagcagcaag 180
gccccaccac catccctgcc tagccccagc agactgccag gcccttccga taccccaatc 240
ctgccccagg cccctcccag actgatctgc gacagccggg tgctggaaag atacctgctg 300
gaagccaaag aggccgagaa catcaccacc ggctgcgccg agcactgcag cctgaacgag 360
aatatcaccg tgcccgacac caaagtgaac ttctacgcct ggaagcggat ggaagtgggc 420
cagcaggccg tggaagtgtg gcagggactg gccctgctga gcgaggccgt gctgagagga 480
caggccctgc tggatgaacag cagccagccc tgggagcccc tgagctgca tgtggataag 540
gccgtgtccg gcctgcggag cctgaccaca ctgctgagag ccctgggcgc tcagaaagag 600
gccatctctc cccctgatgc cgcctctgcc gccctctga gaaccatcac cgccgacacc 660
ttccggaagc tgttccgggt gtacagcaac ttctgcggg gcaagctgaa gctgtacacc 720
ggcgaggcct gccggaccgg cgatagaagc agctccagca aggtccacc cccagcctg 780
ccatcccaa gtagactgcc cgggccctct gacacaccta tcctgccaca gtccagcagc 840
tcaaagctc cccaccatc cctcccatcc ccatccagac tgcttgacc atccgacact 900
ccaattctgc ctgagtaagc ttggcgcgcc 930

<210> 70
<211> 295
<212> PRT
<213> Artificial

<220>
<223> APO-A1-CTP

<400> 70

Met Lys Ala Ala Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
1 5 10 15
Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Pro Gln Ser Pro Trp
20 25 30
Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp
35 40 45
Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys
50 55 60
Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr
65 70 75 80
Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp
85 90 95

Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys
 100 105 110
 Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe
 115 120 125
 Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu
 130 135 140
 Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu
 145 150 155 160
 Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala
 165 170 175
 Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp
 180 185 190
 Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn
 195 200 205
 Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu
 210 215 220
 Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln
 225 230 235 240
 Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala
 245 250 255
 Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln Ser Ser Ser Ser Lys
 260 265 270
 Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
 275 280 285
 Asp Thr Pro Ile Leu Pro Gln
 290 295

<210> 71
 <211> 911
 <212> DNA
 <213> Artificial

<220>
 <223> APO-A1-CTP

<400> 71	
atgaaggccg ccgtgctgac cctggccgtg ctgtttctga ccggctctca ggcccggcac	60
ttctggcagc aggacgagcc tccccagtcc ccctgggaca gagtgaagga cctggccacc	120
gtgtacgtgg acgtgctgaa ggactccggc agagactacg tgtcccagtt cgagggctct	180
gccctgggca agcagctgaa cctgaagctg ctggacaact gggactccgt gacctccacc	240

ttctccaagc tgcgcgaaca gctgggacct gtgaccagc aattctggga caacctggaa 300
 aaagagacag agggcctgag acaggaaatg tccaaggacc tggaagaggt caaagccaag 360
 gtgcagccct acctggacga cttccagaag aaatggcagg aagagatgga actgtaccgg 420
 cagaagggtg aaccctgcg ggccgagctg caggaaggcg ctagacagaa gctgcacgaa 480
 ctgcaggaaa agctgtcccc cctgggagag gaaatgcggg acagagccag agcccacgtg 540
 gacgccctga gaaccacact gggccctac tctgacgagc tgcggcagag gctggccgcc 600
 agactggaag ccctgaaaga gaacggcgga gccgggctgg ccgagtacca cgctaaggct 660
 accgagcacc tgtccaccct gtccgagaag gccaagcccg ccctggaaga tctgcggcag 720
 ggcctgctgc ccgtgctgga atccttcaag gtgtccttcc tgtccgctct ggaagagtac 780
 accaagaagc tgaacaccca gtcctccagc tccaaggccc ctccaccctc cctgcctagc 840
 cctagtagac tgccctgggcc ctccgacacc cccatcctgc cccagtgatg aggatccgcg 900
 gccgcgagct c 911

<210> 72
 <211> 323
 <212> PRT
 <213> Artificial

<220>
 <223> APO-A1-CTP-CTP

<400> 72

Met Lys Ala Ala Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
1 5 10 15

Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Pro Gln Ser Pro Trp
20 25 30

Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp
35 40 45

Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys
50 55 60

Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr
65 70 75 80

Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp
85 90 95

Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys
100 105 110

Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe
115 120 125

Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu
130 135 140

Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu
 145 150 155 160
 Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala
 165 170 175
 Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp
 180 185 190
 Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn
 195 200 205
 Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu
 210 215 220
 Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln
 225 230 235 240
 Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala
 245 250 255
 Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln Ser Ser Ser Ser Lys
 260 265 270
 Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
 275 280 285
 Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro
 290 295 300
 Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile
 305 310 315 320
 Leu Pro Gln

<210> 73
 <211> 995
 <212> DNA
 <213> Artificial

<220>
 <223> APO-A1-CTP-CTP

<400> 73
 atgaaggccg ccgtgctgac cctggccgtg ctgtttctga ccggctctca ggcccggcac 60
 ttctggcagc aggacgagcc tccccagtcc ccctgggaca gagtgaagga cctggccacc 120
 gtgtacgtgg acgtgctgaa ggactccggc agagactacg tgtcccagtt cgagggctct 180
 gccctgggca agcagctgaa cctgaagctg ctggacaact gggactccgt gacctccacc 240
 ttctccaagc tgcgcgaaca gctgggacct gtgaccagg aattctggga caacctggaa 300

aaagagacag agggcctgag acaggaaatg tccaaggacc tggaagaggt caaagccaag	360
gtgcagccct acctggacga cttccagaag aaatggcagg aagagatgga actgtaccgg	420
cagaaggtgg aaccctgctg ggccgagctg caggaaggcg ctagacagaa gctgcacgaa	480
ctgcaggaaa agctgtcccc cctgggagag gaaatgcggg acagagccag agcccacgtg	540
gacgccctga gaaccacct gggcccctac tctgacgagc tgcggcagag gctggccgcc	600
agactggaag ccctgaaaga gaacggcgga gcccggtg ccgagtacca cgctaaggct	660
accgagcacc tgtccacct gtccgagaag gccaagcccg ccctggaaga tctgcggcag	720
ggcctgctgc ccgtgctgga atccttcaag gtgtccttcc tgtccgctct ggaagagtac	780
accaagaagc tgaacaccca gtcctccagc tccaaggccc ctccaccctc cctgcctagc	840
cctagtagac tgctggggcc ctccgacaca ccaatcctgc cacagagcag ctcttctaag	900
gcccctctc catccctgcc atccccctcc cggtgcctg gcccctctga caccctatc	960
ctgcctcagt gatgaaggc tggatccgc gccgc	995