

SEQUENCE LISTING

<110> Amgen Inc.

<120> MULTISPECIFIC TRANSTHYRETIN IMMUNOGLOBULIN FUSIONS

<130> A-2414-WO-PCT

<150> 62/871,247

<151> 2019-07-08

<160> 44

<170> PatentIn version 3.5

<210> 1

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TTR AA

<400> 1

Gly Pro Thr Gly Thr Gly Glu Ser Lys Cys Pro Leu Met Val Lys Val
1 5 10 15

Leu Asp Ala Val Arg Gly Ser Pro Ala Ile Asn Val Ala Val His Val
20 25 30

Phe Arg Lys Ala Ala Asp Asp Thr Trp Glu Pro Phe Ala Ser Gly Lys
35 40 45

Thr Ser Glu Ser Gly Glu Leu His Gly Leu Thr Thr Glu Glu Glu Phe
50 55 60

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

Ala Leu Gly Ile Ser Pro Phe His Glu His Ala Glu Val Val Phe Thr
85 90 95

Ala Asn Asp Ser Gly Pro Arg Arg Tyr Thr Ile Ala Ala Leu Leu Ser
100 105 110

Pro Tyr Ser Tyr Ser Thr Thr Ala Val Val Thr Asn Pro Lys Glu

115

120

125

<210> 2

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine TTR AA

<400> 2

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

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

Phe Lys Lys Thr Ser Glu Gly Ser Trp Glu Pro Phe Ala Ser Gly Lys
 35 40 45

Thr Ala Glu Ser Gly Glu Leu His Gly Leu Thr Thr Asp Glu Lys Phe
 50 55 60

Val Glu Gly Val Tyr Arg Val Glu Leu Asp Thr Lys Ser Tyr Trp Lys
 65 70 75 80

Thr Leu Gly Ile Ser Pro Phe His Glu Phe Ala Asp Val Val Phe Thr
 85 90 95

Ala Asn Asp Ser Gly His Arg His Tyr Thr Ile Ala Ala Leu Leu Ser
 100 105 110

Pro Tyr Ser Tyr Ser Thr Thr Ala Val Val Ser Asn Pro Gln Asn
 115 120 125

<210> 3

<211> 615

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine TTR NA

<400> 3

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tgatgggtcaa agttctagat gctgtccgag gcagtcctgc catcaatgtg gccgtgcatg 180
tggtcagaaa ggctgctgat gacacctggg agccatttgc ctctgggaaa accagtgagt 240
ctggagagct gcatgggctc acaactgagg aggaatttgt agaagggata tacaaagtgg 300
aaatagacac caaatcttac tggaaggcac ttggcatctc cccattccat gagcatgcag 360
aggtgggtatt cacagccaac gactccggcc cccgccgcta caccattgcc gccctgctga 420
gcccctactc ctattccacc acggctgtcg tcaccaatcc caaggaatga gggacttctc 480
ctccagtgga cctgaaggac gagggatggg atttcatgta accaagagta ttccattttt 540
actaaagcac tgttttcacc tcatatgcta tgttagaagt ccaggcagag acaataaaac 600
attcctgtga aaggc 615

<210> 4
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> DNP 3B1 Ab LC AA

<400> 4

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Glu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
65 70 75 80

Pro Leu Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr

85

90

95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
 100 105 110

Tyr Asn Ser Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 5

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> DNP Ab LC NA

<400> 5

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cgctgtgaca tccagatgac ccagtcctca tcctccctgt ctgcatctga aggagacaga 120

gtcaccatca cttgccgggc aagtcagggc attagaaatg atttaggctg gtatcagcag 180

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aaaccaggga aagcccctaa ggcctgcat tatgctgcat ccagtttgca aagtggggtc      240
ccattaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg      300
cagcctgaag attttgcaac ttattactgt ctacagtata atagttaccc gtggacgttc      360
ggccaaggga ccaaggtgga aatcaaactg acggtggctg caccatctgt cttcatcttc      420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac      480
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac      540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc      600
ctgacgctga gcaaagcaga ctacagaaaa caaaagtctt acgcctgcga agtcacccat      660
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<210> 6
<211> 236
<212> PRT
<213> Artificial Sequence

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<220>
<223> DNP 3B1 Ab LC AA w/CPM S230E (EU S176E)

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<400> 6

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1           5           10          15

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```

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
          20          25          30

```

```

Leu Ser Ala Ser Glu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
          35          40          45

```

```

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
          50          55          60

```

```

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
          65          70          75          80

```

```

Pro Leu Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
          85          90          95

```

```

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln

```

100

105

110

Tyr Asn Ser Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 7

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> DNP 3B1 Ab LC NA w/CPM S230E (EU S176E)

<400> 7

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cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctga aggagacaga 120

gtcaccatca cttgccgggc aagtcagggc attagaaatg atttaggctg gtatcagcag 180

aaaccaggga aagcccctaa ggcctgatc tatgctgcat ccagtttgca aagtggggtc 240

ccattaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300

cagcctgaag attttgcaac ttattactgt ctacagtata atagttaccc gtggacgttc 360
ggccaaggga ccaaggtgga aatcaaactg acggtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cgaaagcacc 600
ctgacgctga gcaaagcaga ctacagaaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 8
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> DNP 3B1 Ab HC AA

<400> 8

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly
35 40 45

Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly
50 55 60

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

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

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

Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Tyr Asp Ser Ser Gly Tyr Tyr

115

120

125

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

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 195 200 205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 225 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 245 250 255

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 260 265 270

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 290 295 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 305 310 315 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 325 330 335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
370 375 380

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
405 410 415

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470

<210> 9
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> DNP 3B1 Ab HC NA

<400> 9
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tccctcacct gcactgtctc tgggtggctcc atcagtagtt actactggag ctggatccgg 180
cagccccag ggaagggact ggagtggatt gggtatatct attacagtgg gaacaccaac 240

tccaacccct ccctcaagag tcgagtcacc atatcagtag acacgtccaa gaaccagttc	300
tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagaacc	360
tactatgata gtagtgggta ctactaccgt gcttttgata tctggggcca agggacaatg	420
gtcaccgtct ctagtgcctc caccaagggc ccatcggtct tccccctggc accctcctcc	480
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	540
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttccccgct	600
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc	660
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	720
aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct	780
gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg	840
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	900
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg	960
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac	1020
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1080
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc	1140
ccatccccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc	1200
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag	1260
accacgcctc ccgtgctgga ctccgacggc tccttcctcc tctatagcaa gctcaccgtg	1320
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg	1380
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gt	1422

<210> 10
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DNP Ab HC AA
 w/CPM S230K (EU S183K)

<400> 10

Met	Asp	Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp
1				5				10					15		

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

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly
35 40 45

Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly
50 55 60

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

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

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

Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Tyr Asp Ser Ser Gly Tyr Tyr
115 120 125

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

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
195 200 205

Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
260 265 270

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
290 295 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305 310 315 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
325 330 335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
370 375 380

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
405 410 415

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 465 470

<210> 11
 <211> 1422
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNP Ab HC NA w/CPM S230K (EU S183K)

<400> 11
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 tccctcacct gcactgtctc tgggtggctcc atcagtagtt actactggag ctggatccgg 180
 cagccccag ggaagggact ggagtggatt gggatatatct attacagtgg gaacaccaac 240
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 tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagaacc 360
 tactatgata gtagtgggta ctactaccgt gcttttgata tctggggcca agggacaatg 420
 gtcaccgtct ctagtgcctc caccaagggc ccatcggtct tccccctggc accctcctcc 480
 aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 540
 ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600
 gtcctacagt cctcaggact ctactccctc aagagcgtgg tgaccgtgcc ctccagcagc 660
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720
 aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 780
 gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg 840
 atctcccga cccctgaggt cacatgcgtg gtgggtggacg tgagccacga agaccctgag 900
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gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1140
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 tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1260
 accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg 1320
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380
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<210> 12
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DNP Fab HC AA

<400> 12

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

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

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly
 35 40 45

Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly
 50 55 60

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

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

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

Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Tyr Asp Ser Ser Gly Tyr Tyr
 115 120 125

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

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
195 200 205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys
245

<210> 13
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> DNP Fab HC AA

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tccctcacct gcaactgtctc tgggtggctcc atcagtagtt actactggag ctggatccgg 180
cagccccag ggaagggact ggagtggatt gggatatatct attacagtgg gaacaccaac 240
tccaaccctt ccctcaagag tcgagtcacc atatcagtag acacgtccaa gaaccagttc 300
tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagaacc 360

tactatgata gtagtggtta ctactaccgt gcttttgata tctggggcca agggacaatg	420
gtcaccgtct ctagtgcctc caccaagggc ccatcggtct tccccctggc accctcctcc	480
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	540
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttccccgct	600
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc	660
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aagaaagttg agcccaaadc ttgt	744

<210> 14
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DNP Fab HC AA w/CPM S230K (EU S183K)

<400> 14

Met	Asp	Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp
1				5				10						15	

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

Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly
		35					40					45			

Gly	Ser	Ile	Ser	Ser	Tyr	Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly
	50					55					60				

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

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

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

Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Tyr Asp Ser Ser Gly Tyr Tyr
115 120 125

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

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
195 200 205

Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys
245

<210> 15
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> DNP Fab HC NA w/CPM S230K (EU S183K)

<400> 15
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg ttaagccttc ggagaccctg 120
tccctcacct gcactgtctc tgggtggctcc atcagtagtt actactggag ctggatccgg 180
cagccccag ggaagggact ggagtggatt gggatatctt attacagtgg gaacaccaac 240
tccaaccctt ccctcaagag tcgagtcacc atatcagtag acacgtccaa gaaccagttc 300

tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagaacc	360
tactatgata gtagtgggta ctactaccgt gcttttgata tctggggcca agggacaatg	420
gtcaccgtct ctagtgcctc caccaagggc ccatcggctt tccccctggc accctcctcc	480
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	540
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttccccggct	600
gtcctacagt cctcaggact ctactccctc aagagcgtgg tgaccgtgcc ctccagcagc	660
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	720
aagaaagttg agcccaaadc ttgt	744

<210> 16
 <211> 235
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 655-341 Ab LC AA

<400> 16

Met	Glu	Thr	Pro	Ala	Gln	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Trp	Leu	Pro
1				5				10						15	

Asp	Thr	Thr	Gly	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser
			20					25					30		

Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Gly
		35					40					45			

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

Pro	Ser	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro
65					70					75				80	

Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile
				85					90					95	

Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Phe
			100					105					110		

Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 17
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Ab LC NA

<400> 17
atggaaaccc cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca gggtattagt agaagcgaat tagcctggta ccagcagaaa 180
cctggccagg ctcccagcct cctcatctat ggtgcatcca gcagggccac tggcatccca 240
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 300
cctgaagatt ttgcagtgtta ttactgtcaa caatttggtta gttcaccgtg gacgttcggc 360

caagggacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttccc	420
ccatctgatg agcagttgaa atctggaact gctagcgttg tgtgcctgct gaataacttc	480
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	540
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg	600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag	660
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt	705

<210> 18
 <211> 235
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 655-341 Ab LC AA w/CPM S230K (EU S176K)

<400> 18

Met	Glu	Thr	Pro	Ala	Gln	Leu	Leu	Phe	Leu	Leu	Leu	Trp	Leu	Pro
1				5				10					15	

Asp	Thr	Thr	Gly	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser
			20					25					30		

Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Gly
		35					40					45			

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

Pro	Ser	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro
65					70					75				80	

Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile
				85					90					95	

Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Phe
			100					105					110		

Gly	Ser	Ser	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
			115				120					125			

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 19
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Ab LC NA w/CPM S230K (EU S176K)

<400> 19
atggaaaccc cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60
gaaatttgtt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca ggggtattagt agaagcgaat tagcctggta ccagcagaaa 180
cctggccagg ctcccagcct cctcatctat ggtgcatcca gcagggccac tggcatccca 240
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 300
cctgaagatt ttgcagtgtt ttactgtcaa caatttggtg gttcaccgtg gacgttcggc 360
caagggacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttcccg 420
ccatctgatg agcagttgaa atctggaact gctagcgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	540
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcaa gagcaccctg	600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag	660
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt	705

<210> 20
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 655-341 Ab HC AA

<400> 20

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
1			5					10						15	

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

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

Ser	Ser	Gly	Asp	Tyr	Phe	Trp	Ser	Trp	Ile	Arg	Gln	Leu	Pro	Gly	Lys
	50					55					60				

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

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

Lys	Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala
			100					105					110		

Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Gly	Gly	Asp	Tyr	Ala	Tyr	Gly	Met
		115					120					125			

Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr
	130					135					140				

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

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

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

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

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

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

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

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

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

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

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

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

Leu Ser Leu Ser Pro Gly
465 470

<210> 21
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Ab HC NA

<400> 21
atgaagcacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccctcacc 120
tgcactgtct ctggtggctc catcagcagt ggtgattact tctggagctg gatccgccag 180
ctcccaggga agggcctgga gtggattggg cacatccata acagtgggac cacctactac 240
aatccgtccc tcaagagtcg agttaccata tcagtagaca cgtctaagaa gcagttctcc 300
ctgaggctga gttctgtgac tgccgcggac acggccgtat attactgtgc gagagatcga 360
gggggtgact acgcttatgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 420

tcagcctcca ccaagggccc atccgtcttc cccctggcac cctcctccaa gagcacctct	480
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	540
tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc	600
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag	660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag	720
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	780
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	840
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	900
tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtag	960
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc	1020
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1080
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag	1140
gagatgacca agaaccaggt cagcctgacc tgcctgggtc aaggcttcta tcccagcgac	1200
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1260
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg	1320
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1380
acgcagaaga gcctctccct gtctccgggt	1410

<210> 22
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 655-341 Ab HC AA w/CPM S230E (EU S183E)

<400> 22

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
1				5					10					15	

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

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

Ser Ser Gly Asp Tyr Phe Trp Ser Trp Ile Arg Gln Leu Pro Gly Lys
50 55 60

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

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

Lys Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Arg Asp Arg Gly Gly Asp Tyr Ala Tyr Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
130 135 140

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

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

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

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser
195 200 205

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

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

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

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

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

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

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

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

Leu Ser Leu Ser Pro Gly
465 470

<210> 23
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Ab HC NA w/CPM S230E (EU S183E)

<400> 23
atgaagcacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccctcacc 120
tgcactgtct ctggtggctc catcagcagt ggtgattact tctggagctg gatccgccag 180
ctcccaggga agggcctgga gtggattggg cacatccata acagtgggac cacctactac 240
aatccgtccc tcaagagtcg agttaccata tcagtagaca cgtctaagaa gcagtttctc 300
ctgaggctga gttctgtgac tgccgcggac acggccgtat attactgtgc gagagatcga 360
gggggtgact acgcttatgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 420
tcagcctcca ccaagggcc atccgtcttc cccctggcac cctcctcaa gagcacctct 480
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 540
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 600
tcaggactct actccctcga gagcgtggtg accgtgccct ccagcagctt gggcacccag 660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 780
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 840
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 960
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1080
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag 1140
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1260

gtgctggact cgcacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg	1320
tggcagcagg ggaacgtctt ctcattgctcc gtgatgcatg aggctctgca caaccactac	1380
acgcagaaga gcctctccct gtctccgggt	1410

<210> 24
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 655-341 Fab HC AA

<400> 24

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
1			5					10						15	

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

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

Ser	Ser	Gly	Asp	Tyr	Phe	Trp	Ser	Trp	Ile	Arg	Gln	Leu	Pro	Gly	Lys
	50					55					60				

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

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

Lys	Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala
			100				105						110		

Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Gly	Gly	Asp	Tyr	Ala	Tyr	Gly	Met
		115					120					125			

Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr
	130					135					140				

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

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

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

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

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

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

Pro Lys Ser Cys

<210> 25
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Fab HC NA

<400> 25
atgaagcacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtcccag 60
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tgcactgtct ctggtggctc catcagcagt ggtgattact tctggagctg gatccgccag 180
ctcccaggga agggcctgga gtggattggg cacatccata acagtgggac cacctactac 240
aatccgtccc tcaagagtcg agttaccata tcagtagaca cgtctaagaa gcagttcttc 300
ctgaggctga gttctgtgac tgccgcggac acggccgtat attactgtgc gagagatcga 360
gggggtgact acgcttatgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 420
tcagcctcca ccaagggcc atccgtcttc cccctggcac cctcctcaa gagcacctct 480
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 540

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	600
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcacccag	660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag	720
cccaaattctt gt	732

<210> 26
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 655-341 Fab HC AA w/CPM S230E (EU S183E)

<400> 26

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
1				5					10					15	

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

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

Ser	Ser	Gly	Asp	Tyr	Phe	Trp	Ser	Trp	Ile	Arg	Gln	Leu	Pro	Gly	Lys
	50					55					60				

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

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

Lys	Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala
			100					105					110		

Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Gly	Gly	Asp	Tyr	Ala	Tyr	Gly	Met
		115					120					125			

Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr
	130						135				140				

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

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

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

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser
195 200 205

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

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

Pro Lys Ser Cys

<210> 27
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Fab HC NA w/CPM S230E (EU S183E)

<400> 27
atgaagcacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccttcacc 120
tgcactgtct ctggtggctc catcagcagt ggtgattact tctggagctg gatccgccag 180
ctcccaggga agggcctgga gtggattggg cacatccata acagtgggac cacctactac 240
aatccgtccc tcaagagtcg agttaccata tcagtagaca cgtctaagaa gcagtttctc 300
ctgaggctga gttctgtgac tgccgcggac acggccgtat attactgtgc gagagatcga 360
gggggtgact acgcttatgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 420
tcagcctcca ccaagggcc atccgtcttc cccctggcac cctcctcaa gagcacctct 480

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	540
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	600
tcaggactct actccctcga gagcgtggtg accgtgccct ccagcagctt gggcacccag	660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag	720
cccaaattctt gt	732

<210> 28
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNP Ab LC NA (TTR construct)

<400> 28	
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg	60
cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctga aggagacaga	120
gtcaccatca cttgccgggc aagtcagggc attagaaatg atttaggctg gtatcagcag	180
aaaccaggga aagcccctaa ggcgcctgatc tatgctgcat ccagtttgca aagtggggtc	240
ccattaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg	300
cagcctgaag attttgcaac ttattactgt ctacagtata atagttaccg gtggacgttc	360
ggccaaggga ccaaggtgga aatcaaactg acgggtggctg caccatctgt cttcatcttc	420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac	480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac	540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc	600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat	660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt	708

<210> 29
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DNP Ab LC AA (TTR construct)

<400> 29

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Glu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
65 70 75 80

Pro Leu Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
100 105 110

Tyr Asn Ser Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 30
 <211> 1809
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNP Ab HC NA (TTR construct)

<400> 30
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
 cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg ttaagccttc ggagaccctg 120
 tccctcacct gcaactgtctc tgggtggctcc atcagtagtt actactggag ctggatccgg 180
 cagccccag ggaagggact ggagtggatt gggatatatct attacagtgg gaacaccaac 240
 tccaacccct ccctcaagag tcgagtcacc atatcagtag acacgtccaa gaaccagttc 300
 tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagaacc 360
 tactatgata gtagtgggta ctactaccgt gcttttgata tctggggcca agggacaatg 420
 gtcaccgtct ctagtgcctc caccaagggc ccatcgggtct tccccctggc accctcctcc 480
 aagagcacct ctggggggcac agcgggccctg ggctgcctgg tcaaggacta cttccccgaa 540
 ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600
 gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 660
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720
 aagaaagttg agcccaaatc ttgtgacaaa actcacacat gccaccgtg cccagcacct 780
 gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg 840
 atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 900
 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 960
 gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1020
 tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc 1080
 gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1140

ccatccccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc	1200
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag	1260
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg	1320
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg	1380
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggaggcgg tccaactggt	1440
actggtgaat ctaaagctcc tcttatgggt gcagtcaaag atgctgttcg tggttccccg	1500
gcaattaatg ttgctgtaca tgttttccgt aaagctgctg acgacacctg ggaaccgttc	1560
gctagcggta aaacctccga atccggtgaa ctgcacggtc tgaccaccga agaagaattc	1620
gttgaaggta tctacaaagt tgaaatcgac accaaatcct actggaaagc tttgggtatc	1680
tccccgttcc acgaacacgc tgaagttggt ttcaccgcta acgactccgg tccgcgtcgt	1740
tacacgatcg ctgctctgct gtccccgtac tcctactcca ccaccgctgt tgttaccaac	1800
ccgaaagaa	1809

<210> 31
 <211> 603
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> DNP Ab LC AA (TTR construct)

 <400> 31

Met	Asp	Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp
1				5				10						15	

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

Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly
		35					40					45			

Gly	Ser	Ile	Ser	Ser	Tyr	Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly
	50					55					60				

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

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

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

Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Tyr Asp Ser Ser Gly Tyr Tyr
115 120 125

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

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
195 200 205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
260 265 270

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
290 295 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305 310 315 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
325 330 335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
370 375 380

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
405 410 415

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
450 455 460

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

Thr Gly Glu Ser Lys Ala Pro Leu Met Val Ala Val Lys Asp Ala Val
485 490 495

Arg Gly Ser Pro Ala Ile Asn Val Ala Val His Val Phe Arg Lys Ala
500 505 510

Ala Asp Asp Thr Trp Glu Pro Phe Ala Ser Gly Lys Thr Ser Glu Ser
515 520 525

Gly Glu Leu His Gly Leu Thr Thr Glu Glu Glu Phe Val Glu Gly Ile
530 535 540

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

Ser Pro Phe His Glu His Ala Glu Val Val Phe Thr Ala Asn Asp Ser
565 570 575

Gly Pro Arg Arg Tyr Thr Ile Ala Ala Leu Leu Ser Pro Tyr Ser Tyr
580 585 590

Ser Thr Thr Ala Val Val Thr Asn Pro Lys Glu
595 600

<210> 32
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Ab LC NA (TTR construct)

<400> 32
atggaaacc cagcgagct tctcttctc ctgctactct ggctcccaga taccaccgga 60
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca ggggtattagt agaagcgaat tagcctggta ccagcagaaa 180
cctggccagg ctcccagcct cctcatctat ggtgcatcca gcagggccac tggcatccca 240
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300
cctgaagatt ttgcagtgtg ttactgtcaa caatttggtg gttcaccgtg gacgttcggc 360
caagggacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttcccg 420
ccatctgatg agcagttgaa atctggaact gctagcggtg tgtgcctgct gaataacttc 480
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtactcc 540
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 705

<210> 33

<211> 235

<212> PRT

<213> Artificial Sequence

<220>

<223> 655-341 Ab LC AA (TTR construct)

<400> 33

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly
35 40 45

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

Pro Ser Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
100 105 110

Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 34
<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Ab HC NA (TTR construct)

<400> 34
atgaagcacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccctcacc 120
tgactgtct ctggtggctc catcagcagt ggtgattact tctggagctg gatccgccag 180
ctcccaggga agggcctgga gtggattggg cacatccata acagtgggac cacctactac 240
aatccgtccc tcaagagtcg agttaccata tcagtagaca cgtctaagaa gcagttctcc 300
ctgaggctga gttctgtgac tgccgcggac acggccgtat attactgtgc gagagatcga 360
gggggtgact acgcttatgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 420
tcagcctcca ccaagggcc atccgtcttc cccctggcac cctcctcaa gagcacctct 480
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 540
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 600
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccag 660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720

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cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg      780
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc      840
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      900
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac      960
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc     1020
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     1080
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag     1140
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac     1200
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     1260
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg     1320
tggcagcagg ggaacgtctt ctcattgctc gtgatgcatg aggctctgca caaccactac     1380
acgcagaaga gcctctccct gtctccgggt ggaggcggtc caactggtac tggatgaatct     1440
aaagctcctc ttatggttgc agtcgatgat gctgttcgtg gttccccggc aattaatgtt     1500
gctgtacatg ttttccgtaa agctgctgac gacacctggg aaccgttcgc tagcggtaaa     1560
acctccgaat ccggtgaact gcacggtctg accaccgaag aagaattcgt tgaaggtatc     1620
tacaaagttg aaatcgacac caaatcctac tggaaagctt tgggtatctc cccgttccac     1680
gaacacgctg aagttgtttt caccgctaac gactccggtc cgcgtcgtta cagcatcgct     1740
gctctgctgt ccccgctact ctactccacc accgctgttg ttaccaacc gaaagaa      1797

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<210> 35

<211> 599

<212> PRT

<213> Artificial Sequence

<220>

<223> 655-341 Ab LC AA (TTR construct)

<400> 35

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1           5           10          15

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

```

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

Ser Ser Gly Asp Tyr Phe Trp Ser Trp Ile Arg Gln Leu Pro Gly Lys
50 55 60

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

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

Lys Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Arg Asp Arg Gly Gly Asp Tyr Ala Tyr Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
130 135 140

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

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

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

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

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

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

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

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

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

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

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

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

Leu Ser Leu Ser Pro Gly Gly Gly Gly Pro Thr Gly Thr Gly Glu Ser
465 470 475 480

Lys Ala Pro Leu Met Val Ala Val Asp Asp Ala Val Arg Gly Ser Pro
485 490 495

Ala Ile Asn Val Ala Val His Val Phe Arg Lys Ala Ala Asp Asp Thr
500 505 510

Trp Glu Pro Phe Ala Ser Gly Lys Thr Ser Glu Ser Gly Glu Leu His
515 520 525

Gly Leu Thr Thr Glu Glu Glu Phe Val Glu Gly Ile Tyr Lys Val Glu
530 535 540

Ile Asp Thr Lys Ser Tyr Trp Lys Ala Leu Gly Ile Ser Pro Phe His
545 550 555 560

Glu His Ala Glu Val Val Phe Thr Ala Asn Asp Ser Gly Pro Arg Arg
565 570 575

Tyr Thr Ile Ala Ala Leu Leu Ser Pro Tyr Ser Tyr Ser Thr Thr Ala
580 585 590

Val Val Thr Asn Pro Lys Glu
595

<210> 36
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Fab LC NA (TTR construct)

<400> 36
atggaaacc cagcgagct tctcttctc ctgctactct ggctcccaga taccaccgga 60
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca ggggtattagt agaagcgaat tagcctggta ccagcagaaa 180
cctggccagg ctcccagcct cctcatctat ggtgcatcca gcagggccac tggcatccca 240

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300
 cctgaagatt ttgcagtgtg ttactgtcaa caatttggtg gttcacctg gacgttcggc 360
 caagggacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttccc 420
 ccatctgatg agcagttgaa atctggaact gctagcgttg tgtgcctgct gaataacttc 480
 tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg 600
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660
 ggcttgagct cgcccgtcac aaagagcttc aacaggggag agtgt 705

<210> 37
 <211> 235
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 655-341 Fab LC AA (TTR construct)

<400> 37

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
 20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly
 35 40 45

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

Pro Ser Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
 65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
 100 105 110

Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 38
<211> 1143
<212> DNA
<213> Artificial Sequence

<220>
<223> 655-341 Fab HC NA (TTR construct)

<400> 38
atgaagcacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtcctcacc 120
tgactgtct ctggtggctc catcagcagt ggtgattact tctggagctg gatccgccag 180
ctcccaggga agggcctgga gtggattggg cacatccata acagtgggac cacctactac 240
aatccgtccc tcaagagtcg agttaccata tcagtagaca cgtctaagaa gcagttctcc 300
ctgaggctga gttctgtgac tgccgcggac acggccgtat attactgtgc gagagatcga 360

```

gggggtgact acgcttatgg tatggacgtc tggggccaag ggaccacggt caccgtctcc      420
tcagcctcca ccaagggccc atccgtcttc cccctggcac cctcctccaa gagcacctct      480
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg      540
tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc      600
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag      660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag      720
cccaaattct gtggaggagg tccaactggt actggtgaat ctaaagctcc tcttatggtt      780
gcagtcgatg atgctgttcg tggttccccg gcaattaatg ttgctgtaca tgttttccgt      840
aaagctgctg acgacacctg ggaaccgttc gctagcggta aaacctccga atccggtgaa      900
ctgcacggtc tgaccaccga agaagaattc gttgaaggta tctacaaagt tgaaatcgac      960
accaaattct actggaaagc tttgggtatc tccccgttcc acgaacacgc tgaagttggt    1020
ttcaccgcta acgactccgg tccgcgtcgt tacacgatcg ctgctctgct gtccccgtac    1080
tcctactcca ccaccgtgt tgttaccaac ccgaaagaag gcggtcacca tcaccatcac    1140
cac                                                                    1143

```

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<210> 39
<211> 381
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> 655-341 Fab HC AA (TTR construct)

```

```

<400> 39

```

```

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1           5           10           15

```

```

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

```

```

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

```

```

Ser Ser Gly Asp Tyr Phe Trp Ser Trp Ile Arg Gln Leu Pro Gly Lys
50           55           60

```

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

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

Lys Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Arg Asp Arg Gly Gly Asp Tyr Ala Tyr Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
130 135 140

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

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

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

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

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

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

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

Pro Leu Met Val Ala Val Asp Asp Ala Val Arg Gly Ser Pro Ala Ile
260 265 270

Asn Val Ala Val His Val Phe Arg Lys Ala Ala Asp Asp Thr Trp Glu
275 280 285

Pro Phe Ala Ser Gly Lys Thr Ser Glu Ser Gly Glu Leu His Gly Leu
290 295 300

Thr Thr Glu Glu Glu Phe Val Glu Gly Ile Tyr Lys Val Glu Ile Asp
305 310 315 320

Thr Lys Ser Tyr Trp Lys Ala Leu Gly Ile Ser Pro Phe His Glu His
325 330 335

Ala Glu Val Val Phe Thr Ala Asn Asp Ser Gly Pro Arg Arg Tyr Thr
340 345 350

Ile Ala Ala Leu Leu Ser Pro Tyr Ser Tyr Ser Thr Thr Ala Val Val
355 360 365

Thr Asn Pro Lys Glu Gly Gly His His His His His His
370 375 380

<210> 40
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> DNP Fab LC NA (TTR construct)

<400> 40
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctga aggagacaga 120
gtcaccatca cttgccgggc aagtcagggc attagaaatg atttaggctg gtatcagcag 180
aaaccaggga aagcccctaa ggcctgatc tatgctgcat ccagtttgca aagtggggtc 240
ccattaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt ctacagtata atagttaccc gtggacgttc 360
ggccaaggga ccaaggtgga aatcaaactg acgggtggctg caccatctgt cttcatcttc 420
ccgcatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc	600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat	660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt	708

<210> 41
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DNP Fab LC AA (TTR construct)

<400> 41

Met	Asp	Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp
1				5				10						15	

Leu	Arg	Gly	Ala	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser
		20					25					30			

Leu	Ser	Ala	Ser	Glu	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser
		35					40					45			

Gln	Gly	Ile	Arg	Asn	Asp	Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys
	50					55					60				

Ala	Pro	Lys	Arg	Leu	Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val
65					70					75					80

Pro	Leu	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr
				85					90					95	

Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln
			100					105					110		

Tyr	Asn	Ser	Tyr	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile
		115					120					125			

Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp
130						135					140				

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 42
<211> 1155
<212> PRT
<213> Artificial Sequence

<220>
<223> DNP Fab HC NA (TTR construct)

<400> 42

Ala Thr Gly Gly Ala Cys Ala Thr Gly Ala Gly Gly Gly Thr Gly Cys
1 5 10 15

Cys Cys Gly Cys Thr Cys Ala Gly Cys Thr Cys Cys Thr Gly Gly Gly
20 25 30

Gly Cys Thr Cys Cys Thr Gly Cys Thr Gly Cys Thr Gly Thr Gly Gly
35 40 45

Cys Thr Gly Ala Gly Ala Gly Gly Thr Gly Cys Gly Cys Gly Cys Thr
50 55 60

Gly Thr Cys Ala Gly Gly Thr Gly Cys Ala Gly Cys Thr Gly Cys Ala
65 70 75 80

Gly Gly Ala Gly Thr Cys Gly Gly Gly Cys Cys Cys Ala Gly Gly Ala
85 90 95

Cys Thr Gly Gly Thr Thr Ala Ala Gly Cys Cys Thr Thr Cys Gly Gly
100 105 110

Ala Gly Ala Cys Cys Cys Thr Gly Thr Cys Cys Cys Thr Cys Ala Cys
115 120 125

Cys Thr Gly Cys Ala Cys Thr Gly Thr Cys Thr Cys Thr Gly Gly Thr
130 135 140

Gly Gly Cys Thr Cys Cys Ala Thr Cys Ala Gly Thr Ala Gly Thr Thr
145 150 155 160

Ala Cys Thr Ala Cys Thr Gly Gly Ala Gly Cys Thr Gly Gly Ala Thr
165 170 175

Cys Cys Gly Gly Cys Ala Gly Cys Cys Cys Cys Cys Ala Gly Gly Gly
180 185 190

Ala Ala Gly Gly Gly Ala Cys Thr Gly Gly Ala Gly Thr Gly Gly Ala
195 200 205

Thr Thr Gly Gly Gly Thr Ala Thr Ala Thr Cys Thr Ala Thr Thr Ala
210 215 220

Cys Ala Gly Thr Gly Gly Gly Ala Ala Cys Ala Cys Cys Ala Ala Cys
225 230 235 240

Thr Cys Cys Ala Ala Cys Cys Cys Cys Thr Cys Cys Cys Thr Cys Ala
245 250 255

Ala Gly Ala Gly Thr Cys Gly Ala Gly Thr Cys Ala Cys Cys Ala Thr
260 265 270

Ala Thr Cys Ala Gly Thr Ala Gly Ala Cys Ala Cys Gly Thr Cys Cys
275 280 285

Ala Ala Gly Ala Ala Cys Cys Ala Gly Thr Thr Cys Thr Cys Cys Cys
290 295 300

Thr Gly Ala Ala Gly Cys Thr Gly Ala Gly Cys Thr Cys Thr Gly Thr
305 310 315 320

Gly Ala Cys Cys Gly Cys Thr Gly Cys Gly Gly Ala Cys Ala Cys Gly
325 330 335

Gly Cys Cys Gly Thr Gly Thr Ala Thr Thr Ala Cys Thr Gly Thr Gly
340 345 350

Cys Gly Ala Gly Ala Ala Cys Cys Thr Ala Cys Thr Ala Thr Gly Ala
355 360 365

Thr Ala Gly Thr Ala Gly Thr Gly Gly Thr Thr Ala Cys Thr Ala Cys
370 375 380

Thr Ala Cys Cys Gly Thr Gly Cys Thr Thr Thr Thr Gly Ala Thr Ala
385 390 395 400

Thr Cys Thr Gly Gly Gly Gly Cys Cys Ala Ala Gly Gly Gly Ala Cys
405 410 415

Ala Ala Thr Gly Gly Thr Cys Ala Cys Cys Gly Thr Cys Thr Cys Thr
420 425 430

Ala Gly Thr Gly Cys Cys Thr Cys Cys Ala Cys Cys Ala Ala Gly Gly
435 440 445

Gly Cys Cys Cys Ala Thr Cys Gly Gly Thr Cys Thr Thr Cys Cys Cys
450 455 460

Cys Cys Thr Gly Gly Cys Ala Cys Cys Cys Thr Cys Cys Thr Cys Cys
465 470 475 480

Ala Ala Gly Ala Gly Cys Ala Cys Cys Thr Cys Thr Gly Gly Gly Gly
485 490 495

Gly Cys Ala Cys Ala Gly Cys Gly Gly Cys Cys Cys Thr Gly Gly Gly
500 505 510

Cys Thr Gly Cys Cys Thr Gly Gly Thr Cys Ala Ala Gly Gly Ala Cys
515 520 525

Thr Ala Cys Thr Thr Cys Cys Cys Cys Gly Ala Ala Cys Cys Gly Gly
530 535 540

Thr Gly Ala Cys Gly Gly Thr Gly Thr Cys Gly Thr Gly Gly Ala Ala
545 550 555 560

Cys Thr Cys Ala Gly Gly Cys Gly Cys Cys Cys Thr Gly Ala Cys Cys
565 570 575

Ala Gly Cys Gly Gly Cys Gly Thr Gly Cys Ala Cys Ala Cys Cys Thr
580 585 590

Thr Cys Cys Cys Gly Gly Cys Thr Gly Thr Cys Cys Thr Ala Cys Ala
595 600 605

Gly Thr Cys Cys Thr Cys Ala Gly Gly Ala Cys Thr Cys Thr Ala Cys
610 615 620

Thr Cys Cys Cys Thr Cys Ala Gly Cys Ala Gly Cys Gly Thr Gly Gly
625 630 635 640

Thr Gly Ala Cys Cys Gly Thr Gly Cys Cys Cys Thr Cys Cys Ala Gly
645 650 655

Cys Ala Gly Cys Thr Thr Gly Gly Gly Cys Ala Cys Cys Cys Ala Gly
660 665 670

Ala Cys Cys Thr Ala Cys Ala Thr Cys Thr Gly Cys Ala Ala Cys Gly
675 680 685

Thr Gly Ala Ala Thr Cys Ala Cys Ala Ala Gly Cys Cys Cys Ala Gly
690 695 700

Cys Ala Ala Cys Ala Cys Cys Ala Ala Gly Gly Thr Gly Gly Ala Cys
705 710 715 720

Ala Ala Gly Ala Ala Ala Gly Thr Thr Gly Ala Gly Cys Cys Cys Ala
725 730 735

Ala Ala Thr Cys Thr Thr Gly Thr Gly Gly Ala Gly Gly Ala Gly Gly
740 745 750

Thr Cys Cys Ala Ala Cys Thr Gly Gly Thr Ala Cys Thr Gly Gly Thr
755 760 765

Gly Ala Ala Thr Cys Thr Ala Ala Ala Gly Cys Thr Cys Cys Thr Cys
770 775 780

Thr Thr Ala Thr Gly Gly Thr Thr Gly Cys Ala Gly Thr Cys Ala Ala
785 790 795 800

Ala Gly Ala Thr Gly Cys Thr Gly Thr Thr Cys Gly Thr Gly Gly Thr
805 810 815

Thr Cys Cys Cys Cys Gly Gly Cys Ala Ala Thr Thr Ala Ala Thr Gly
820 825 830

Thr Thr Gly Cys Thr Gly Thr Ala Cys Ala Thr Gly Thr Thr Thr Thr
835 840 845

Cys Cys Gly Thr Ala Ala Ala Gly Cys Thr Gly Cys Thr Gly Ala Cys
850 855 860

Gly Ala Cys Ala Cys Cys Thr Gly Gly Gly Ala Ala Cys Cys Gly Thr
865 870 875 880

Thr Cys Gly Cys Thr Ala Gly Cys Gly Gly Thr Ala Ala Ala Ala Cys
885 890 895

Cys Thr Cys Cys Gly Ala Ala Thr Cys Cys Gly Gly Thr Gly Ala Ala
900 905 910

Cys Thr Gly Cys Ala Cys Gly Gly Thr Cys Thr Gly Ala Cys Cys Ala
915 920 925

Cys Cys Gly Ala Ala Gly Ala Ala Gly Ala Ala Thr Thr Cys Gly Thr
930 935 940

Thr Gly Ala Ala Gly Gly Thr Ala Thr Cys Thr Ala Cys Ala Ala Ala
945 950 955 960

Gly Thr Thr Gly Ala Ala Ala Thr Cys Gly Ala Cys Ala Cys Cys Ala
965 970 975

Ala Ala Thr Cys Cys Thr Ala Cys Thr Gly Gly Ala Ala Ala Gly Cys
980 985 990

Thr Thr Thr Gly Gly Gly Thr Ala Thr Cys Thr Cys Cys Cys Cys Gly
995 1000 1005

Thr Thr Cys Cys Ala Cys Gly Ala Ala Cys Ala Cys Gly Cys Thr
1010 1015 1020

Gly Ala Ala Gly Thr Thr Gly Thr Thr Thr Thr Cys Ala Cys Cys
1025 1030 1035

Gly Cys Thr Ala Ala Cys Gly Ala Cys Thr Cys Cys Gly Gly Thr
1040 1045 1050

Cys Cys Gly Cys Gly Thr Cys Gly Thr Thr Ala Cys Ala Cys Gly
1055 1060 1065

Ala Thr Cys Gly Cys Thr Gly Cys Thr Cys Thr Gly Cys Thr Gly
1070 1075 1080

Thr Cys Cys Cys Gly Thr Ala Cys Thr Cys Cys Thr Ala Cys
1085 1090 1095

Thr Cys Cys Ala Cys Cys Ala Cys Cys Gly Cys Thr Gly Thr Thr
1100 1105 1110

Gly Thr Thr Ala Cys Cys Ala Ala Cys Cys Cys Gly Ala Ala Ala
1115 1120 1125

Gly Ala Ala Gly Gly Cys Gly Gly Thr Cys Ala Cys Cys Ala Thr
1130 1135 1140

Cys Ala Cys Cys Ala Thr Cys Ala Cys Cys Ala Cys
1145 1150 1155

<210> 43
<211> 385
<212> PRT
<213> Artificial Sequence

<220>
<223> DNP Fab HC AA (TTR construct)

<400> 43

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly
35 40 45

Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly
50 55 60

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

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

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

Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Tyr Asp Ser Ser Gly Tyr Tyr
115 120 125

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

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
195 200 205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys Gly Gly Gly Pro Thr Gly Thr Gly
245 250 255

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

Ser Pro Ala Ile Asn Val Ala Val His Val Phe Arg Lys Ala Ala Asp
275 280 285

Asp Thr Trp Glu Pro Phe Ala Ser Gly Lys Thr Ser Glu Ser Gly Glu
290 295 300

Leu His Gly Leu Thr Thr Glu Glu Glu Phe Val Glu Gly Ile Tyr Lys
305 310 315 320

Val Glu Ile Asp Thr Lys Ser Tyr Trp Lys Ala Leu Gly Ile Ser Pro
325 330 335

Phe His Glu His Ala Glu Val Val Phe Thr Ala Asn Asp Ser Gly Pro
340 345 350

Arg Arg Tyr Thr Ile Ala Ala Leu Leu Ser Pro Tyr Ser Tyr Ser Thr
355 360 365

Thr Ala Val Val Thr Asn Pro Lys Glu Gly Gly His His His His His
370 375 380

His
385

<210> 44
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Human TTR NA

<400> 44
ggccaactg gtaccggtga atccaagtgt cctctgatgg tcaaagttct agatgctgtc 60
cgaggcagtc ctgccatcaa tgtggccgtg catgtgttca gaaaggctgc tgatgacacc 120
tgggagccat ttgcctctgg gaaaaccagt gagtctggag agctgcatgg gtcacaact 180
gaggaggaat ttgtagaagg gatatacaaa gtggaaatag acaccaaadc ttactggaag 240
gcacttggca tctccccatt ccatgagcat gcagaggtgg tattcacagc caacgactcc 300
ggccccgcc gctacaccat tgccgccctg ctgagcccct actcctattc caccacggct 360
gtcgtcacca atccaagga a 381