

PCTIL2013050107-seq1-000001-EN.txt
SEQUENCE LISTING

<110> PROLOR BIOTECH INC.
FIMA, UDI EYAL
HART, GILI

<120> LONG-ACTING COAGULATION FACTORS AND METHODS OF PRODUCING SAME

<130> P-9520-PC5

<150> 13/372,540

<151> 2012-02-14

<160> 45

<170> PatentIn version 3.5

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<212> PRT

<213> Homo sapiens

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Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg
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<400> 9

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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
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<213> Homo sapiens

<400> 10

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
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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
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 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
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 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

Pro Arg 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 Gln Trp Leu Gln Lys Leu Met Arg Ser Gln 420
425 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Gly Cys Gly Arg 435
440 445

<210> 11
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<212> DNA
<213> Homo sapiens
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120
tgcgcacaag cgttccctga gagctcgg ccgggtctcc ttgagagagg gtccaaggag
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gagcagtgct ccttcgagga ggcgcgggag atcttcaagg acgcggagag gacgaagctg
240
gagcagtgatt cttaagtga tggggaccag tgtgccctaa gtccatgcca gaatgggggc
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360
aactgtaga cgacaagga tgaccagctg atctgttga acgagaacgg cggctgtgag
420
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480
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780
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1260
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1356

<210> 12

<211> 1442

<212> DNA

<213> Artificial Sequence

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<223> CTP-modified Factor VII

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cgcgccaacg cgcttcctgga ggagctgcgg ccgggctccc tggagagggg gtgcaaggag	180
gagcagtgtc ccttcgagga ggcccgggag atcttcaagg acgcggagag gacgaagctg	240
ttctggattt cttacagtga tggggaccag tgtgcctcaa gtccatgcca gaatgggggc	300
tcctgcaagg accagctcca gtcctatatc tgcttctgcc tccctgcctt cgagggccgg	360
aactgtgaga cgcacaagga tgaccagctg atctgtgtga acgagaacgg cggctgtgag	420
cagtactgca gtgaccacac gggcaccaag cgctcctgtc ggtgccacga ggggtactct	480
ctgctggcag acggggtgtc ctgcacacc acagttgaat atccatgtgg aaaaatacct	540
attctagaaa aaagaaatgc cagcaaacc caaggccgaa ttgtgggggg caaggtgtgc	600
cccaaagggg agtgtccatg gcaggtcctg ttgttggtga atggagctca gttgtgtggg	660
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aactggagga acctgatcgc ggtgctgggc gagcacgacc tcagcgagca cgacggggat	780
gagcagagcc ggcgggtggc gcaggtcatc atcccagca cgtacgtccc gggcaccacc	840
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cccctctgcc tgcccgaacg gacgttctct gagaggacgc tggccttcgt gcgttctca	960
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tcccaaata tcacggagta catgttctgt gccggctact cggatggcag caaggactcc	1140
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ggcatcgtga gctggggcca gggctgcgcc accgtgggcc acttcggcgt gtacaccagg	1260
gtgtcccagt acatcgagtg gctgcagaaa ctgatgagaa gcgagcccag acccggcgtg	1320
ctgctgagag ccccttccc cagcagcagc tccaaggccc ctcccctag cctgcccagc	1380
cctagcagac tgcctgggcc cagcgacacc cccatcctgc ccagtgagg atccgcggcc	1440
gc	1442

<210> 13

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> CTP-modified Factor VII

<400> 13

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
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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
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Ser Asp Thr Pro Ile Leu Pro Gln
465 470

<210> 14
<211> 1535
<212> DNA
<213> Artificial Sequence

<220>
<223> CTP-modified Factor VII

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 180 cgcgccaaag cgtccctgga gagctcgg ccggctccc tggagaggga gtgcaaggag
 240 gagcagtgt ccttcaggga ggcggggag atctcaagg acgaggagag gacgaagt
 300 ttttgattt ctacagta tgggagcag tgtgccca gtccatgcca gaatggggc
 360 tcttgcaagg accagctca gtcctatc tgcctcgt tccctgctt cgaaggccgg
 420 aactgtaga cgaaggga tgaccagt atctgtga acgaagaagg cggctgtgag
 480 cagtactga gtgaccacac gggcaccag cgtccctgtc ggtgccaga ggggtactt
 540 ctgctggcag acggggtgtc ctgacacac acagtgaat atccatgtg aaaaatactt
 600 atttagaaa aagaatatc cagcaaac caagccga tgtggggg caaggtgtg
 660 cccaagggt agtgcctatg gcaagtctg ttgtgtga atgagctca gttgtgtgg
 720 gggaccctga tcaaccat ctggtgtgtc tccggccc actgttcga caaatcaag
 780 aactgagga acctgctgc ggtgctggc gagcagacc tcagcagga cgaagggat
 840 gagcagagc ggcgggtg gcaggtatc atcccgca cgtacgtcc gggcaccac
 900 aaccagaca tgcgctgt ccgctgac cagccgtgtg tccatcaga ccatgtgtg
 960 cccctcgtc tgcggagc gacgttctt gagagagc tggccttct gcgttctca
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 1140 tcccaata tcacggagta catgttctt gcggctact cggatggcag caaggaactc
 1200 tgaaggggg acagtggag ccacatgac acccatacc ggggcacgt gtaccctgac
 1260 ggcattctga gctggggca ggcctgccc accgtggcc acttcggcgt gtacacagg
 1320 gtgtccagt acatcagtg gctgcagaa ctgatgaaa ggcagccag accggcgtg
 1380 ctgttagag cccctccc cagcagcag tccaaggccc ctccccctag cctgcccagc
 1440 ctagcagac tgcctggcc ctccgacaca ccaatctgc cacagagcag ctctctaag
 1500 gccccttc catccctgc atccctcc cggctggcag gcccctga caccctatc
 1535 ctgctcagt gatgaagtc tggatccgc gccgc

<210> 15
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 <213> Artificial Sequence

<220>
 <223> CTP-modified Factor VII

<400> 15

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 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
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Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro
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Ile Leu Pro Gln
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<210> 16

<211> 1404

<212> DNA

<213> Homo sapiens

<400> 16

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acaaaattct gaatcggcca aagagggtata attcaggtaa attggaagag tttgttcaag 180

ggaaccttga gagagaatgt atggaagaaa agtgtagttt tgaagaagca cgagaagttt 240

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<210> 17
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 17

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 35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
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 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> 18
 <211> 1502
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CTP-modified Factor IX

<400> 18
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 aacaaaattc tgaatcgccc aaagaggtat aattcaggtta aattggaaga gtttgttcaa 180
 gggaaccttg agagagaatg tatggaagaa aagtgtagtt ttgaagaagc acgagaagtt 240
 ttgaaaaca ctgaaagaac aactgaattt tggaagcagt atgttgatgg agatcagttg 300
 gagtccaatc catgttttaa tggcggcagt tgcaaggatg acattaattc ctatgaatgt 360
 tgggtgtccct ttggatttga aggaagaac tgtgaattag atgtaacatg taacattaag 420
 aatggcagat gcgagcagtt ttgtaaaaat agtgtgata acaagggtgt ttgtcctgt 480
 actgagggat atcgacttgc agaaaaccag aagtcctgtg aaccagcagt gccatttcca 540
 tgtggaagag tttctgtttc aaaaacttct aagctcaccg gtgctgagac tgtttttcct 600
 gatgtggact atgtaaattc tactgaagct gaaaccattt tggataacat cactcaaagc 660
 acccaatcat ttaatgactt cactcgagtt gttggtggag aagatgcaa accaggtcaa 720
 ttcccttggc aggttggttt gaatggtaaa gttgatgcat tctgtggagg ctctatcggt 780
 aatgaaaaat ggattgtaac tgctgcccac tgtgttgaaa ctggtgttaa aattacagtt 840
 gtcgcaggtg aacataatat tgaggagaca gaacatacag agcaaaagcg aaatgtgatt 900
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gc 1502

<210> 19
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> CTP-modified Factor IX

<400> 19

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
 485

<210> 20
 <211> 1585
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CTP-modified Factor IX

<400> 20
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 aacaaaattc tgaatcggcc aaagaggtat aattcaggta aattggaaga gtttgttcaa 180
 gggaaccttg agagagaatg tatggaagaa aagtgtagtt ttgaagaagc acgagaagtt 240
 tttgaaaaca ctgaaagaac aactgaattt tggaagcagt atgttgatgg agatcagttg 300
 gagtccaatc catgtttaaa tggcggcagt tgcaaggatg acattaattc ctatgaatgt 360
 tgggtgtccct ttggatttga aggaagaac tgtgaattag atgtaacatg taacattaag 420
 aatggcagat gcgagcagtt ttgtaaaaat agtgtgata acaagggtgg ttgtcctgt 480
 actgagggat atcgacttgc agaaaaccag aagtcctgtg aaccagcagt gccatttcca 540
 tgtggaagag tttctgtttc acaaacttct aagctcacc gtgctgagac tgtttttcct 600
 gatgtggact atgtaaattc tactgaagct gaaaccattt tggataacat cactcaaagc 660
 acccaatcat ttaatgactt cactcgagtt gttggtggag aagatgccaa accagggtcaa 720
 ttcccttggc aggttgtttt gaatggtaaa gttgatgcat tctgtggagg ctctatcggt 780
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<210> 21
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> CTP-modified Factor IX

<400> 21

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
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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> 22
<211> 2413
<212> DNA
<213> Homo sapiens

<400> 22
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gctgtgcgca tccctggagg ccagcggtg gccaacagtg tggcacggaa gcatgggttc 180
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ggcatcgaga agaaccaccc ggacttggca ggcaattatg atcctggggc cagttttgat 540
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 1440 ctacaccgagc ccaagacat cgggaaacgg ctggaagtg ggaagaccgt gaccgctgc
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 1620 ctgttgtag ctagccaca tgaactacc gcatgtggt ttaatgacty ggccttcac
 1680 acaactcatt cctggatga ggaactcctt ggcgaatggg tcctagatg tgaacaacac
 1740 agcgaagcca acaactatg gacgtgacc aagtaccac tcgtactcta tggaccgccc
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 2040 gacctgacag actgcctcag ctgcccagc cagcctcct tggaccctgt ggaacagat
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 2413 tgaacggcc cgc

<210> 23
 <211> 794
 <212> PRT
 <213> Homo sapiens
 <400> 23

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 1 5 10 15

Leu Val Leu Leu 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> 24

<211> 1621

<212> DNA

<213> Artificial Sequence

<220>

<223> CTP-modified Factor VII

<400> 24

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gagcagtgt ccttcgagga ggcccgagg atcttcaagg acgcggagag gacgaagctg	240
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tcctgcaagg accagctcca gtcctatatc tgcttctgcc tccctgcctt cgagggccgg	360
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ccaggccctt ctgatacacc catcctccca cagtgatgag gatccgcggc cgcttaatta 1620
a 1621

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<210> 25
 <211> 528
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CTP-modified Factor VII

<400> 25

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

<210> 26
<211> 1607
<212> DNA
<213> Artificial Sequence

<220>
<223> CTP-modified Factor VII

<400> 26
ctcgaggaca tgggtctccca ggccctcagg ctctctgcc ttctgcttgg gcttcagggc 60
tgcttggtctg cagtcttcgt aaccaggag gaagcccacg gcgtcctgca ccggcgccgg 120
cgcgccaacg cgttcctgga ggagctgcgg ccgggctccc tggagagggg gtgcaaggag 180
gagcagtgcct ccttcgagga ggcccgggag atcttcaagg acgcggagag gacgaagctg 240
ttctggattt cttacagtga tggggaccag tgtgcctcaa gtccatgcca gaatgggggc 300

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tcctgcaagg accagctcca gtcctatatc tgcttctgcc tccctgcctt cgagggcccg 360
aactgtgaga cgcacaagga tgaccagctg atctgtgtga acgagaacgg cggctgtgag 420
cagtactgca gtgaccacac gggcaccaag cgctcctgtc ggtgccacga ggggtactct 480
ctgctggcag acgggggtgtc ctgcacaccc acagttgaat atccatgtgg aaaaatacct 540
attctagaaa aaagaaatgc cagcaaacc ccaaggccgaa ttgtgggggg caaggtgtgc 600
cccaaagggg agtgtccatg gcaggtcctg ttgttgggtga atggagctca gttgtgtggg 660
gggaccctga tcaacaccat ctgggtgggtc tccgcggccc actgtttcga caaaatcaag 720
aactggagga acctgatcgc ggtgctgggc gagcacgacc tcagcgagca cgacggggat 780
gagcagagcc ggcgggtggc gcaggtcatc atccccagca cgtacgtccc gggcaccacc 840
aaccacgaca tcgcgctgct ccgcctgcac cagcccgtgg tcctcactga ccatgtggtg 900
cccccttgcc tgcccgaacg gacgttctct gagaggacgc tggccttcgt gcgcttctca 960
ttggtcagcg gctggggcca gctgctggac cgtggcgcca cggccctgga gctcatggtc 1020
ctcaacgtgc cccggctgat gaccaggac tgccctgcagc agtcacggaa ggtgggagac 1080
tccccaaata tcacggagta catgttctgt gccggctact cggatggcag caaggactcc 1140
tgcaaggggg acagtggagg cccacatgcc acccactacc ggggcacgtg gtacctgacc 1200
ggcatcgtga gctggggcca gggctgcgcc accgtgggcc acttcggcgt gtacaccagg 1260
gtgtcccagt acatcgagt gctgcagaaa ctgatgagaa gcgagcccag acccggcgtg 1320
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cctagcagac tgcctgggcc cagtacacc cctatcctgc ctacgtccag ctccagcaag 1440
gccccacccc ctagcctgcc ttctccttct cggctgcctg gccccagcga tactccaatt 1500
ctgccccagt cctccagcag taaggctccc cctccatctc tgccatcccc cagcagactg 1560
ccaggccctt ctgatacacc catcctccca cagtgatgag gatccgc 1607

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<210> 27

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> CTP-modified Factor VII

<400> 27

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

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

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His Gly Val Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu
35           40           45

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

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

Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
 85 90 95

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

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

Gln Leu Ile Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser
 130 135 140

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

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

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

Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
 195 200 205

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

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

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

His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro
 260 265 270

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

Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu
 290 295 300

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

Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu
 325 330 335

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

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

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

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

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

Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
 420 425 430

Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ser
 435 440 445

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

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

Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
 485 490 495

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

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

Leu Pro Gln Gly
 530

<210> 28
 <211> 1775
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CTP-modified Factor VII

<400> 28
 ctcgaggaca tggctctccca ggccctcagg ctctctgcc ttctgcttgg gcttcagggc 60
 tgccctggctg cagtcttcgt aaccaggag gaagcccacg gcgtcctgca ccggcgccgg 120

180 cgcgcccaacg cgttccctgga ggaagctgcgg ccgggctccc tggagaggga gtgcagaaggag
 240 gagcagtgct ccttcgagga gggccgggag atcttcaagg acgcgagag gagcgaagctg
 300 ttctgattt ctacagtgga tggggaccag tgtgccctcaa gtccatgccaa gaatgggggc
 360 tccctgaagg accagctcaa gtccatatc tgcctctgcc tccctgcctt cgaaggccgg
 420 aactgtgaga cgcacaagga tgaccagctg atctgtgtga acgagaacgg cggctgtgag
 480 cagtactgca gtgaccacac gggcaccaa gctcctgtc ggtgccaga ggggtactct
 540 ctgtctgag acgggtgtc ctgcacaccc acagttgaat atccatgtgg aaaaataact
 600 attctagaaa aagaatatg cagcaaaacc caaggccgaa ttgtggggg caaggtgtg
 660 ccaaaaggg agtgcctatg gcaggtcctg ttgttgtga atgagctca gttgtgtgg
 720 gggaacctga tcaaacacat ctggtgtgtc tccgcgccc actgtttcga caaaatcaag
 780 aactggagga acctgatcg ggtgtgtggc gagcacaacc tcagcgagca cgaagggat
 840 gagcagagcc ggggtgtggc gtaggtcatc atcccagca cgtacgtccc gggcacaccc
 900 aaccaagaca tgcgctgtc ccgcttcac cagcccggtg tccctactga ccatgtgtg
 960 cccctctgc tgcggaaag gacgttctt gagagagcgc tggccttctg gcgttctca
 1020 ttgttcagcg gctggggcca gctgttgga cgtgcggcca cggccctgga gctcatgtc
 1080 ctcaacgtgc ccgctgat gaccagga tgcttcagc agtcacgaa ggtgggagac
 1140 tcccaata tcaaggagta catgttctgt gccgctact cggatggcag caaggactcc
 1200 tgcaaggggg acagtggagg ccccatgccc acccatac ggggcacgtg gtaccctgac
 1260 ggcatctgga gctggggcca gggctgcgc accgtggccc attcggcgt gtacacacagg
 1320 gtgtccagt acatcagtg gctgcagaaa ctgatgaaa gcgagcccaa accggcgtg
 1380 ctgttgagag cccctccc cagcagcagc tccaaggccc cttcccctag cctgcccagc
 1440 cctagcagac tgcctggccc ctctgacac cctatccctg ctacgtccag ctctcttaag
 1500 gtccacacac cttccctgcc tagcccttca agactggcag gccctagcga tacaccaatt
 1560 ctgcccagct ccttcagcag caaggtcccc ccaactagcc tgccttctcc atcaaggctg
 1620 cctggcccat cगतatcccc aatttgcct cagagcagct ctacgaagc accctccccc
 1680 agtctgccc ctccaagcag actccctgc ccttcagaca ctccaactc cccaagctc
 1740 tctagctcta aagctccacc tccagcctg cccaagcccta gtagactccc cgaaccttct
 1775 gatataccca tctgcccga gtgatgagga tccgc

<210> 29
 <211> 589
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CTP-modified Factor VII

<400> 29

Leu Glu Asp Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu
 1 5 10 15
 Gly Leu Gln Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala
 20 25 30
 His Gly Val Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu
 35 40 45
 Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser
 50 55 60
 Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu
 65 70 75 80
 Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
 85 90 95
 Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe
 100 105 110
 Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp
 115 120 125
 Gln Leu Ile Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser
 130 135 140
 Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser
 145 150 155 160
 Leu Leu Ala Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys
 165 170 175
 Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly
 180 185 190
 Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
 195 200 205
 Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile
 210 215 220
 Asn Thr Ile Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys
 225 230 235 240
 Asn Trp Arg Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu
 245 250 255
 His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro
 260 265 270

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

Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu
 290 295 300

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

Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu
 325 330 335

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

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

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

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

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

Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
 420 425 430

Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ser
 435 440 445

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

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

Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser
 485 490 495

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

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

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

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

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

Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser
580 585

<210> 30
<211> 1673
<212> DNA
<213> Artificial Sequence

<220>
<223> CTP-modified Factor IX

<400> 30
tctagagtcg accccgccat gcagcgcgtg aacatgatca tggcagaatc accaggcctc 60
atcaccatct gccttttagg atatctactc agtgctgaat gtacagtttt tcttgatcat 120
gaaaacgcca acaaaattct gaatcggcca aagaggata attcaggtaa attggaagag 180
tttgttcaag ggaaccttga gagagaatgt atggaagaaa agtgtagttt tgaagaagca 240
cgagaagttt ttgaaaacac tgaaagaaca actgaatttt ggaagcagta tgttgatgga 300
gatcagtgtg agtccaatcc atgtttaaat ggcggcagtt gcaaggatga cattaattcc 360
tatgaatgtt ggtgtccctt tggatttgaa ggaaagaact gtgaattaga tgtaacatgt 420
aacattaaga atggcagatg cgagcagttt tgtaaaaata gtgctgataa caagggtggt 480
tgctcctgta ctgagggata tcgacttgca gaaaaccaga agtcctgtga accagcagtg 540
ccatttccat gtggaagagt ttctgtttca caaacttcta agctcaccg tgctgaggca 600
gtttttcctg atgtggacta tgtaaattct actgaagctg aaaccatttt ggataacatc 660
actcaaagca cccaatcatt taatgacttc actcgagttg ttggtggaga agatgccaaa 720
ccagggtcaat tcccttgga ggttgttttg aatggtaaag ttgatgcatt ctgtggaggc 780
tctatcgta atgaaaaatg gattgtaact gctgccact gtgttgaaac tgggtgttaa 840
attacagttg tcgcaggtga acataatatt gaggagacag aacatacaga gcaaaagcga 900
aatgtgattc gaattattcc tcaccacaac tacaatgcag ctattaataa gtacaaccat 960
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ccacttgttg accgagccac atgtcttcga tctacaaagt tcaccatcta taacaacatg 1200
ttctgtgctg gcttccatga aggaggtaga gattcatgtc aaggagatag tgggggaccc 1260
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tgtgcaatga aaggcaaata tggaatatat accaaggat cccggtatgt caactggatt 1380
aaggaaaaaa caaagctcac tagctccagc agcaaggccc ctcccccgag cctgccctcc 1440

ccaagcaggc tgcctgggcc cagtgcacc cctatcctgc ctcagtccag ctccagcaag 1500
 gccccacccc ctaccctgcc ttctccttct cggtgcctg gccccagcga tactccaatt 1560
 ctgccccagt cctccagcag taaggctccc cctccatctc tgccatcccc cagcagactg 1620
 ccaggccctt ctgatacacc catcctccca cagtgatgag gatccgcggc cgc 1673

<210> 31
 <211> 545
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CTP-modified Factor IX

<400> 31

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 Ala 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> 32
<211> 1757
<212> DNA
<213> Artificial Sequence

<220>
<223> CTP-modified Factor IX

<400> 32
tctagagtcg accccgccat gcagcgcgtg aacatgatca tggcagaatc accaggcctc 60
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gaaaacgcca acaaaattct gaatcggcca aagaggtata attcaggtaa attggaagag 180
tttgttcaag ggaaccttga gagagaatgt atggaagaaa agtgtagttt tgaagaagca 240
cgagaagttt ttgaaaacac tgaaagaaca actgaatttt ggaagcagta tgttgatgga 300
gatcagtgtg agtccaatcc atgttttaaat ggcggcagtt gcaaggatga cattaattcc 360
tatgaatgtt ggtgtccctt tggatttgaa ggaaagaact gtgaattaga tgtaacatgt 420
aacattaaga atggcagatg cgagcagttt tgtaaaaata gtgctgataa caagggtggtt 480
tgctcctgta ctgagggata tcgacttgca gaaaaccaga agtcctgtga accagcagtg 540
ccatttccat gtggaagagt ttctgtttca caaacttcta agctcaccg tgctgaggca 600
gtttttcctg atgtggacta tgtaaatctt actgaagctg aaaccatttt ggataacatc 660
actcaaagca cccaatcatt taatgacttc actcgagttg ttggtggaga agatgccaaa 720
ccagggtcaat tcccttggca ggttgttttg aatggtaaag ttgatgcatt ctgtggaggc 780
tctatcgta atgaaaaatg gattgtaact gctgccact gtgttgaaac tgggtgttaa 840
attacagttg tcgcaggtga acataatatt gaggagacag aacatacaga gcaaaagcga 900
aatgtgattc gaattattcc tcaccacaac tacaatgcag ctattaataa gtacaaccat 960
gacattgccc ttctggaact ggacgaaccc ttagtgctaa acagctacgt tacacctatt 1020
tgcattgctg acaaggaata cacgaacatc ttctcaaat ttggatctgg ctatgtaagt 1080

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ttctgtgctg gcttccatga aggaggtaga gattcatgtc aaggagatag tgggggaccc 1260
catgttactg aagtggaagg gaccagtttc ttaactggaa ttattagctg ggggtgaagag 1320
tgtgcaatga aaggcaaata tggaatatat accaagggtat cccgggtatgt caactggatt 1380
aaggaaaaaa caaagctcac tagctccagc agcaaggccc ctcccccgag cctgccctcc 1440
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gccccaccac cttccctgcc tagcccttca agactgccag gccctagcga tacaccaatt 1560
ctgccccagt cctccagcag caaggctccc ccacctagcc tgccttctcc atcaaggctg 1620
cctggcccat ccgatacccc aattttgcct cagagcagct ctagcaaggc acctcccccc 1680
agtctgccct ctccaagcag actccctggc cttcagaca ctcccattct gccacagtga 1740
tgaggatccg cggccgc 1757

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<210> 33
 <211> 583
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CTP-modified Factor IX
 <400> 33

Ser Arg Val Asp Pro Ala Met Gln Arg Val Asn Met Ile Met Ala Glu
 1 5 10 15

Ser Pro Gly Leu Ile Thr Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala
 20 25 30

Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala Asn Lys Ile Leu Asn
 35 40 45

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

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

Arg Glu Val Phe Glu Asn Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln
 85 90 95

Tyr Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly
 100 105 110

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

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

Gly Arg Cys Glu Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val
 145 150 155 160

Cys Ser Cys Thr Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys
 165 170 175

Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser Val Ser Gln Thr
 180 185 190

Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr Val
 195 200 205

Asn Ser Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr
 210 215 220

Gln Ser Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys
 225 230 235 240

Pro Gly Gln Phe Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala
 245 250 255

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

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

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

Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His
 305 310 315 320

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

Val Thr Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu
 340 345 350

Lys Phe Gly Ser Gly Tyr Val Ser Gly Trp Gly Arg Val Phe His Lys
 355 360 365

Gly Arg Ser Ala Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp
 370 375 380

Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met
 385 390 395 400

Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp
 405 410 415

Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr
 420 425 430

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

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

Lys Leu Thr Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser
 465 470 475 480

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

Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu
 500 505 510

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

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

Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro
 545 550 555 560

Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile
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Leu Pro Gln Gly Ser Ala Ala
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<210> 34
 <211> 1840
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CTP-modified Factor IX

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 aaaacgcaa caaaattctg aatcggccaa agaggtataa ttcaggtaaa ttggaagagt 180
 ttgttcaagg gaaccttgag agagaatgta tggaagaaaa gtgtagtttt gaagaagcac 240
 gagaagtttt tgaaaacact gaaagaacaa ctgaattttg gaagcagtat gttgatggag 300
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gctcctgtac	tgagggatat	cgacttgcag	aaaaccagaa	gtcctgtgaa	ccagcagtgc	540
catttccatg	tggaagagtt	tctgtttcac	aaactttctaa	gctcaccctg	gctgaggcag	600
tttttcctga	tgtggactat	gtaaattcta	ctgaagctga	aaccattttg	gataacatca	660
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caggtcaatt	cccttggcag	gttgttttga	atggtaaagt	tgatgcattc	tgtggaggct	780
ctatcgtaa	tgaaaaatgg	attgtaactg	ctgcccactg	tgttgaaact	ggtgttaaaa	840
ttacagttgt	cgcaggtgaa	cataatattg	aggagacaga	acatacagag	caaaagcgaa	900
atgtgattcg	aattattcct	caccacaact	acaatgcagc	tattaataag	tacaaccatg	960
acattgccct	tctggaactg	gacgaacctt	tagtgctaaa	cagctacgtt	acacctattt	1020
gcattgctga	caaggaatac	acgaacatct	tcctcaaatt	tggtatctggc	tatgtaagt	1080
gctggggaag	agtcttccac	aaaggagat	cagctttagt	tcttcagtac	cttagagttc	1140
cacttgttga	ccgagccaca	tgtcttcgat	ctacaaagtt	caccatctat	aacaacatgt	1200
tctgtgctgg	cttccatgaa	ggaggtagag	attcatgtca	aggagatagt	gggggacccc	1260
atgttactga	agtggaaggg	accagtttct	taactggaat	tattagctgg	ggtgaagagt	1320
gtgcaatgaa	aggcaaatat	ggaatatata	ccaaggtatc	ccggtatgtc	aactggatta	1380
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caagcaggct	gcctggggcc	tctgacaccc	ctatcctgcc	tcagtccagc	tcctctaagg	1500
ctccaccacc	ttccctgcct	agcccttcaa	gactgccagg	ccctagcgat	acaccaattc	1560
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<220>
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<400> 35

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

Cys Thr Val Phe Leu Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg
35 40 45

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

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

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

Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser
100 105 110

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

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

Arg Cys Glu Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys
145 150 155 160

Ser Cys Thr Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu
165 170 175

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

Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn
195 200 205

Ser Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln
210 215 220

Ser Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro
225 230 235 240

Gly Gln Phe Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe
245 250 255

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

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

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

Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp
305 310 315 320

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

Thr Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys
340 345 350

Phe Gly Ser Gly Tyr Val Ser Gly Trp Gly Arg Val Phe His Lys Gly
355 360 365

Arg Ser Ala Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg
370 375 380

Ala Thr Cys Leu Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe
385 390 395 400

Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser
405 410 415

Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly
420 425 430

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

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

Leu Thr Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro
465 470 475 480

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

Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro
500 505 510

Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Ser Ser Ser Ser Lys Ala
515 520 525

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

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

Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu
565 570 575

Pro Gln Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro
580 585 590

Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser
595 600 605

Ala Ala
610

<210> 36
<211> 20
<212> DNA
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<220>
<223> Primer 101 for FIX-(CTP)2

<400> 36
gtttagtga cgcgcagaat 20

<210> 37
<211> 20
<212> DNA
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<220>
<223> Primer 103-R for FIX-(CTP)2

<400> 37
ttgaggaaga tggtcgtgta 20

<210> 38
<211> 20
<212> DNA
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<220>
<223> Primer 98 for FIX-(CTP)2

<400> 38
attacagttg tcgcaggtga 20

<210> 39
<211> 30
<212> DNA
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<220>
<223> Primer 99-Rfor FIX-(CTP)2

<400> 39
gctggagcta gtgagctttg ttttttcctt 30

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<223> Primer 100 for FIX-(CTP)2

<400> 40

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<210> 41

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Primer 27-R for FIX-(CTP)2

<400> 41

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<210> 42

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 75

<400> 42

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20

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 122r

<400> 43

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27

<210> 44

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 123

<400> 44

gtgctgaggc agtttttcct gatgtggact at

32

<210> 45

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 124r

<400> 45

caacacagtg ggcagcag

18