

SEQUENCE LISTING

<110> Nykode Therapeutics AS
 <120> Co-expression of constructs and immunoinhibitory compounds
 <130> P6010PC00
 <160> 179
 <170> PatentIn version 3.5
 <210> 1
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dimerization unit

<400> 1

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Glu Pro Lys Ser
 1 5 10 15

Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser
 20 25 30

Gly Gly Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 35 40 45

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 50 55 60

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 65 70 75 80

Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp
 85 90 95

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 100 105 110

Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala
 115 120 125

Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 130 135 140

<210> 2
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Signal peptide of mIg VH

<400> 2

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
 1 5 10 15

Val Gln Cys

<210> 3
 <211> 650
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VB5049*

<400> 3

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
 1 5 10 15

Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr
 20 25 30

Ser Leu Gly Asn Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile
 35 40 45

Lys Gly Trp Leu Ala Trp Tyr Gln Gln Lys Ser Gly Asn Ala Pro Gln
 50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ile Phe Thr Ile Ser Asn
 85 90 95

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

Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
130 135 140

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Phe Tyr Met Asn
165 170 175

Trp Ile Arg Gln Pro Pro Gly Gln Ala Pro Glu Trp Leu Gly Val Ile
180 185 190

Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Val Asn Thr Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Gln Asn Ile Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly
245 250 255

Gln Gly Val Met Val Thr Val Ser Ser Glu Leu Lys Thr Pro Leu Gly
260 265 270

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys
275 280 285

Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln
290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
 340 345 350

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
 370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Ser Pro
 405 410 415

Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser Pro Phe
 420 425 430

Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp Ala Glu
 435 440 445

Ala Gln Pro Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
 450 455 460

Asp Val Glu Glu Asn Pro Gly Pro Met Pro Gly Ser Ala Leu Leu Cys
 465 470 475 480

Cys Leu Leu Leu Leu Thr Gly Met Arg Ile Ser Arg Gly Gln Tyr Ser
 485 490 495

Arg Glu Asp Asn Asn Cys Thr His Phe Pro Val Gly Gln Ser His Met
 500 505 510

Leu Leu Glu Leu Arg Thr Ala Phe Ser Gln Val Lys Thr Phe Phe Gln
 515 520 525

Thr Lys Asp Gln Leu Asp Asn Ile Leu Leu Thr Asp Ser Leu Met Gln
530 535 540

Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln
545 550 555 560

Phe Tyr Leu Val Glu Val Met Pro Gln Ala Glu Lys His Gly Pro Glu
565 570 575

Ile Lys Glu His Leu Asn Ser Leu Gly Glu Lys Leu Lys Thr Leu Arg
580 585 590

Met Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser
595 600 605

Lys Ala Val Glu Gln Val Lys Ser Asp Phe Asn Lys Leu Gln Asp Gln
610 615 620

Gly Val Tyr Lys Ala Met Asn Glu Phe Asp Ile Phe Ile Asn Cys Ile
625 630 635 640

Glu Ala Tyr Met Met Ile Lys Met Lys Ser
645 650

<210> 4
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> VB5052*

<400> 4

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
1 5 10 15

Leu Cys Asn Gln Val Leu Ser Ala Pro Leu Ala Ala Asp Thr Pro Thr
20 25 30

Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile
35 40 45

Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Ser Val Ile
50 55 60

Phe Leu Thr Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu
65 70 75 80

Trp Ala Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Glu Leu
85 90 95

Lys Thr Pro Leu Gly Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp
100 105 110

Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
130 135 140

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
145 150 155 160

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly
165 170 175

Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp
180 185 190

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
195 200 205

Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His
210 215 220

Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu
225 230 235 240

Gly Gly Leu Ser Pro Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp
245 250 255

Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys
260 265 270

Asp Gln Asp Ala Glu Ala Gln Pro
275 280

<210> 5
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> VB5051*

<400> 5

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln Cys Ser Pro Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp
20 25 30

Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys
35 40 45

Asp Gln Asp Ala Glu Ala Gln Pro
50 55

<210> 6
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving peptide

<400> 6

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 7
<211> 19

<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving peptide

<400> 7

Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn
1				5				10					15		

Pro Gly Pro

<210> 8
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving peptide

<400> 8

Gln	Cys	Thr	Asn	Tyr	Ala	Leu	Leu	Lys	Leu	Ala	Gly	Asp	Val	Glu	Ser
1				5				10					15		

Asn Pro Gly Pro
20

<210> 9
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving peptide

<400> 9

Val	Lys	Gln	Thr	Leu	Asn	Phe	Asp	Leu	Leu	Lys	Leu	Ala	Gly	Asp	Val
1				5				10					15		

Glu Ser Asn Pro Gly Pro
20

<210> 10
<211> 81

<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding amino acids 1-27 of SEQ ID NO: 1

<400> 10

gagctcaaaa cccacttgg tgacacaact cacacagagc ccaaattcttg tgacacacct 60

cccccgtagc caaggtgccc a 81

<210> 11

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding amino acids 38-144 of SEQ ID NO: 1

<400> 11

ggacagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 60

aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag 120

tgggagagca gcgggcagcc ggagaacaac tacaacacca cgcctcccat gctggactcc 180

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 240

aacatcttct catgctccgt gatgcatgag gctctgcaca accgcttcac gcagaagagc 300

ctctccctgt ctccgggtaa a 321

<210> 12

<211> 432

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 1

<400> 12

gagctcaaaa cccacttgg tgacacaact cacacagagc ccaaattcttg tgacacacct 60

cccccgtagc caaggtgccc aggcggtgga agcagcggag gtggaagtgg aggacagccc 120

cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc 180

agcctgacct gcctggtcaa aggcttctac ccagcgcaca tcgccgtgga gtgggagagc 240

agcgggcagc cggagaacaa ctacaacacc acgcctccca tgctggactc cgacggctcc 300

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacatcttc 360
 tcatgctccg tgatgcatga ggctctgcac aaccgcttca cgcagaagag cctctccctg 420
 tctccgggta aa 432

<210> 13
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Signal peptide hCCL3L1

<400> 13

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
 1 5 10 15

Leu Cys Asn Gln Val Leu Ser
 20

<210> 14
 <211> 70
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCCL3L1

<400> 14

Ala Pro Leu Ala Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr
 1 5 10 15

Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser
 20 25 30

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

Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser
 50 55 60

Asp Leu Glu Leu Ser Ala
 65 70

<210> 15
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> scFv with specificity for murine CD205

<400> 15

Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr Ser Leu Gly
1 5 10 15

Asn Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Lys Gly Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Ser Gly Asn Ala Pro Gln Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Tyr Ile Phe Thr Ile Ser Asn Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Gln Ser Phe Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Leu Glu
115 120 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
130 135 140

Ala Ala Ser Gly Phe Thr Phe Asn Asp Phe Tyr Met Asn Trp Ile Arg
145 150 155 160

Gln Pro Pro Gly Gln Ala Pro Glu Trp Leu Gly Val Ile Arg Asn Lys
165 170 175

Gly Asn Gly Tyr Thr Thr Glu Val Asn Thr Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Ser Arg Asp Asn Thr Gln Asn Ile Leu Tyr Leu Gln Met Asn
195 200 205

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

Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly Gln Gly Val
225 230 235 240

Met Val Thr Val Ser Ser
245

<210> 16
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> MOG (27-63)*

<400> 16

Ser Pro Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser
1 5 10 15

Pro Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp
20 25 30

Ala Glu Ala Gln Pro
35

<210> 17
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide mIL-10

<400> 17

Met Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Leu Thr Gly Met

1 5 10 15

Arg Ile

<210> 18
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> mIL-10

<400> 18

Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His Phe Pro
1 5 10 15

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

Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile Leu Leu
35 40 45

Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro Gln Ala
65 70 75 80

Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu Gly Glu
85 90 95

Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser Asp Phe
115 120 125

Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu Phe Asp
130 135 140

Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met Lys Ser

145 150 155 160

<210> 19
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> MOG (27-63)

<400> 19

Ser Pro Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser
1 5 10 15

Pro Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp
 20 25 30

Ala Glu Gln Ala Pro
 35

<210> 20
<211> 862
<212> PRT
<213> Artificial Sequence

<220>
<223> VB5062

<400> 20

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr
 20 25 30

Ser Leu Gly Asn Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile
 35 40 45

Lys Gly Trp Leu Ala Trp Tyr Gln Gln Lys Ser Gly Asn Ala Pro Gln
 50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ile Phe Thr Ile Ser Asn
85 90 95

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

Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
130 135 140

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Phe Tyr Met Asn
165 170 175

Trp Ile Arg Gln Pro Pro Gly Gln Ala Pro Glu Trp Leu Gly Val Ile
180 185 190

Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Val Asn Thr Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Gln Asn Ile Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly
245 250 255

Gln Gly Val Met Val Thr Val Ser Ser Glu Leu Lys Thr Pro Leu Gly
260 265 270

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys
275 280 285

Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln

290

295

300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
 340 345 350

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
 370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Ser Pro
 405 410 415

Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser Pro Phe
 420 425 430

Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp Ala Glu
 435 440 445

Gln Ala Pro Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
 450 455 460

Asp Val Glu Glu Asn Pro Gly Pro Met Pro Pro Ser Gly Leu Arg Leu
 465 470 475 480

Leu Pro Leu Leu Leu Pro Leu Pro Trp Leu Leu Val Leu Thr Pro Gly
 485 490 495

Arg Pro Ala Ala Gly Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu
 500 505 510

Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
515 520 525

Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu Val Pro Pro Gly Pro
530 535 540

Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val
545 550 555 560

Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr
565 570 575

Ala Lys Glu Val Thr Arg Val Leu Met Val Asp Arg Asn Asn Ala Ile
580 585 590

Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile Tyr Met Phe Phe Asn
595 600 605

Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro Pro Leu Leu Ser Arg
610 615 620

Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser Val Glu Gln His Val
625 630 635 640

Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp Arg Tyr Leu Gly Asn
645 650 655

Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp Leu Ser Phe Asp Val
660 665 670

Thr Gly Val Val Arg Gln Trp Leu Asn Gln Gly Asp Gly Ile Gln Gly
675 680 685

Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser Lys Asp Asn Lys Leu
690 695 700

His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg Arg Gly Asp Leu Gly
705 710 715 720

Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro

725

730

735

Leu Glu Arg Ala Gln His Leu His Ser Ser Arg His Arg Arg Ala Leu
740 745 750

Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
755 760 765

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
770 775 780

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
785 790 795 800

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
805 810 815

Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Ala
820 825 830

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
835 840 845

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
850 855 860

<210> 21

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> VB5063

<400> 21

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr
20 25 30

Ser Leu Gly Asn Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile

35

40

45

Lys Gly Trp Leu Ala Trp Tyr Gln Gln Lys Ser Gly Asn Ala Pro Gln
 50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ile Phe Thr Ile Ser Asn
 85 90 95

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

Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
 130 135 140

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Phe Tyr Met Asn
 165 170 175

Trp Ile Arg Gln Pro Pro Gly Gln Ala Pro Glu Trp Leu Gly Val Ile
 180 185 190

Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Val Asn Thr Ser Val Lys
 195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Gln Asn Ile Leu Tyr Leu
 210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
 225 230 235 240

Arg Gly Gly Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly
 245 250 255

Gln Gly Val Met Val Thr Val Ser Ser Glu Leu Lys Thr Pro Leu Gly
260 265 270

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys
275 280 285

Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln
290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
340 345 350

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Ser Pro
405 410 415

Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser Pro Phe
420 425 430

Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp Ala Glu
435 440 445

Gln Ala Pro Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
450 455 460

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Cys Leu Gly Leu Arg Arg

465 470 475 480
 Tyr Lys Ala Gln Leu Gln Leu Pro Ser Arg Thr Trp Pro Phe Val Ala
 485 490 495
 Leu Leu Thr Leu Leu Phe Ile Pro Val Phe Ser Glu Ala Ile Gln Val
 500 505 510
 Thr Gln Pro Ser Val Val Leu Ala Ser Ser His Gly Val Ala Ser Phe
 515 520 525
 Pro Cys Glu Tyr Ser Pro Ser His Asn Thr Asp Glu Val Arg Val Thr
 530 535 540
 Val Leu Arg Gln Thr Asn Asp Gln Met Thr Glu Val Cys Ala Thr Thr
 545 550 555 560
 Phe Thr Glu Lys Asn Thr Val Gly Phe Leu Asp Tyr Pro Phe Cys Ser
 565 570 575
 Gly Thr Phe Asn Glu Ser Arg Val Asn Leu Thr Ile Gln Gly Leu Arg
 580 585 590
 Ala Val Asp Thr Gly Leu Tyr Leu Cys Lys Val Glu Leu Met Tyr Pro
 595 600 605
 Pro Pro Tyr Phe Val Gly Met Gly Asn Gly Thr Gln Ile Tyr Val Ile
 610 615 620
 Asp Pro Glu Pro Cys Pro Asp Ser Asp
 625 630

 <210> 22
 <211> 583
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> VB5064

 <400> 22
 Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly

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

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
 225 230 235 240

Arg Gly Gly Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly
 245 250 255

Gln Gly Val Met Val Thr Val Ser Ser Glu Leu Lys Thr Pro Leu Gly
 260 265 270

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys
 275 280 285

Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln
 290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
 340 345 350

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
 370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Met Tyr
 405 410 415

Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu Leu Val
 420 425 430

Asn Ser Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala Glu Ala

435

440

445

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu Glu Gln
 450 455 460

Leu Leu Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn Tyr Arg
 465 470 475 480

Asn Leu Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu Pro Lys
 485 490 495

Gln Ala Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu Leu Gly
 500 505 510

Pro Leu Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe Gln Leu
 515 520 525

Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val Val Lys
 530 535 540

Leu Lys Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp Glu Ser
 545 550 555 560

Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys Gln Ser
 565 570 575

Ile Ile Ser Thr Ser Pro Gln
 580

<210> 23
 <211> 569
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VB5065

<400> 23

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
 1 5 10 15

Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr

30

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly
245 250 255

Gln Gly Val Met Val Thr Val Ser Ser Glu Leu Lys Thr Pro Leu Gly
260 265 270

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys
275 280 285

Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln
290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
340 345 350

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Met Asn
405 410 415

Ala Thr His Cys Ile Leu Ala Leu Gln Leu Phe Leu Met Ala Val Ser
420 425 430

Gly Cys Tyr Cys His Gly Thr Val Ile Glu Ser Leu Glu Ser Leu Asn
435 440 445

Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser Leu Phe

450

455

460

Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys Ile Leu
 465 470 475 480

Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys
 485 490 495

Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser His Leu
 500 505 510

Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala Phe Met
 515 520 525

Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg Gln Ala
 530 535 540

Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu Ser Ser
 545 550 555 560

Leu Arg Lys Arg Lys Arg Ser Arg Cys
 565

<210> 24

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide mTGF beta 1

<400> 24

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
 1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
 20 25

<210> 25

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> mTGF beta 1

<400> 25

Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
1 5 10 15

Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
20 25 30

Pro Pro Ser Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val
35 40 45

Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala
50 55 60

Asp Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr
65 70 75 80

Arg Val Leu Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys
85 90 95

Asp Ile Ser His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg
100 105 110

Glu Ala Val Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu
115 120 125

Gln Arg Leu Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys
130 135 140

Tyr Ser Asn Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro
145 150 155 160

Thr Asp Thr Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg
165 170 175

Gln Trp Leu Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala
180 185 190

His Cys Ser Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn

195

200

205

Gly Ile Ser Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met
 210 215 220

Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln
 225 230 235 240

His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys
 245 250 255

Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp
 260 265 270

Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr
 275 280 285

His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp
 290 295 300

Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly
 305 310 315 320

Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro
 325 330 335

Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn
 340 345 350

Met Ile Val Arg Ser Cys Lys Cys Ser
 355 360

<210> 26

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide mCLTA-4

<400> 26

Met Ala Cys Leu Gly Leu Arg Arg Tyr Lys Ala Gln Leu Gln Leu Pro

1	5	10	15
Ser	Arg	Thr	Trp
			20
Pro	Phe	Val	Ala
			25
Leu	Leu	Thr	Leu
			30
Phe	Ile	Pro	
Val	Phe	Ser	
		35	
<210> 27			
<211> 126			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> mCLTA-4 extracellular domain			
<220>			
<221> DOMAIN			
<222> (1)..(126)			
<223> extracellular domain			
<400> 27			
Glu	Ala	Ile	Gln
			5
Val	Thr	Gln	Pro
			10
Ser	Val	Val	Leu
			15
Ala	Ser	Ser	His
Gly	Val	Ala	Ser
			20
Phe	Pro	Cys	Glu
			25
Tyr	Ser	Pro	Ser
			30
His	Asn	Thr	Asp
Glu	Val	Arg	Val
			35
Thr	Val	Leu	Arg
			40
Gln	Thr	Asn	Asp
			45
Gln	Met	Thr	Glu
Val	Cys	Ala	Thr
			50
Thr	Phe	Thr	Glu
			55
Lys	Asn	Thr	Val
			60
Gly	Phe	Leu	Asp
Tyr	Pro	Phe	Cys
			65
Ser	Gly	Thr	Phe
			70
Asn	Glu	Ser	Arg
			75
Val	Asn	Leu	Thr
			80
Ile	Gln	Gly	Leu
			85
Arg	Ala	Val	Asp
			90
Thr	Gly	Leu	Tyr
			95
Cys	Lys	Val	
Glu	Leu	Met	Tyr
			100
Pro	Pro	Pro	Tyr
			105
Phe	Val	Gly	Met
			110
Gly	Asn	Gly	Thr

Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
115 120 125

<210> 28
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide mIL-2

<400> 28

Met Tyr Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu
1 5 10 15

Leu Val Asn Ser
20

<210> 29
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> mIL-2

<400> 29

Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala Glu Ala Gln Gln
1 5 10 15

Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu Glu Gln Leu Leu
20 25 30

Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn Tyr Arg Asn Leu
35 40 45

Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu Pro Lys Gln Ala
50 55 60

Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu Leu Gly Pro Leu
65 70 75 80

Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe Gln Leu Glu Asp

85

90

95

Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val Val Lys Leu Lys
 100 105 110

Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp Glu Ser Ala Thr
 115 120 125

Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys Gln Ser Ile Ile
 130 135 140

Ser Thr Ser Pro Gln
 145

<210> 30
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Signal peptide mIFN gamma

<400> 30

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

Val Ser Gly Cys Tyr Cys
 20

<210> 31
 <211> 133
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mIFN gamma

<400> 31

His Gly Thr Val Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe Asn
 1 5 10 15

Ser Ser Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp
 20 25 30

Arg Asn Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile
35 40 45

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

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

Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys
85 90 95

Phe Glu Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu
100 105 110

Ile Arg Val Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg
115 120 125

Lys Arg Ser Arg Cys
130

<210> 32
<211> 650
<212> PRT
<213> Artificial Sequence

<220>
<223> VB5049

<400> 32

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr
20 25 30

Ser Leu Gly Asn Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile
35 40 45

Lys Gly Trp Leu Ala Trp Tyr Gln Gln Lys Ser Gly Asn Ala Pro Gln
50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ile Phe Thr Ile Ser Asn
85 90 95

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

Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
130 135 140

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Phe Tyr Met Asn
165 170 175

Trp Ile Arg Gln Pro Pro Gly Gln Ala Pro Glu Trp Leu Gly Val Ile
180 185 190

Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Val Asn Thr Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Gln Asn Ile Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly
245 250 255

Gln Gly Val Met Val Thr Val Ser Ser Glu Leu Lys Thr Pro Leu Gly
260 265 270

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys

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

Arg Glu Asp Asn Asn Cys Thr His Phe Pro Val Gly Gln Ser His Met
500 505 510

Leu Leu Glu Leu Arg Thr Ala Phe Ser Gln Val Lys Thr Phe Phe Gln
515 520 525

Thr Lys Asp Gln Leu Asp Asn Ile Leu Leu Thr Asp Ser Leu Met Gln
530 535 540

Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln
545 550 555 560

Phe Tyr Leu Val Glu Val Met Pro Gln Ala Glu Lys His Gly Pro Glu
565 570 575

Ile Lys Glu His Leu Asn Ser Leu Gly Glu Lys Leu Lys Thr Leu Arg
580 585 590

Met Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser
595 600 605

Lys Ala Val Glu Gln Val Lys Ser Asp Phe Asn Lys Leu Gln Asp Gln
610 615 620

Gly Val Tyr Lys Ala Met Asn Glu Phe Asp Ile Phe Ile Asn Cys Ile
625 630 635 640

Glu Ala Tyr Met Met Ile Lys Met Lys Ser
645 650

<210> 33
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> VB5052

<400> 33

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
1 5 10 15

Leu Cys Asn Gln Val Leu Ser Ala Pro Leu Ala Ala Asp Thr Pro Thr
20 25 30

Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile
35 40 45

Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Ser Val Ile
50 55 60

Phe Leu Thr Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu
65 70 75 80

Trp Ala Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Glu Leu
85 90 95

Lys Thr Pro Leu Gly Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp
100 105 110

Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
130 135 140

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
145 150 155 160

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly
165 170 175

Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp
180 185 190

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
195 200 205

Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His
210 215 220

Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu

225						230						235						240
Gly	Gly	Leu	Ser	Pro	Gly	Lys	Asn	Ala	Thr	Gly	Met	Glu	Val	Gly	Trp			
				245					250					255				
Tyr	Arg	Ser	Pro	Phe	Ser	Arg	Val	Val	His	Leu	Tyr	Arg	Asn	Gly	Lys			
			260					265					270					
Asp	Gln	Asp	Ala	Glu	Gln	Ala	Pro											
		275					280											

Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr
 20 25 30

Ser Leu Gly Asn Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile
 35 40 45

Lys Gly Trp Leu Ala Trp Tyr Gln Gln Lys Ser Gly Asn Ala Pro Gln
 50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ile Phe Thr Ile Ser Asn
 85 90 95

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

Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
 130 135 140

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Phe Tyr Met Asn
 165 170 175

Trp Ile Arg Gln Pro Pro Gly Gln Ala Pro Glu Trp Leu Gly Val Ile
 180 185 190

Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Val Asn Thr Ser Val Lys
 195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Gln Asn Ile Leu Tyr Leu
 210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala

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

Gln Ala Pro
450

<210> 36
<211> 1062
<212> PRT
<213> Artificial Sequence

<220>
<223> VB5044

<400> 36

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr
20 25 30

Ser Leu Gly Asn Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile
35 40 45

Lys Gly Trp Leu Ala Trp Tyr Gln Gln Lys Ser Gly Asn Ala Pro Gln
50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ile Phe Thr Ile Ser Asn
85 90 95

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

Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
130 135 140

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Phe Tyr Met Asn
165 170 175

Trp Ile Arg Gln Pro Pro Gly Gln Ala Pro Glu Trp Leu Gly Val Ile
180 185 190

Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Val Asn Thr Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Gln Asn Ile Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly
245 250 255

Gln Gly Val Met Val Thr Val Ser Ser Glu Leu Lys Thr Pro Leu Gly
260 265 270

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys
275 280 285

Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln
290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
340 345 350

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile

370

375

380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Ser Pro
 405 410 415

Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser Pro Phe
 420 425 430

Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp Ala Glu
 435 440 445

Gln Ala Pro Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
 450 455 460

Asp Val Glu Glu Asn Pro Gly Pro Met Pro Gly Ser Ala Leu Leu Cys
 465 470 475 480

Cys Leu Leu Leu Leu Thr Gly Met Arg Ile Ser Arg Gly Gln Tyr Ser
 485 490 495

Arg Glu Asp Asn Asn Cys Thr His Phe Pro Val Gly Gln Ser His Met
 500 505 510

Leu Leu Glu Leu Arg Thr Ala Phe Ser Gln Val Lys Thr Phe Phe Gln
 515 520 525

Thr Lys Asp Gln Leu Asp Asn Ile Leu Leu Thr Asp Ser Leu Met Gln
 530 535 540

Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln
 545 550 555 560

Phe Tyr Leu Val Glu Val Met Pro Gln Ala Glu Lys His Gly Pro Glu
 565 570 575

Ile Lys Glu His Leu Asn Ser Leu Gly Glu Lys Leu Lys Thr Leu Arg
 580 585 590

Met Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser
595 600 605

Lys Ala Val Glu Gln Val Lys Ser Asp Phe Asn Lys Leu Gln Asp Gln
610 615 620

Gly Val Tyr Lys Ala Met Asn Glu Phe Asp Ile Phe Ile Asn Cys Ile
625 630 635 640

Glu Ala Tyr Met Met Ile Lys Met Lys Ser Gly Ser Gly Ala Thr Asn
645 650 655

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
660 665 670

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
675 680 685

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
690 695 700

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
705 710 715 720

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
725 730 735

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
740 745 750

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
755 760 765

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
770 775 780

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
785 790 795 800

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val

45/122

Ala Ser Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
1025 1030 1035

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn
1040 1045 1050

Met Ile Val Arg Ser Cys Lys Cys Ser
1055 1060

<210> 37
<211> 1224
<212> PRT
<213> Artificial Sequence

<220>
<223> VB5054

<400> 37

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr
20 25 30

Ser Leu Gly Asn Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile
35 40 45

Lys Gly Trp Leu Ala Trp Tyr Gln Gln Lys Ser Gly Asn Ala Pro Gln
50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ile Phe Thr Ile Ser Asn
85 90 95

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

Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
130 135 140

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Phe Tyr Met Asn
165 170 175

Trp Ile Arg Gln Pro Pro Gly Gln Ala Pro Glu Trp Leu Gly Val Ile
180 185 190

Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Val Asn Thr Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Gln Asn Ile Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly
245 250 255

Gln Gly Val Met Val Thr Val Ser Ser Glu Leu Lys Thr Pro Leu Gly
260 265 270

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys
275 280 285

Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln
290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn

48/122

Phe Tyr Leu Val Glu Val Met Pro Gln Ala Glu Lys His Gly Pro Glu
565 570 575

Ile Lys Glu His Leu Asn Ser Leu Gly Glu Lys Leu Lys Thr Leu Arg
580 585 590

Met Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser
595 600 605

Lys Ala Val Glu Gln Val Lys Ser Asp Phe Asn Lys Leu Gln Asp Gln
610 615 620

Gly Val Tyr Lys Ala Met Asn Glu Phe Asp Ile Phe Ile Asn Cys Ile
625 630 635 640

Glu Ala Tyr Met Met Ile Lys Met Lys Ser Gly Ser Gly Ala Thr Asn
645 650 655

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
660 665 670

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
675 680 685

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
690 695 700

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
705 710 715 720

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
725 730 735

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
740 745 750

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
755 760 765

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu

770

775

780

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
785 790 795 800

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
805 810 815

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
820 825 830

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
835 840 845

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
850 855 860

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
865 870 875 880

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
885 890 895

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
900 905 910

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
915 920 925

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
930 935 940

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
945 950 955 960

Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys
965 970 975

Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn
980 985 990

Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr
 995 1000 1005

Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
 1010 1015 1020

Ala Ser Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
 1025 1030 1035

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn
 1040 1045 1050

Met Ile Val Arg Ser Cys Lys Cys Ser Gly Ser Gly Glu Gly Arg
 1055 1060 1065

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
 1070 1075 1080

Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Ile Val Val Tyr Ser
 1085 1090 1095

Leu Ser Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp
 1100 1105 1110

Lys His Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp
 1115 1120 1125

Met Pro Val Thr Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu
 1130 1135 1140

Phe Ser Phe Lys Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile
 1145 1150 1155

Phe Glu Gln Gly Leu Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala
 1160 1165 1170

Leu Asn Met Thr Ala Ser Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr
 1175 1180 1185

Pro Glu Thr Asp Cys Glu Thr Gln Val Thr Thr Tyr Ala Asp Phe

1190

1195

1200

Ile Asp Ser Leu Lys Thr Phe Leu Thr Asp Ile Pro Phe Glu Cys
 1205 1210 1215

Lys Lys Pro Val Gln Lys
 1220

<210> 38
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Signal peptide mGM-CSF

<400> 38

Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Ile Val Val Tyr Ser Leu
 1 5 10 15

Ser

<210> 39
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mGM-CSF

<400> 39

Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His Val
 1 5 10 15

Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val Thr
 20 25 30

Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys Lys
 35 40 45

Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu Arg
 50 55 60

Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser Tyr
65 70 75 80

Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr Gln
85 90 95

Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu Thr
100 105 110

Asp Ile Pro Phe Glu Cys Lys Lys Pro Val Gln Lys
115 120

<210> 40
<211> 476
<212> PRT
<213> Artificial Sequence

<220>
<223> VB5068

<400> 40

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

Tyr Ser Ala Thr Ala Leu Leu Ile Asn Arg Leu Pro Val Val Asp Lys
20 25 30

Leu Pro Val Pro Leu Asp Asp Ile Ile Pro Ser Phe Asp Pro Leu Lys
35 40 45

Met Leu Leu Lys Thr Leu Gly Ile Ser Val Glu His Leu Val Thr Gly
50 55 60

Leu Lys Lys Cys Val Asp Glu Leu Gly Pro Glu Ala Ser Glu Ala Val
65 70 75 80

Lys Lys Leu Leu Glu Ala Leu Ser His Leu Val Glu Leu Lys Thr Pro
85 90 95

Leu Gly Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro
100 105 110

Pro Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly
115 120 125

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
130 135 140

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu
165 170 175

Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
180 185 190

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
195 200 205

Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
210 215 220

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu
225 230 235 240

Ser Pro Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser
245 250 255

Pro Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp
260 265 270

Ala Glu Gln Ala Pro Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
275 280 285

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro Gly Ser Ala Leu
290 295 300

Leu Cys Cys Leu Leu Leu Leu Thr Gly Met Arg Ile Ser Arg Gly Gln
305 310 315 320

Tyr Ser Arg Glu Asp Asn Asn Cys Thr His Phe Pro Val Gly Gln Ser

325

330

335

His Met Leu Leu Glu Leu Arg Thr Ala Phe Ser Gln Val Lys Thr Phe
 340 345 350

Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile Leu Leu Thr Asp Ser Leu
 355 360 365

Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
 370 375 380

Ile Gln Phe Tyr Leu Val Glu Val Met Pro Gln Ala Glu Lys His Gly
 385 390 395 400

Pro Glu Ile Lys Glu His Leu Asn Ser Leu Gly Glu Lys Leu Lys Thr
 405 410 415

Leu Arg Met Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
 420 425 430

Lys Ser Lys Ala Val Glu Gln Val Lys Ser Asp Phe Asn Lys Leu Gln
 435 440 445

Asp Gln Gly Val Tyr Lys Ala Met Asn Glu Phe Asp Ile Phe Ile Asn
 450 455 460

Cys Ile Glu Ala Tyr Met Met Ile Lys Met Lys Ser
 465 470 475

<210> 41
 <211> 625
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VB5069

<400> 41

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

Leu Gly Val Ala Thr Ser Leu Glu Val Ser Glu Ser Pro Gly Ser Val

30

Thr Cys Leu Leu Asp Leu Gln Val Ile Ser Pro Gln Pro Arg Ser Val
225 230 235 240

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Glu Pro Lys Ser
245 250 255

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

Gly Gly Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
275 280 285

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
290 295 300

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
305 310 315 320

Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp
325 330 335

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
340 345 350

Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala
355 360 365

Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

Gly Leu Gly Gly Leu Ser Pro Gly Lys Asn Ala Thr Gly Met Glu Val
385 390 395 400

Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu Tyr Arg Asn
405 410 415

Gly Lys Asp Gln Asp Ala Glu Gln Ala Pro Gly Ser Gly Glu Gly Arg
420 425 430

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
435 440 445

Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Leu Thr Gly Met Arg

450

455

460

Ile Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His Phe
 465 470 475 480

Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe Ser
 485 490 495

Gln Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile Leu
 500 505 510

Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys Gln
 515 520 525

Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro Gln
 530 535 540

Ala Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu Gly
 545 550 555 560

Glu Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg Phe
 565 570 575

Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser Asp
 580 585 590

Phe Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu Phe
 595 600 605

Asp Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met Lys
 610 615 620

Ser
 625

<210> 42
 <211> 554
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VB5070

<400> 42

Met Trp Val Arg Gln Val Pro Trp Ser Phe Thr Trp Ala Val Leu Gln
1 5 10 15

Leu Ser Trp Gln Ser Gly Trp Leu Leu Glu Val Pro Asn Gly Pro Trp
20 25 30

Arg Ser Leu Thr Phe Tyr Pro Ala Trp Leu Thr Val Ser Glu Gly Ala
35 40 45

Asn Ala Thr Phe Thr Cys Ser Leu Ser Asn Trp Ser Glu Asp Leu Met
50 55 60

Leu Asn Trp Asn Arg Leu Ser Pro Ser Asn Gln Thr Glu Lys Gln Ala
65 70 75 80

Ala Phe Cys Asn Gly Leu Ser Gln Pro Val Gln Asp Ala Arg Phe Gln
85 90 95

Ile Ile Gln Leu Pro Asn Arg His Asp Phe His Met Asn Ile Leu Asp
100 105 110

Thr Arg Arg Asn Asp Ser Gly Ile Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125

His Pro Lys Ala Lys Ile Glu Glu Ser Pro Gly Ala Glu Leu Val Val
130 135 140

Thr Glu Arg Ile Leu Glu Thr Ser Thr Arg Tyr Pro Ser Pro Ser Pro
145 150 155 160

Lys Pro Glu Gly Arg Phe Gln Gly Met Glu Leu Lys Thr Pro Leu Gly
165 170 175

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys
180 185 190

Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln
195 200 205

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 210 215 220

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 225 230 235 240

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
 245 250 255

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 260 265 270

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
 275 280 285

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 290 295 300

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Ser Pro
 305 310 315 320

Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser Pro Phe
 325 330 335

Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp Ala Glu
 340 345 350

Gln Ala Pro Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
 355 360 365

Asp Val Glu Glu Asn Pro Gly Pro Met Pro Gly Ser Ala Leu Leu Cys
 370 375 380

Cys Leu Leu Leu Leu Thr Gly Met Arg Ile Ser Arg Gly Gln Tyr Ser
 385 390 395 400

Arg Glu Asp Asn Asn Cys Thr His Phe Pro Val Gly Gln Ser His Met
 405 410 415

Leu Leu Glu Leu Arg Thr Ala Phe Ser Gln Val Lys Thr Phe Phe Gln

420

425

430

Thr Lys Asp Gln Leu Asp Asn Ile Leu Leu Thr Asp Ser Leu Met Gln
 435 440 445

Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln
 450 455 460

Phe Tyr Leu Val Glu Val Met Pro Gln Ala Glu Lys His Gly Pro Glu
 465 470 475 480

Ile Lys Glu His Leu Asn Ser Leu Gly Glu Lys Leu Lys Thr Leu Arg
 485 490 495

Met Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser
 500 505 510

Lys Ala Val Glu Gln Val Lys Ser Asp Phe Asn Lys Leu Gln Asp Gln
 515 520 525

Gly Val Tyr Lys Ala Met Asn Glu Phe Asp Ile Phe Ile Asn Cys Ile
 530 535 540

Glu Ala Tyr Met Met Ile Lys Met Lys Ser
 545 550

<210> 43

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide mSCGB3A2

<400> 43

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

Tyr Ser Ala Thr Ala
 20

<210> 44

<211> 70
<212> PRT
<213> Artificial Sequence

<220>
<223> mSCGB3A2

<400> 44

Leu Leu Ile Asn Arg Leu Pro Val Val Asp Lys Leu Pro Val Pro Leu
1 5 10 15

Asp Asp Ile Ile Pro Ser Phe Asp Pro Leu Lys Met Leu Leu Lys Thr
20 25 30

Leu Gly Ile Ser Val Glu His Leu Val Thr Gly Leu Lys Lys Cys Val
35 40 45

Asp Glu Leu Gly Pro Glu Ala Ser Glu Ala Val Lys Lys Leu Leu Glu
50 55 60

Ala Leu Ser His Leu Val
65 70

<210> 45
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide mVSIG3

<400> 45

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

Leu Gly Val Ala Thr Ser
20

<210> 46
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> mVSIG3 extracellular domain

<220>

<221> DOMAIN

<222> (1)..(218)

<223> extracellular domain

<400> 46

Leu Glu Val Ser Glu Ser Pro Gly Ser Val Gln Val Ala Arg Gly Gln
1 5 10 15

Thr Ala Val Leu Pro Cys Ala Phe Ser Thr Ser Ala Ala Leu Leu Asn
20 25 30

Leu Asn Val Ile Trp Met Val Ile Pro Leu Ser Asn Ala Asn Gln Pro
35 40 45

Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met Phe Asp Gly Ala Leu
50 55 60

Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr Met Pro Ala Thr Asn
65 70 75 80

Val Ser Ile Phe Ile Asn Asn Thr Gln Leu Ser Asp Thr Gly Thr Tyr
85 90 95

Gln Cys Leu Val Asn Asn Leu Pro Asp Arg Gly Gly Arg Asn Ile Gly
100 105 110

Val Thr Gly Leu Thr Val Leu Val Pro Pro Ser Ala Pro Gln Cys Gln
115 120 125

Ile Gln Gly Ser Gln Asp Leu Gly Ser Asp Val Ile Leu Leu Cys Ser
130 135 140

Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu Trp Glu Lys Leu Asp
145 150 155 160

Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln Asp Gln Val Gln Gly
165 170 175

Thr Val Thr Ile Arg Asn Ile Ser Ala Leu Ser Ser Gly Leu Tyr Gln

180

185

190

Cys Val Ala Ser Asn Ala Ile Gly Thr Ser Thr Cys Leu Leu Asp Leu
 195 200 205

Gln Val Ile Ser Pro Gln Pro Arg Ser Val
 210 215

<210> 47
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Signal peptide mPD-1

<400> 47

Met Trp Val Arg Gln Val Pro Trp Ser Phe Thr Trp Ala Val Leu Gln
 1 5 10 15

Leu Ser Trp Gln Ser Gly Trp Leu
 20

<210> 48
 <211> 145
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mPD-1 extracellular domain

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> extracellular domain

<400> 48

Leu Glu Val Pro Asn Gly Pro Trp Arg Ser Leu Thr Phe Tyr Pro Ala
 1 5 10 15

Trp Leu Thr Val Ser Glu Gly Ala Asn Ala Thr Phe Thr Cys Ser Leu
 20 25 30

Ser Asn Trp Ser Glu Asp Leu Met Leu Asn Trp Asn Arg Leu Ser Pro

35

40

45

Ser Asn Gln Thr Glu Lys Gln Ala Ala Phe Cys Asn Gly Leu Ser Gln
 50 55 60

Pro Val Gln Asp Ala Arg Phe Gln Ile Ile Gln Leu Pro Asn Arg His
 65 70 75 80

Asp Phe His Met Asn Ile Leu Asp Thr Arg Arg Asn Asp Ser Gly Ile
 85 90 95

Tyr Leu Cys Gly Ala Ile Ser Leu His Pro Lys Ala Lys Ile Glu Glu
 100 105 110

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

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

Met
 145

<210> 49
 <211> 784
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VB5076

<400> 49

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
 1 5 10 15

Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Thr
 20 25 30

Ser Leu Gly Asn Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile
 35 40 45

Lys Gly Trp Leu Ala Trp Tyr Gln Gln Lys Ser Gly Asn Ala Pro Gln

50

55

60

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ile Phe Thr Ile Ser Asn
85 90 95

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

Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
130 135 140

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Phe Tyr Met Asn
165 170 175

Trp Ile Arg Gln Pro Pro Gly Gln Ala Pro Glu Trp Leu Gly Val Ile
180 185 190

Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Val Asn Thr Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Gln Asn Ile Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
225 230 235 240

Arg Gly Gly Pro Tyr Tyr Tyr Ser Gly Asp Asp Ala Pro Tyr Trp Gly
245 250 255

Gln Gly Val Met Val Thr Val Ser Ser Glu Leu Lys Thr Pro Leu Gly
260 265 270

Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys
275 280 285

Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln
290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
340 345 350

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Lys Glu
405 410 415

Val Asp Arg Leu Glu Asp Glu Leu Val Asn Glu Lys Glu Lys Tyr Lys
420 425 430

Ser Ile Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Tyr Lys Glu
435 440 445

Gln Ile Lys Thr Leu Thr Asn Lys Leu Lys Ala Ala Glu Ala Arg Ala
450 455 460

Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Gln Leu Lys Glu
465 470 475 480

Ala Arg Phe Leu Ala Glu Glu Ala Asp Arg Lys Tyr Asp Glu Val Gly

485

490

495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Leu Asn Arg Arg Ile
500 505 510

Gln Leu Leu Glu Glu Asp Leu Glu Arg Ser Glu Glu Arg Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Asp Leu Asp Gln Val Gln Glu Ser Leu
530 535 540

Leu Lys Ala Asn Asn Gln Leu Val Glu Lys Asp Gly Gly Gly Gly Ser
545 550 555 560

Gly Gly Gly Gly Ser Glu Gln Gln Asn Lys Glu Ala Asn Asn Arg Ala
565 570 575

Glu Lys Ser Glu Glu Glu Val His Asn Gly Ser Gly Glu Gly Arg Gly
580 585 590

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro
595 600 605

Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Leu Thr Gly Met Arg Ile
610 615 620

Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His Phe Pro
625 630 635 640

Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe Ser Gln
645 650 655

Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile Leu Leu
660 665 670

Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
675 680 685

Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro Gln Ala
690 695 700

Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu Gly Glu
705 710 715 720

Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg Phe Leu
725 730 735

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser Asp Phe
740 745 750

Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu Phe Asp
755 760 765

Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met Lys Ser
770 775 780

<210> 50
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Met e 1

<400> 50

Lys Glu Val Asp Arg Leu Glu Asp Glu Leu Val Asn Glu Lys Glu Lys
1 5 10 15

Tyr Lys Ser Ile Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Tyr
20 25 30

Lys Glu Gln Ile Lys Thr Leu Thr Asn Lys Leu Lys Ala Ala Glu Ala
35 40 45

Arg Ala Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Gln Leu
50 55 60

Lys Glu Ala Arg Phe Leu Ala Glu Glu Ala Asp Arg Lys Tyr Asp Glu
65 70 75 80

Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Leu Asn Arg
85 90 95

Arg Ile Gln Leu Leu Glu Glu Asp Leu Glu Arg Ser Glu Glu Arg Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Leu Asp Gln Val Gln Glu
115 120 125

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

Gly Ser Gly Gly Gly Gly Ser Glu Gln Gln Asn Lys Glu Ala Asn Asn
145 150 155 160

Arg Ala Glu Lys Ser Glu Glu Glu Val His Asn
165 170

<210> 51
<211> 161
<212> PRT
<213> Artificial Sequence

<220>
<223> hCTLA4 extracellular domain

<220>
<221> SIGNAL
<222> (1)..(35)
<223> Signal peptide

<220>
<221> DOMAIN
<222> (36)..(161)
<223> extracellular domain

<400> 51

Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1 5 10 15

Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20 25 30

Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

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

Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
 65 70 75 80

Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
 85 90 95

Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
 100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160

Asp

<210> 52
 <211> 170
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hPD-1 extracellular domain

<220>
 <221> SIGNAL
 <222> (1)..(23)
 <223> signal peptide

<220>
 <221> DOMAIN
 <222> (24)..(170)
 <223> extracellular domain

<400> 52

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln

1	5	10	15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp	20	25	30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp	35	40	45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val	50	55	60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala	65	70	75
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg	85	90	95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg	100	105	110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu	115	120	125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val	130	135	140
Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro	145	150	155
Arg Pro Ala Gly Gln Phe Gln Thr Leu Val	165	170	

<210> 53
 <211> 178
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hIL-10

<220>
 <221> SIGNAL

<222> (1)..(18)

<223> signal peptide

<400> 53

Met His Ser Ser Ala Leu Leu Cys Cys Leu Val Leu Leu Thr Gly Val
1 5 10 15

Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
20 25 30

Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe
35 40 45

Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
50 55 60

Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
65 70 75 80

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
85 90 95

Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
100 105 110

Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg
115 120 125

Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
130 135 140

Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
145 150 155 160

Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
165 170 175

Arg Asn

<210> 54

<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> hTGF beta - 1

<220>
<221> SIGNAL
<222> (1)..(29)
<223> signal peptide

<400> 54

Met Pro Pro Ser Gly Leu Arg Leu Leu Leu Leu Leu Leu Pro Leu Leu
1 5 10 15

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

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

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

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe Thr
225 230 235 240

Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu Gln
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
275 280 285

Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys
290 295 300

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

Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr
325 330 335

Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala
340 345 350

Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr
355 360 365

Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val

370

375

380

Arg Ser Cys Lys Cys Ser
385 390

<210> 55
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> hIL-2

<220>
<221> SIGNAL
<222> (1)..(20)
<223> signal peptide

<400> 55

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

Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
20 25 30

Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
35 40 45

Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
50 55 60

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65 70 75 80

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
85 90 95

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
100 105 110

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
115 120 125

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
130 135 140

Cys Gln Ser Ile Ile Ser Thr Leu Thr
145 150

<210> 56
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> hGM-CSF

<220>
<221> SIGNAL
<222> (1)..(17)
<223> signal peptide

<400> 56

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys

115

120

125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 130 135 140

<210> 57

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> hIFN- gamma

<220>

<221> SIGNAL

<222> (1)..(23)

<223> signal peptide

<400> 57

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

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
 20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
 35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
 50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
 65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
 85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
 100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
 115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145 150 155 160

Gly Arg Arg Ala Ser Gln
165

<210> 58
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> hTGF beta 2

<400> 58

Met His Tyr Cys Val Leu Ser Ala Phe Leu Ile Leu His Leu Val Thr
1 5 10 15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Glu Glu Val Pro
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Asp Glu
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Pro Phe Phe
100 105 110

Pro Ser Glu Thr Val Cys Pro Val Val Thr Thr Pro Ser Gly Ser Val
115 120 125

Gly Ser Leu Cys Ser Arg Gln Ser Gln Val Leu Cys Gly Tyr Leu Asp
130 135 140

Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg Ile Val Arg Phe
145 150 155 160

Asp Val Ser Ala Met Glu Lys Asn Ala Ser Asn Leu Val Lys Ala Glu
165 170 175

Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg Val Pro Glu Gln
180 185 190

Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp Leu Thr Ser Pro
195 200 205

Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr Arg Ala Glu Gly
210 215 220

Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val His Glu Trp Leu His
225 230 235 240

His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu His Cys Pro Cys
245 250 255

Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro Asn Lys Ser Glu
260 265 270

Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr Ser Thr Tyr Thr
275 280 285

Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys Lys Asn Ser Gly
290 295 300

Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser Tyr Arg Leu Glu
305 310 315 320

Ser Gln Gln Thr Asn Arg Arg Lys Lys Arg Ala Leu Asp Ala Ala Tyr
325 330 335

Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr Ile

340 345 350
 Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly
 355 360 365

 Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser Ser
 370 375 380

 Asp Thr Gln His Ser Arg Val Leu Ser Leu Tyr Asn Thr Ile Asn Pro
 385 390 395 400

 Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro Leu
 405 410 415

 Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro Lys Ile Glu Gln Leu Ser
 420 425 430

 Asn Met Ile Val Lys Ser Cys Lys Cys Ser
 435 440

 <210> 59
 <211> 412
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> hTGF beta 3

 <400> 59

 Met Lys Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn
 1 5 10 15

 Phe Ala Thr Val Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe
 20 25 30

 Gly His Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu
 35 40 45

 Ser Lys Leu Arg Leu Thr Ser Pro Pro Glu Pro Thr Val Met Thr His
 50 55 60

 Val Pro Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu

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

Asp Asn Pro Gly Gln Gly Gly Gln Arg Lys Lys Arg Ala Leu Asp Thr
 290 295 300

Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu
 305 310 315 320

Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro
 325 330 335

Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg
 340 345 350

Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu
 355 360 365

Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu
 370 375 380

Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln
 385 390 395 400

Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
 405 410

<210> 60
 <211> 1173
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hTGF beta 1

<400> 60
 atgccgccct ccgggctgcg gctgctgccg ctgctgctac cgctgctgtg gctactggtg 60
 ctgacgcctg gccggccggc cgcgggacta tccacctgca agactatcga catggagctg 120
 gtgaagcgga agcgcacga ggccatccgc ggccagatcc tgtccaagct gcggctcgcc 180
 agccccccga gccagggggga ggtgccgccc ggcccgtgc ccgaggccgt gctcgccctg 240
 tacaacagca cccgcgaccg ggtggccggg gagagtgcag aaccggagcc cgagcctgag 300
 gccgactact acgccaagga ggtcaccgc gtgctaattg tggaaccaca caacgaaatc 360

tatgacaagt tcaagcagag tacacacagc atatatatgt tcttcaacac atcagagctc	420
cgagaagcgg tacctgaacc cgtgttgctc tcccgggcag agctgcgtct gctgaggctc	480
aagttaaaag tggagcagca cgtggagctg taccagaaat acagcaacaa ttcctggcga	540
tacctcagca accggctgct ggcacccagc gactcgccag agtggttatc ttttgatgtc	600
accggagttg tgcggcagtg gttgagccgt ggaggggaaa ttgagggtt tgccttagc	660
gcccactgct cctgtgacag cagggataac aactgcaag tggacatcaa cgggttctact	720
accggccgcc gaggtgacct ggccaccatt catggcatga accggccttt cctgcttctc	780
atggccaccc cgctggagag ggcccagcat ctgcaaagct cccggcaccg ccgagccctg	840
gacaccaact attgcttcag ctccacggag aagaactgct gcgtgcggca gctgtacatt	900
gacttccgca aggacctcgg ctggaagtgg atccacgagc ccaagggtta ccatgccaac	960
ttctgcctcg ggccctgccc ctacatttgg agcctggaca cgcagtacag caaggtcctg	1020
gccctgtaca accagcataa cccgggcgcc tcggcggcgc cgtgctgcgt gccgcaggcg	1080
ctggagccgc tgcccatcgt gtactacgtg ggccgcaagc ccaaggtgga gcagctgtcc	1140
aacatgatcg tgcgctcctg caagtgcagc tga	1173

<210> 61
 <211> 1329
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hTGF beta 2

<400> 61	
atgcactact gtgtgctgag cgcttttctg atcctgcatc tggtcacggt cgcgctcagc	60
ctgtctacct gcagcacact cgatatggac cagttcatgc gcaagaggat cgaggcgatc	120
cgcgggcaga tcctgagcaa gctgaagctc accagtcccc cagaagacta tcctgagccc	180
gaggaagtcc ccccggagggt gatttccatc tacaacagca ccagggactt gctccaggag	240
aaggcgagcc ggagggcggc cgcctgcgag cgcgagagga gcgacgaaga gtactacgcc	300
aaggaggttt acaaaataga catgccgccc ttcttcccct ccgaaactgt ctgcccagtt	360
gttacaacac cctctggctc agtgggcagc ttgtgctcca gacagtcca ggtgctctgt	420
gggtaccttg atgcatccc gccactttc tacagaccct acttcagaat tgttcgattt	480

gacgtctcag caatggagaa gaatgcttcc aatttggtga aagcagagtt cagagtcttt	540
cgtttgcaga acccaaaagc cagagtgcct gaacaacgga ttgagctata tcagattctc	600
aagtccaaag atttaacatc tccaaccag cgctacatcg acagcaaagt tgtgaaaaca	660
agagcagaag gcgaatggct ctccttcgat gtaactgatg ctgttcatga atggcttcac	720
cataaagaca ggaacctggg atttaaaata agcttacact gtccctgctg cacttttgta	780
ccatctaata attacatcat ccaaataaa agtgaagaac tagaagcaag atttgcaggt	840
attgatggca cctccacata taccagtggg gatcagaaaa ctataaagtc cactaggaaa	900
aaaaacagtg ggaagacccc acatctcctg ctaatgttat tgcctccta cagacttgag	960
tcacaacaga ccaaccggcg gaagaagcgt gctttggatg cggcctattg ctttagaaat	1020
gtgcaggata attgctgcct acgtccactt tacattgatt tcaagaggga tctagggtgg	1080
aatggatac acgaaccaa aggttacaat gccaaacttct gtgctggagc atgcccgtat	1140
ttatggagtt cagacactca gcacagcagg gtcctgagct tatataatac cataaatcca	1200
gaagcatctg cttctccttg ctgcgtgtcc caagatttag aacctctaac cattctctac	1260
tacattggca aaacaccaa gattgaacag ctttctaata tgattgtaaa gtcttgcaaa	1320
tgcagctaa	1329

<210> 62
 <211> 930
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hTGF beta 3

<400> 62	
atgaagatgc acttgcaaag ggctctggtg gtcctggccc tgctgaactt tgccacggtc	60
agcctctctc tgtccacttg caccaccttg gacttcggcc acatcaagaa gaagagggtg	120
gaagccatta ggggacagat cttgagcaag ctcaggctca ccagcccccc tgagccaacg	180
gtgatgaccc acgtccccta tcaggctctg gccctttaca acagcaccgc ggagctgctg	240
gaggagatgc atggggagag ggaggaaggc tgcaccaggg aaaacaccga gtcggaatac	300
tatgcaaaag aaatccataa attcgacatg atccaggggc tggcggagca caacgaactg	360
gctgtctgcc ctaaaggaat tacctccaag gttttccgct tcaatgtgtc ctcagtggag	420

aaaaatagaa ccaacctatt ccgagcagaa ttccgggtct tgcgggtgcc caaccccagc	480
tctaagcgga atgagcagag gatcgagctc ttccagatcc ttcggccaga tgagcacatt	540
gccaacagc gctatatcgg tggcaagaat ctgccacac ggggcactgc cgagtggctg	600
tcctttgatg tctactgacac tgtgcgtgag tggctgttga gaagagagtc caacttaggt	660
ctagaaatca gcattcactg tccatgtcac acctttcagc ccaatggaga tctcctggaa	720
aacattcacg aggtgatgga aatcaaattc aaaggcgtgg acaatgagga tgaccatggc	780
cgtggagatc tggggcgcct caagaagcag aaggatcacc acaaccctca tctaatacctc	840
atgatgattc cccacaccg gctcgacaac ccgggccagg ggggtcagag gaagaagcgg	900
gctttggaca ccaattactg cttccggtga	930

<210> 63
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hIL-10

<400> 63	
atgcacagct cagcactgct ctgttgccctg gtcctcctga ctggggtgag ggccagccca	60
ggccagggca cccagtctga gaacagctgc acccacttcc caggcaacct gcctaacatg	120
cttcgagatc tccgagatgc cttcagcaga gtgaagactt tctttcaaata gaaggatcag	180
ctggacaact tgttgtaaaa ggagtccttg ctggaggact ttaagggtta cctgggttgc	240
caagccttgt ctgagatgat ccagttttac ctggaggagg tgatgccccca agctgagaac	300
caagacccag acatcaaggc gcatgtgaac tccctggggg agaacctgaa gaccctcagg	360
ctgaggctac ggcgctgtca tcgatttctt ccctgtgaaa acaagagcaa ggccgtggag	420
caggtgaaga atgcctttaa taagctccaa gagaaaggca tctacaaagc catgagttag	480
tttgacatct tcatcaacta catagaagcc tacatgacaa tgaagatacg aaactga	537

<210> 64
 <211> 93
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hSCGB3A2

<220>
 <221> SIGNAL
 <222> (1)..(21)
 <223> signal peptide

<400> 64

Met Lys Leu Val Thr Ile Phe Leu Leu Val Thr Ile Ser Leu Cys Ser
 1 5 10 15

Tyr Ser Ala Thr Ala Phe Leu Ile Asn Lys Val Pro Leu Pro Val Asp
 20 25 30

Lys Leu Ala Pro Leu Pro Leu Asp Asn Ile Leu Pro Phe Met Asp Pro
 35 40 45

Leu Lys Leu Leu Leu Lys Thr Leu Gly Ile Ser Val Glu His Leu Val
 50 55 60

Glu Gly Leu Arg Lys Cys Val Asn Glu Leu Gly Pro Glu Ala Ser Glu
 65 70 75 80

Ala Val Lys Lys Leu Leu Glu Ala Leu Ser His Leu Val
 85 90

<210> 65
 <211> 282
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hSCGB3A2

<400> 65

atgaagctgg taactatctt cctgctggtg accatcagcc ttgtagtta ctctgctact 60
 gccttcctca tcaacaaagt gccccttcct gttgacaagt tggcaccttt acctctggac 120
 aacattcttc cttttatgga tccattaaag cttcttctga aaactctggg catttctgtt 180
 gagcaccttg tggaggggct aaggaagtgt gtaaatagagc tgggaccaga ggcttctgaa 240
 gctgtgaaga aactgctgga ggcgctatca cacttggtgt ga 282

<210> 66

<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> hVSIG-3

<220>
<221> SIGNAL
<222> (1)..(22)
<223> signal peptide

<220>
<221> DOMAIN
<222> (23)..(241)
<223> extracellular domain

<400> 66

Met Thr Ser Gln Arg Ser Pro Leu Ala Pro Leu Leu Leu Leu Ser Leu
1 5 10 15

His Gly Val Ala Ala Ser Leu Glu Val Ser Glu Ser Pro Gly Ser Ile
20 25 30

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

Ser Ala Ala Leu Ile Asn Leu Asn Val Ile Trp Met Val Thr Pro Leu
50 55 60

Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln
65 70 75 80

Met Phe Asp Gly Ala Pro Arg Phe His Gly Arg Val Gly Phe Thr Gly
85 90 95

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

Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp Ile
115 120 125

Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro Pro
130 135 140

Ser Ala Pro His Cys Gln Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp
145 150 155 160

Val Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr
165 170 175

Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr
180 185 190

Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu
195 200 205

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

Thr Cys Leu Leu Asp Leu Gln Val Ile Ser Pro Gln Pro Arg Asn Ile
225 230 235 240

Gly

<210> 67
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> hVSIG-3 extracellular domain

<220>
<221> misc_feature
<222> (1)..(723)
<223> extracellular domain

<400> 67
atgacttctc agcggtcccc tctggcgcct ttgctgctcc tctctctgca cggtgttgca 60
gcatccctgg aagtgtcaga gagccctggg agtatccagg tggcccgggg tcagccagca 120
gtcctgccct gcactttcac taccagcgct gccctcatta acctcaatgt catttggatg 180
gtcactcctc tctccaatgc caaccaacct gaacaggtca tcctgtatca gggtggacag 240
atgtttgatg gtgcccccg gttccacggg agggtaggat ttacaggcac catgccagct 300

accaatgtct ctatcttcat taataacact cagttatcag acactggcac ctaccagtgc	360
ctgggtcaaca accttccaga catagggggc aggaacattg gggtcaccgg tctcacagtg	420
ttagttcccc cttctgcccc acactgccaa atccaaggat cccaggatat tggcagcgat	480
gtcatcctgc tctgtagctc agaggaaggc attcctcgac caacttacct ttgggagaag	540
ttagacaata ccctcaaact acctccaaca gctactcagg accaggtcca gggaacagtc	600
accatccgga acatcagtgc cctgtcttca ggtttgtacc agtgcgtggc ttctaagtct	660
attggaacca gcacctgtct tctggatctc caggttattt caccagcc caggaacatt	720
gga	723

<210> 68
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus of 2A self-cleaving peptide; X can be any amino acid

<220>
 <221> SITE
 <222> (2)..(2)
 <223> X can be any amino acid

<220>
 <221> SITE
 <222> (4)..(4)
 <223> X can be any amino acid

<400> 68

Asp	Xaa	Glu	Xaa	Asn	Pro	Gly	Pro
1				5			

<210> 69
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Self-cleaving peptide

<400> 69

Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro
-----	-----	-----	-----	-----	-----	-----	-----

1

5

<210> 70

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Self-cleaving peptide

<400> 70

Asp Val Glu Ser Asn Pro Gly Pro

1

5

<210> 71

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Self-cleaving peptide

<400> 71

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu

1

5

10

15

Glu Asn Pro Gly Pro

20

<210> 72

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Self-cleaving peptide

<400> 72

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val

1

5

10

15

Glu Glu Asn Pro Gly Pro

20

<210> 73

<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving peptide

<400> 73

Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1 5 10 15

Val Glu Ser Asn Pro Gly Pro
20

<210> 74
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving peptide

<400> 74

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15

Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 75
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 75

Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
1 5 10

<210> 76
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Linker

<400> 76

Gly Gly Gly Ser Gly
1 5

<210> 77

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 77

Gly Gly Ser Gly Gly
1 5

<210> 78

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 78

Ser Gly Ser Ser Gly Ser
1 5

<210> 79

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 79

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 80

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<220>

<221> SITE

<222> (1)..(5)

<223> can be repeated m times, where m is an integer from 1 to 5

<400> 80

Gly Gly Gly Gly Ser
1 5

<210> 81

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<220>

<221> SITE

<222> (1)..(5)

<223> can be repeated m times, where m is an integer from 1 to 5

<400> 81

Gly Gly Gly Ser Ser
1 5

<210> 82

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<220>

<221> SITE

<222> (1)..(5)

<223> can be repeated m times, where m is an integer from 1 to 5

<400> 82

Gly Gly Ser Gly Gly

1 5

<210> 83
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> SITE
<222> (1)..(5)
<223> can be repeated m times, where m is an integer from 1 to 5

<400> 83

Gly Gly Gly Ser Gly
1 5

<210> 84
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> SITE
<222> (1)..(6)
<223> can be repeated m times, where m is an integer from 1 to 5

<400> 84

Ser Gly Ser Ser Gly Ser
1 5

<210> 85
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 85

Leu Gly Gly Gly Ser

1 5

<210> 86
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 86

Gly Leu Gly Gly Ser
1 5

<210> 87
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 87

Gly Gly Leu Gly Ser
1 5

<210> 88
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 88

Gly Gly Gly Leu Ser
1 5

<210> 89
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 89

Gly Gly Gly Gly Leu
1 5

<210> 90
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 90

Leu Gly Gly Ser Gly
1 5

<210> 91
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 91

Gly Leu Gly Ser Gly
1 5

<210> 92
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 92

Gly Gly Leu Ser Gly
1 5

<210> 93
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 93

Gly Gly Gly Leu Gly
1 5

<210> 94

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 94

Gly Gly Gly Ser Leu
1 5

<210> 95

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 95

Leu Gly Gly Ser Ser
1 5

<210> 96

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 96

Gly Leu Gly Ser Ser
1 5

<210> 97

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 97

Gly Gly Leu Ser Ser
1 5

<210> 98

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 98

Leu Gly Leu Gly Ser
1 5

<210> 99

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 99

Gly Leu Gly Leu Ser
1 5

<210> 100

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 100

Gly Leu Leu Gly Ser
1 5

<210> 101

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 101

Leu Gly Gly Leu Ser
1 5

<210> 102

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 102

Gly Leu Gly Gly Leu
1 5

<210> 103

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 103

Leu Gly Leu Ser Gly
1 5

<210> 104

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 104

Gly Leu Leu Ser Gly
1 5

<210> 105

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

<220>
<223> Linker

<400> 105

Gly Gly Leu Ser Leu
1 5

<210> 106
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 106

Gly Gly Leu Leu Gly
1 5

<210> 107
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 107

Gly Leu Gly Ser Leu
1 5

<210> 108
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 108

Leu Gly Leu Ser Ser
1 5

<210> 109
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 109

Gly Gly Leu Leu Ser
1 5

<210> 110
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 110

Leu Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 111
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 111

Gly Leu Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 112
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 112

Gly Gly Leu Gly Ser Gly Gly Gly Gly Ser

1 5 10

<210> 113
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> tetramerization unit

<400> 113

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

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

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

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

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

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

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

Ala Ala Cys Cys Gly
115

<210> 114
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 114

Gly Gly Gly Gly Leu Gly Gly Gly Gly Ser
1 5 10

<210> 115
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 115

Leu Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10

<210> 116
<211> 180
<212> DNA
<213> Artificial Sequence

<220>
<223> trimerization unit

<400> 116
gctgggcagg tgaggatctg ggccacatac cagaccatgc tggacaagat ccgggaggtg 60
ccggagggct ggctcatctt tgtggccgag agggaagagc tctatgtacg cgttagaaat 120
ggcttccgga aggtgctgct ggaggcccgg acagccctcc cgagaggcac gggcaatgag 180

<210> 117
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> trimerization unit

<400> 117

Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys
1 5 10 15

Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
20 25

<210> 118

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

<220>
<223> Linker

<400> 118

Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly
1 5 10

<210> 119
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> IgM hinge

<400> 119
gccgaactcc cgcccaaggt gtccgtgttc gtccctcccc gcgatggggtt cttcggcaat 60
ccacgaaaat ccaaactgat ttgtcaggcc accggcttct ccccccgaca gatccaggtg 120
agttggctac gagagggtaa acaggtgggg agcggagtga ccactgacca ggtgcaggcc 180
gaggccaagg aaagcggacc cacaacatac aaagtgacaa gcactctgac gattaaggag 240
tcagactggc tcggccaatc catgtttaca tgccgggttg atcacagagg gttgaccttc 300
caacagaacg catccagtat gtgcgttcca gat 333

<210> 120
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> t cell epitope

<400> 120

Ser Ile Ile Asn Phe Glu Lys Leu
1 5

<210> 121
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Linker

<400> 121

Leu Gly Gly Ser Ser Gly Gly Gly Ser Ser
1 5 10

<210> 122

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 122

Gly Leu Gly Ser Ser Gly Gly Gly Ser Ser
1 5 10

<210> 123

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 123

Gly Gly Leu Ser Ser Gly Gly Gly Ser Ser
1 5 10

<210> 124

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 124

Gly Gly Gly Leu Ser Gly Gly Gly Ser Ser
1 5 10

<210> 125

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 125

Gly Gly Gly Ser Leu Gly Gly Gly Ser Ser
1 5 10

<210> 126

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 126

Leu Gly Gly Gly Ser Leu Gly Gly Gly Ser
1 5 10

<210> 127

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 127

Gly Leu Gly Gly Ser Gly Leu Gly Gly Ser
1 5 10

<210> 128

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 128

Gly Gly Leu Gly Ser Gly Gly Leu Gly Ser
1 5 10

<210> 129

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

<220>
<223> Linker

<400> 129

Gly Gly Gly Leu Ser Gly Gly Gly Leu Ser
1 5 10

<210> 130
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 130

Gly Gly Gly Gly Leu Gly Gly Gly Gly Leu
1 5 10

<210> 131
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 131

Leu Gly Gly Ser Gly Leu Gly Gly Ser Gly
1 5 10

<210> 132
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 132

Gly Leu Gly Ser Gly Gly Leu Gly Ser Gly
1 5 10

<210> 133
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 133

Gly Gly Leu Ser Gly Gly Gly Leu Ser Gly
1 5 10

<210> 134
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 134

Gly Gly Gly Leu Gly Gly Gly Gly Leu Gly
1 5 10

<210> 135
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 135

Gly Gly Gly Ser Leu Gly Gly Gly Ser Leu
1 5 10

<210> 136
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 136

Leu Gly Gly Ser Ser Leu Gly Gly Ser Ser

1	5	10
---	---	----

<210> 137
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 137

Gly	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Ser	Ser
1				5					10

<210> 138
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 138

Gly	Gly	Leu	Ser	Ser	Gly	Gly	Leu	Ser	Ser
1				5					10

<210> 139
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 139

Gly	Ser	Gly	Gly	Gly	Ala
1				5	

<210> 140
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 140

Gly Ser Gly Gly Gly Ala Gly Ser Gly Gly Gly Ala
1 5 10

<210> 141
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 141

Gly Ser Gly Gly Gly Ala Gly Ser Gly Gly Gly Ala Gly Ser Gly Gly
1 5 10 15

Gly Ala

<210> 142
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 142

Gly Ser Gly Gly Gly Ala Gly Ser Gly Gly Gly Ala Gly Ser Gly Gly
1 5 10 15

Gly Ala Gly Ser Gly Gly Gly Ala
20

<210> 143
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 143

Gly Glu Asn Leu Tyr Phe Gln Ser Gly Gly
1 5 10

<210> 144
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 144

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser
1 5 10

<210> 145
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 145

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
1 5 10

<210> 146
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 146

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10

<210> 147
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 147

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

1 5 10

<210> 148
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 148

Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly
1 5 10

<210> 149
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 149

Gly Gly Gly Ser Ser Ser
1 5

<210> 150
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 150

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
1 5 10 15

<210> 151
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 151

Gly Leu Gly Gly Leu Ala Ala Ala
1 5

<210> 152
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 152

Lys Pro Glu Pro Lys Pro Ala Pro Ala Pro Lys Pro
1 5 10

<210> 153
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 153

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
1 5 10

<210> 154
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> SITE
<222> (1)..(5)
<223> can be repeated m times, where m is an integer from 1 to 5

<400> 154

Glu Ala Ala Ala Lys
1 5

<210> 155

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

<220>
<223> Linker

<400> 155

Gly Gly Gly Leu Ser Gly Gly Gly Gly Ser
1 5 10

<210> 156
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 156

Gly Leu Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10

<210> 157
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 157

Gly Gly Leu Ser Gly Gly Gly Gly Ser Gly
1 5 10

<210> 158
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 158

Gly Gly Gly Leu Gly Gly Gly Gly Ser Gly
1 5 10

<210> 159
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 159

Gly Gly Gly Ser Leu Gly Gly Gly Ser Gly
1 5 10

<210> 160
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 160

Pro Ser Arg Leu Glu Glu Glu Leu Arg Arg Arg Leu Thr Glu Pro
1 5 10 15

<210> 161
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 161

Ser Ala Cys Tyr Cys Glu Leu Ser
1 5

<210> 162
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 162

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu

1 5 10 15

<210> 163
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 163

Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu
1 5 10

<210> 164
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 164

Gly Gly Ser Ala Gly Gly Ser Gly Ser Gly Ser Ser Gly Gly Ser Ser
1 5 10 15

Gly Ala Ser Gly Thr Gly Thr Ala Gly Gly Thr Gly Ser Gly Ser Gly
20 25 30

Thr Gly Ser Gly
35

<210> 165
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 165

Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
1 5 10 15

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser

20

25

30

Gly Gly Gly Ser
35

<210> 166
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 166

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
1 5 10 15

<210> 167
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> T cell epitope

<400> 167

His Cys Leu Gly Lys Trp Leu Gly His Pro Asp Lys Phe
1 5 10

<210> 168
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> T cell epitope

<400> 168

Ala His Ser Leu Glu Arg Val Cys His Cys Leu Gly Lys Trp Leu Gly
1 5 10 15

His Pro Asp Lys Phe Val Gly Ile Thr Tyr Ala Leu Thr
20 25

<210> 169

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

<220>
<223> T cell epitope

<400> 169

Asn Thr Trp Thr Thr Cys Gln Ser Ile Ala Phe Pro Ser Lys
1 5 10

<210> 170
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> T cell epitope

<400> 170

Ala Val Pro Val Tyr Ile Tyr Phe Asn Thr Trp Thr Thr Cys Gln Ser
1 5 10 15

Ile Ala Phe Pro Ser Lys Thr Ser Ala Ser Ile Gly Ser Leu
20 25 30

<210> 171
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> T cell epitope

<400> 171

Val His Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Ser
1 5 10 15

Gln Gly Lys Gly Arg
20

<210> 172
<211> 36
<212> PRT
<213> Artificial Sequence

<220>

<223> T cell epitope

<400> 172

Arg Thr Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val
1 5 10 15

Thr Pro Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser
20 25 30

Leu Ser Arg Phe
35

<210> 173

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 173

His Glu Tyr Gly Ala Glu Ala Leu Glu Arg Ala Gly
1 5 10

<210> 174

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 174

Gly Leu Ser Gly Leu
1 5

<210> 175

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 175

Gly Gly Gly Gly Ser
1 5

<210> 176
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 176

Glu Ala Ala Ala Lys
1 5

<210> 177
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> SITE
<222> (1)..(5)
<223> can be repeated m times, where m is an integer from 1 to 5

<400> 177

Glu Ala Ala Ala Lys Gly Ser
1 5

<210> 178
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> SITE
<222> (1)..(4)
<223> can be repeated m times, where m is an integer from 1 to 5

<400> 178

Glu Ala Ala Lys Gly Ser
1 5

<210> 179
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 179

Gly Pro Ser Arg Leu Glu Glu Glu Leu Arg Arg Arg Leu Thr Glu Pro
1 5 10 15

Gly