

SEQUENCE LISTING

<110> Nykode Therapeutics AS

<120> Tolerance-inducing constructs and composition and their use for the treatment of immune disorders

<130> P5967PC00

<160> 220

<170> PatentIn version 3.5

<210> 1

<211> 144

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<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> 468
<212> PRT
<213> Artificial sequence

<220>
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<220>
<221> MISC_FEATURE
<223> VB5003

<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 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 Pro Ser Val Ile Phe Leu Thr
 260 265 270

Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln
 275 280 285

Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Glu Leu Lys Thr Pro Leu
 290 295 300

Gly Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 305 310 315 320

Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly
 325 330 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 340 345 350

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 355 360 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn
 370 375 380

Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe
 385 390 395 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 405 410 415

Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr
 420 425 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Met
 435 440 445

Glu Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu Tyr
 450 455 460

Arg Asn Gly Lys
465

<210> 3
<211> 484
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5004

<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 Pro Ser Val Ile Phe Leu Thr
 260 265 270

Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln
 275 280 285

Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Glu Leu Lys Thr Pro Leu
 290 295 300

Gly Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 305 310 315 320

Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly
 325 330 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 340 345 350

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 355 360 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn
 370 375 380

Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe
 385 390 395 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 405 410 415

Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr
 420 425 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Ser
 435 440 445

Pro Gly Lys Asn Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser Pro
 450 455 460

Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp Ala
 465 470 475 480

Glu Ala Gln Pro

<210> 4
 <211> 294
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5012

<400> 4

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 Pro Ser Val Ile Phe
 85 90 95

Leu Thr Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
 100 105 110

Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Glu Leu Lys Thr
 115 120 125

Pro Leu Gly Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro
 130 135 140

Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser
145 150 155 160

Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
165 170 175

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
180 185 190

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro
195 200 205

Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
210 215 220

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
225 230 235 240

Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg
245 250 255

Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly
260 265 270

Leu Met Glu Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His
275 280 285

Leu Tyr Arg Asn Gly Lys
290

<210> 5
<211> 631
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5013

<400> 5

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
20 25 30

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

Ser Ala Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile 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 Leu 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 Arg
 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 Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu 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 Ser Val
 225 230 235 240

Gly Val Ile Ala Gly Ala Val Gly Thr Gly Ala Val Leu Ile Val Ile
 245 250 255

Cys Leu Ala Leu Ile Ser Gly Ala Phe Phe Tyr Trp Arg Ser Lys Asn
 260 265 270

Lys Glu Glu Glu Glu Glu Ile Pro Asn Glu Ile Arg Glu Asp Asp
 275 280 285

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

Ser Ser Glu Asn Asn Thr Leu Thr Ser Ser Asn Thr Tyr Asn Ser Arg
 305 310 315 320

Tyr Trp Asn Asn Asn Pro Lys Pro His Arg Asn Thr Glu Ser Phe Asn
 325 330 335

His Phe Ser Asp Leu Arg Gln Ser Phe Ser Gly Asn Ala Val Ile Pro
 340 345 350

Ser Ile Tyr Ala Asn Gly Asn His Leu Val Leu Gly Pro His Lys Thr
 355 360 365

Leu Val Val Thr Ala Asn Arg Gly Ser Ser Pro Gln Val Leu Pro Arg
 370 375 380

Asn Asn Gly Ser Val Ser Arg Lys Pro Trp Pro Gln His Thr His Ser
 385 390 395 400

Tyr Thr Val Ser Gln Met Thr Leu Glu Arg Ile Gly Ala Val Pro Val
 405 410 415

Met Val Pro Ala Gln Ser Arg Ala Gly Ser Leu Val Pro Ser Val Ile
 420 425 430

Phe Leu Thr Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu
 435 440 445

Trp Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Glu Leu Lys
 450 455 460

Thr Pro Leu Gly Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr
 465 470 475 480

Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly
 485 490 495

Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 500 505 510

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 515 520 525

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln
 530 535 540

Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
 545 550 555 560

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
565 570 575

Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
580 585 590

Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly
595 600 605

Gly Leu Met Glu Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val
610 615 620

His Leu Tyr Arg Asn Gly Lys
625 630

<210> 6
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Murine IgVH signal peptide (1-19)

<400> 6

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

Val Gln Cys

<210> 7
<211> 467
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5016

<400> 7

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 Pro Ser Val Ile Phe Leu Thr
 260 265 270

Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln
 275 280 285

Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Glu Leu Lys Thr Pro Leu
290 295 300

Gly Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
305 310 315 320

Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly
325 330 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
340 345 350

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
355 360 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn
370 375 380

Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe
385 390 395 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
405 410 415

Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr
420 425 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Thr
435 440 445

Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val Leu Leu Glu Tyr
450 455 460

Val Thr Leu
465

<210> 8
<211> 381
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5005

<400> 8

Met Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Leu Thr Gly Met
1 5 10 15

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
275 280 285

Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro
290 295 300

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
305 310 315 320

Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met
325 330 335

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

Pro Gly Lys Gly Leu Gly Gly Leu Met Glu Val Gly Trp Tyr Arg Ser
355 360 365

Pro Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys
370 375 380

<210> 9
<211> 397
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5006

<400> 9

Met Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Thr Gly Met
1 5 10 15

Arg Ile Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His
20 25 30

Phe Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe
35 40 45

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

Leu Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys
65 70 75 80

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro

85

90

95

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

Gly Glu Lys Leu Lys Thr Leu Arg Met 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 Ser
 130 135 140

Asp Phe Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu
 145 150 155 160

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

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

Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser Asp Leu Glu
 195 200 205

Leu Ser Ala Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Glu
 210 215 220

Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly
 225 230 235 240

Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val
 245 250 255

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 260 265 270

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 275 280 285

Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro
 290 295 300

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 305 310 315 320

Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met
 325 330 335

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

Pro Gly Lys Gly Leu Gly Gly Leu Ser Pro Gly Lys Asn Ala Thr Gly
355 360 365

Met Glu Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu
370 375 380

Tyr Arg Asn Gly Lys Asp Gln Asp Ala Glu Ala Gln Pro
385 390 395

<210> 10
<211> 593
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5009

<400> 10

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 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 Asp 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 Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
115 120 125

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

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

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

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
180 185 190

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

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

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

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
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

Ser 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 Pro Ser Val Ile Phe Leu Thr Lys Arg Gly
385 390 395 400

Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val

405

410

415

Ser Asp Leu Glu Leu Ser Ala Glu Leu Lys Thr Pro Leu Gly Asp Thr
 420 425 430

Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
 435 440 445

Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln Pro Arg
 450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 465 470 475 480

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 485 490 495

Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn
 500 505 510

Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 515 520 525

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser
 530 535 540

Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser
 545 550 555 560

Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Met Glu Val Gly
 565 570 575

Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly
 580 585 590

Lys

<210> 11
 <211> 364
 <212> PRT
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<220>
 <223> Artificial Sequence

<220>
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 <223> VB5017

<400> 11

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
260 265 270

Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met
275 280 285

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
290 295 300

Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His
305 310 315 320

Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro
325 330 335

Gly Lys Gly Leu Gly Gly Leu Met Glu Val Gly Trp Tyr Arg Ser Pro
340 345 350

Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys
355 360

<210> 12
<211> 468
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5022

<400> 12

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 Pro Ser Val Ile Phe Leu Thr
 260 265 270

Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln
 275 280 285

Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Glu Leu Lys Thr Pro Leu
 290 295 300

Gly Asp Thr Thr His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 305 310 315 320

Cys Pro Arg Cys Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly
 325 330 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 340 345 350

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
355 360 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn
370 375 380

Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe
385 390 395 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
405 410 415

Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr
420 425 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Ala
435 440 445

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

Ala Arg Ala Glu
465

<210> 13
<211> 435
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5003b

<400> 13

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 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	
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
 385 390 395 400

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

Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu Tyr Arg
 420 425 430

Asn Gly Lys
 435

<210> 14
 <211> 348
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5005b

<400> 14

Met Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Thr Gly Met
 1 5 10 15

Arg Ile Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His
 20 25 30

Phe Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe
 35 40 45

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

Leu Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys
 65 70 75 80

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

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

Gly Glu Lys Leu Lys Thr Leu Arg Met 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 Ser
130 135 140

Asp Phe Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu
145 150 155 160

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

Lys Ser Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Glu Pro
180 185 190

Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly
195 200 205

Ser Ser Gly Gly Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr
210 215 220

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
225 230 235 240

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
245 250 255

Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met
260 265 270

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
275 280 285

Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His
290 295 300

Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro
305 310 315 320

Gly Lys Gly Leu Gly Gly Leu Met Glu Val Gly Trp Tyr Arg Ser Pro
325 330 335

Phe Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys

<210> 15
 <211> 331
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5017a

<400> 15

Met Ala Cys Leu Gly Leu Arg Arg Tyr Lys Ala Gln Leu Gln Leu Pro
 1 5 10 15

Ser Arg Thr Trp Pro Phe Val Ala Leu Leu Thr Leu Leu Phe Ile Pro
 20 25 30

Val Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val Val Leu Ala
 35 40 45

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

Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr Asn Asp Gln
 65 70 75 80

Met Thr Glu Val Cys Ala Thr Thr Phe Thr Glu Lys Asn Thr Val Gly
 85 90 95

Phe Leu Asp Tyr Pro Phe Cys Ser Gly Thr Phe Asn Glu Ser Arg Val
 100 105 110

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

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

Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly Ser
 180 185 190

Ser Gly Gly Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
195 200 205

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
225 230 235 240

Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu
245 250 255

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

Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu
275 280 285

Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
290 295 300

Lys Gly Leu Gly Gly Leu Met Glu Val Gly Trp Tyr Arg Ser Pro Phe
305 310 315 320

Ser Arg Val Val His Leu Tyr Arg Asn Gly Lys
325 330

<210> 16
<211> 426
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5046

<400> 16

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
20 25 30

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

Ser Ala Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile 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 Leu 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 Arg
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 Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu 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 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
 420 425

<210> 17
 <211> 451
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB50048

<400> 17

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
 450

<210> 18
 <211> 279
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5052

<400> 18

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

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

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

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

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

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

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

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

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

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

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

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

Gln Asp Ala Glu Gln Ala Pro
 275

<210> 19
 <211> 364
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5058

<400> 19

Met Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Leu Thr Gly Met
1 5 10 15

Arg Ile Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His
20 25 30

Phe Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe
35 40 45

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

Leu Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys
65 70 75 80

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

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

Gly Glu Lys Leu Lys Thr Leu Arg Met 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 Ser
130 135 140

Asp Phe Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu
145 150 155 160

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

Lys Ser Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Glu Pro
180 185 190

Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly
195 200 205

Ser Ser Gly Gly Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr
210 215 220

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
225 230 235 240

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
245 250 255

Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met
 260 265 270

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 275 280 285

Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His
 290 295 300

Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro
 305 310 315 320

Gly Lys Gly Leu Gly Gly Leu Ser Pro Gly Lys Asn Ala Thr Gly Met
 325 330 335

Glu Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu Tyr
 340 345 350

Arg Asn Gly Lys Asp Gln Asp Ala Glu Gln Ala Pro
 355 360

<210> 20
 <211> 576
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5059

<400> 20

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 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 Asp 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 Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
115 120 125

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

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

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

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
180 185 190

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

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

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

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
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

Ser 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 Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr
 385 390 395 400

His Thr Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
 405 410 415

Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gln Pro Arg Glu
 420 425 430

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 435 440 445

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 450 455 460

Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr
 465 470 475 480

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 485 490 495

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys
 500 505 510

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

Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu Ser Pro Gly Lys Asn
 530 535 540

Ala Thr Gly Met Glu Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val
 545 550 555 560

Val His Leu Tyr Arg Asn Gly Lys Asp Gln Asp Ala Glu Gln Ala Pro
 565 570 575

<210> 21

<211> 277

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> VB5060

<400> 21

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
275

<210> 22
<211> 347
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5061

<400> 22

Met Ala Cys Leu Gly Leu Arg Arg Tyr Lys Ala Gln Leu Gln Leu Pro
1 5 10 15

Ser Arg Thr Trp Pro Phe Val Ala Leu Leu Thr Leu Leu Phe Ile Pro
20 25 30

Val Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val Val Leu Ala
35 40 45

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

Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr Asn Asp Gln
65 70 75 80

Met Thr Glu Val Cys Ala Thr Thr Phe Thr Glu Lys Asn Thr Val Gly
85 90 95

Phe Leu Asp Tyr Pro Phe Cys Ser Gly Thr Phe Asn Glu Ser Arg Val
100 105 110

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

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

Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly Ser
180 185 190

Ser Gly Gly Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
195 200 205

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
225 230 235 240

Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu
245 250 255

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

Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu
275 280 285

Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
290 295 300

Lys Gly Leu Gly Gly Leu Ser Pro Gly Lys Asn Ala Thr Gly Met Glu
305 310 315 320

Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu Tyr Arg
325 330 335

Asn Gly Lys Asp Gln Asp Ala Glu Gln Ala Pro
340 345

<210> 23
<211> 355
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE

<223> VB5071

<400> 23

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
 355

<210> 24
 <211> 56
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5051

<400> 24

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 Gln Ala Pro
 50 55

<210> 25
 <211> 39
 <212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> VB5014b

<400> 25

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

Val Gln Cys Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val
20 25 30

Leu Leu Glu Tyr Val Thr Leu
35

<210> 26

<211> 262

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> VB5015b

<400> 26

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

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

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

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

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

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

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

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

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

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

Gly Leu Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val Leu
 245 250 255

Leu Glu Tyr Val Thr Leu
 260

<210> 27
 <211> 434
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5016b

<400> 27

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 Thr Asn
 405 410 415

Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val Leu Leu Glu Tyr Val
 420 425 430

Thr Leu

<210> 28
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> misc_feature
 <223> Dimerization unit

<400> 28
 gagcccaaatt cttgtgacac acctcccccg tgcccaaggt gccca

45

<210> 29
 <211> 171
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Met e 1 antigenic unit

<400> 29

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> 30
<211> 274
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Met e 1 antigenic unit

<400> 30

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

Gly Tyr

<210> 31
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> The indicated sequence can be repeated m times, where m is an integer greater than or equal to 1

<400> 31

Glu Ala Ala Lys Gly Ser
 1 5

<210> 32
 <211> 434
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5024◆

<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 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

<210> 33
<211> 153
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Human IL2

<400> 33

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> 34
<211> 413
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5030

<400> 34

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

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

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

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

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

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

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

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

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

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

Gly Leu Lys Glu Val Asp Arg Leu Glu Asp Glu Leu Val Asn Glu Lys
245 250 255

Glu Lys Tyr Lys Ser Ile Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
260 265 270

Ala Tyr Lys Glu Gln Ile Lys Thr Leu Thr Asn Lys Leu Lys Ala Ala
275 280 285

Glu Ala Arg Ala Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn
290 295 300

Gln Leu Lys Glu Ala Arg Phe Leu Ala Glu Glu Ala Asp Arg Lys Tyr
305 310 315 320

Asp Glu Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Leu
325 330 335

Asn Arg Arg Ile Gln Leu Leu Glu Glu Asp Leu Glu Arg Ser Glu Glu
340 345 350

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Leu Asp Gln Val
355 360 365

Gln Glu Ser Leu Leu Lys Ala Asn Asn Gln Leu Val Glu Lys Asp Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Gln Gln Asn Lys Glu Ala
385 390 395 400

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

<210> 35
 <211> 516
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5079◆

<400> 35

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

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

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

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

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

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

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

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

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

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

Gly Leu Met Lys Leu Glu Lys Asp Asn Ala Met Asp Arg Ala Asp Thr
 245 250 255

Leu Glu Gln Gln Asn Lys Glu Ala Asn Asn Arg Ala Glu Lys Ser Glu
 260 265 270

Glu Glu Val Phe Gly Leu Gln Lys Lys Leu Gln Gln Leu Glu Asn Asp
 275 280 285

Leu Asp Ser Val Gln Glu Ala Leu Leu Lys Ala Asn Gln His Leu Glu
 290 295 300

Glu Lys Asp Lys Ala Leu Ser Asn Ala Glu Gly Glu Val Ala Ala Leu
 305 310 315 320

Asn Arg Arg Ile Gln Leu Leu Glu Glu Asp Leu Glu Arg Ser Glu Glu
 325 330 335

Arg Leu Asn Thr Ala Thr Thr Lys Leu Ala Glu Ala Ser Gln Ala Ala
 340 345 350

Asp Glu Ser Glu Arg Met Arg Lys Val Leu Glu Asn Arg Ser Leu Ser
 355 360 365

Asp Glu Glu Arg Met Asp Ala Leu Glu Asn Gln Leu Lys Glu Ala Arg
 370 375 380

Phe Leu Ala Glu Glu Ala Asp Arg Lys Tyr Asp Glu Val Ala Arg Lys
 385 390 395 400

Leu Ala Met Val Glu Ala Asp Leu Glu Arg Ala Glu Glu Arg Ala Glu
 405 410 415

Thr Gly Glu Ser Lys Ile Val Glu Leu Glu Glu Glu Leu Arg Val Val
 420 425 430

Gly Asn Asn Leu Lys Ser Leu Glu Val Ser Glu Glu Lys Ala Asn Gln
 435 440 445

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

Lys Ala Ala Glu Ala Arg Ala Glu Phe Ala Glu Arg Ser Val Gln Lys
465 470 475 480

Leu Gln Lys Glu Val Asp Arg Leu Glu Asp Glu Leu Val Asn Glu Lys
485 490 495

Glu Lys Tyr Lys Ser Ile Thr Asp Glu Leu Asp Gln Thr Phe Ser Glu
500 505 510

Leu Ser Gly Tyr
515

<210> 36
<211> 462
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence

<220>
<221> misc_feature
<223> Human IL2

<400> 36
atgtacagga tgcaactcct gtcttgcatc gcactaagtc ttgcacttgt cacaaacagt 60
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 120
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 180
acatttaagt ttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 240
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta 300
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 360
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 420
tggattacct tttgtcaaag catcatctca acactgactt ga 462

<210> 37
<211> 56
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5001b

<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 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> 38
<211> 279
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5002b

<400> 38

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

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

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

Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

130

135

140

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

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

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

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

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

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

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

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

Gln Asp Ala Glu Ala Gln Pro
 275

<210> 39
 <211> 451
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> VB5004b

<400> 39

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
450

<210> 40
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<220>
<221> MISC_FEATURE
<223> VB5006b

<400> 40

Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Leu Thr Gly Met Arg
1 5 10 15

Ile Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His Phe
20 25 30

Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe Ser
35 40 45

Gln Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile Leu
 50 55 60

Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys Gln
 65 70 75 80

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

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

Glu Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg Phe
 115 120 125

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

Phe Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu Phe
 145 150 155 160

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

Ser Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Glu Pro Lys
 180 185 190

Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Gly Gly Ser
 195 200 205

Ser Gly Gly Gly Ser Gly Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 210 215 220

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 245 250 255

Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu
 260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 275 280 285

Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu
 290 295 300

Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
305 310 315 320

Lys Gly Leu Gly Gly Leu Ser Pro Gly Lys Asn Ala Thr Gly Met Glu
325 330 335

Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu Tyr Arg
340 345 350

Asn Gly Lys Asp Gln Asp Ala Glu Ala Gln Pro
355 360

<210> 41
<211> 277
<212> PRT
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<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> VB5012b

<400> 41

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 Ala Gln Pro
 275

<210> 42
 <211> 180
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<220>
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<220>
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<400> 42
 gctgggcagg tgaggatctg ggccacatac cagaccatgc tggacaagat ccgggaggtg 60
 ccggaggggct ggctcatctt tgtggccgag agggaagagc tctatgtacg cgtagaaat 120
 ggcttccgga aggtgctgct ggaggcccg acagccctcc cgagaggcac gggcaatgag 180

<210> 43
 <211> 27
 <212> PRT
 <213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Trimerization unit

<400> 43

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> 44
<211> 117
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Tetramerization unit

<400> 44
aagcctctgg acggagagta ttctactctc cagatccggg gccccgaaag gttcgaaatg 60
ttccgggagc ttaacgaggc cttggagctg aaagacgcac aggccggaaa ggaaccg 117

<210> 45
<211> 8
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> OVA (257-264)

<400> 45

Ser Ile Ile Asn Phe Glu Lys Leu
1 5

<210> 46
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Dimerization unit

<400> 46

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
1 5 10 15

<210> 47
<211> 333
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> IgM hinge

<400> 47
gccgaactcc cgcccaaggt gtccgtgttc gtccctcccc gcgatgggtt cttcggcaat 60
ccacgaaaat ccaaactgat ttgtcaggcc accggcttct ccccccgaca gatccaggtg 120
agttggctac gagagggtaa acaggtgggg agcggagtga cactgacca ggtgcaggcc 180
gaggccaagg aaagcggacc cacaacatac aaagtgacaa gcactctgac gattaaggag 240
tcagactggc tcggccaatc catgtttaca tgccgggttg atcacagagg gttgaccttc 300
caacagaacg catccagtat gtgcgttcca gat 333

<210> 48
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Murine Ig VH signal peptide

<400> 48
Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15

Val Gln

<210> 49
<211> 246
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Murine scFv anti-DEC205

<400> 49
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 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> 50
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Natural leader sequence murine IL-10

<400> 50

Met Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Leu Thr Gly Met
1 5 10 15

Arg Ile

<210> 51

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

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<221> MISC_FEATURE

<223> Linker

<400> 51

Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
1 5 10

<210> 52

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 52

Gly Gly Gly Ser Gly
1 5

<210> 53

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 53

Gly Gly Gly Gly Ser

1 5

<210> 54
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 54

Ser Gly Ser Ser Gly Ser
1 5

<210> 55
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 55

Gly Gly Ser Gly Gly
1 5

<210> 56
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 56

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 57
<211> 15
<212> PRT
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<220>
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<220>
<221> MISC_FEATURE
<223> Linker

<400> 57

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 58
<211> 20
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<223> Linker

<400> 58

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 59
<211> 25
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 59

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 60
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 60

Gly Gly Gly Ser Ser
1 5

<210> 61
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 61

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
1 5 10

<210> 62
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 62

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
1 5 10 15

<210> 63
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 63

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly
1 5 10 15

Gly Gly Ser Ser
20

<210> 64

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 64

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Gly Ser Ser
20 25

<210> 65

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 65

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10

<210> 66

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 66

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

<210> 67

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 67

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15

Gly Gly Ser Gly
20

<210> 68

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 68

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Gly Ser Gly
20 25

<210> 69

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 69

Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser Gly Ser
1 5 10

<210> 70

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 70

Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser
1 5 10 15

Gly Ser

<210> 71

<211> 24

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 71

Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser
1 5 10 15

Gly Ser Ser Gly Ser Ser Gly Ser
20

<210> 72

<211> 30

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 72

Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser
1 5 10 15

Gly Ser Ser Gly Ser Ser Gly Ser Ser Gly Ser Ser Gly Ser
20 25 30

<210> 73

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 73

Leu Gly Gly Gly Ser
1 5

<210> 74

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 74

Gly Leu Gly Gly Ser
1 5

<210> 75

<211> 5

<212> PRT

<213> Artificial sequence

<220>

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<220>

<221> MISC_FEATURE

<223> Linker

<400> 75

Gly Gly Leu Gly Ser
1 5

<210> 76
<211> 5
<212> PRT
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<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 76

Gly Gly Gly Leu Ser
1 5

<210> 77
<211> 5
<212> PRT
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<220>
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<220>
<221> MISC_FEATURE
<223> Linker

<400> 77

Gly Gly Gly Gly Leu
1 5

<210> 78
<211> 5
<212> PRT
<213> Artificial sequence

<220>
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<220>
<221> MISC_FEATURE
<223> Linker

<400> 78

Leu Gly Gly Ser Gly
1 5

<210> 79
<211> 5
<212> PRT
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<220>

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<220>

<221> MISC_FEATURE

<223> Linker

<400> 79

Gly Leu Gly Ser Gly

1 5

<210> 80

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 80

Gly Gly Leu Ser Gly

1 5

<210> 81

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 81

Gly Gly Gly Leu Gly

1 5

<210> 82

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 82

Gly Gly Gly Ser Leu
1 5

<210> 83
<211> 5
<212> PRT
<213> Artificial sequence

<220>
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<220>
<221> MISC_FEATURE
<223> Linker

<400> 83

Leu Gly Gly Ser Ser
1 5

<210> 84
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 84

Gly Leu Gly Ser Ser
1 5

<210> 85
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 85

Gly Gly Leu Ser Ser
1 5

<210> 86
<211> 5
<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 86

Leu Gly Leu Gly Ser

1 5

<210> 87

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 87

Gly Leu Gly Leu Ser

1 5

<210> 88

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 88

Gly Leu Leu Gly Ser

1 5

<210> 89

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 89

Leu Gly Gly Leu Ser
1 5

<210> 90

<211> 5

<212> PRT

<213> Artificial sequence

<220>

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<220>

<221> MISC_FEATURE

<223> Linker

<400> 90

Gly Leu Gly Gly Leu
1 5

<210> 91

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 91

Gly Leu Gly Gly Leu Gly Leu Gly Gly Leu
1 5 10

<210> 92

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 92

Gly Leu Gly Gly Leu Gly Leu Gly Gly Leu Gly Leu Gly Gly Leu
1 5 10 15

<210> 93
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 93

Gly Leu Gly Gly Leu Gly Leu Gly Gly Leu Gly Leu Gly Gly Leu Gly
1 5 10 15

Leu Gly Gly Leu
20

<210> 94
<211> 25
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 94

Gly Leu Gly Gly Leu Gly Leu Gly Gly Leu Gly Leu Gly Gly Leu Gly
1 5 10 15

Leu Gly Gly Leu Gly Leu Gly Gly Leu
20 25

<210> 95
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 95

Leu Gly Leu Ser Gly
1 5

<210> 96
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 96

Gly Leu Leu Ser Gly
1 5

<210> 97
<211> 5
<212> PRT
<213> Artificial sequence

<220>
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<220>
<221> MISC_FEATURE
<223> Linker

<400> 97

Gly Gly Leu Ser Leu
1 5

<210> 98
<211> 5
<212> PRT
<213> Artificial sequence

<220>
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<220>
<221> MISC_FEATURE
<223> Linker

<400> 98

Gly Gly Leu Leu Gly
1 5

<210> 99
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 99

Gly Leu Gly Ser Leu
1 5

<210> 100
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 100

Leu Gly Leu Ser Ser
1 5

<210> 101
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 101

Gly Gly Leu Leu Ser
1 5

<210> 102
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 102

Leu Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10

<210> 103
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 103

Gly Leu Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 104
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 104

Gly Gly Leu Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 105
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 105

Gly Gly Gly Leu Ser Gly Gly Gly Gly Ser
1 5 10

<210> 106
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 106

Gly Gly Gly Gly Leu Gly Gly Gly Gly Ser
1 5 10

<210> 107
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 107

Leu Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10

<210> 108
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 108

Gly Leu Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10

<210> 109
<211> 10
<212> PRT
<213> Artificial sequence

<220>
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<220>
<221> MISC_FEATURE
<223> Linker

<400> 109

Gly Gly Leu Ser Gly Gly Gly Gly Ser Gly
1 5 10

<210> 110

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 110

Gly Gly Gly Leu Gly Gly Gly Gly Ser Gly
1 5 10

<210> 111

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 111

Gly Gly Gly Ser Leu Gly Gly Gly Ser Gly
1 5 10

<210> 112

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 112

Leu Gly Gly Ser Ser Gly Gly Gly Ser Ser
1 5 10

<210> 113

<211> 10

<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 113

Gly Leu Gly Ser Ser Gly Gly Gly Ser Ser
1 5 10

<210> 114
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 114

Gly Gly Leu Ser Ser Gly Gly Gly Ser Ser
1 5 10

<210> 115
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 115

Gly Gly Gly Leu Ser Gly Gly Gly Ser Ser
1 5 10

<210> 116
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>

<221> MISC_FEATURE
<223> Linker

<400> 116

Gly Gly Gly Ser Leu Gly Gly Gly Ser Ser
1 5 10

<210> 117
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 117

Leu Gly Gly Gly Ser Leu Gly Gly Gly Ser
1 5 10

<210> 118
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 118

Gly Leu Gly Gly Ser Gly Leu Gly Gly Ser
1 5 10

<210> 119
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 119

Gly Gly Leu Gly Ser Gly Gly Leu Gly Ser
1 5 10

<210> 120
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 120

Gly Gly Gly Leu Ser Gly Gly Gly Leu Ser
1 5 10

<210> 121
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 121

Gly Gly Gly Gly Leu Gly Gly Gly Gly Leu
1 5 10

<210> 122
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 122

Leu Gly Gly Ser Gly Leu Gly Gly Ser Gly
1 5 10

<210> 123
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 123

Gly Leu Gly Ser Gly Gly Leu Gly Ser Gly
1 5 10

<210> 124
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 124

Gly Gly Leu Ser Gly Gly Gly Leu Ser Gly
1 5 10

<210> 125
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 125

Gly Gly Gly Leu Gly Gly Gly Gly Leu Gly
1 5 10

<210> 126
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 126

Gly Gly Gly Ser Leu Gly Gly Gly Ser Leu
1 5 10

<210> 127
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 127

Leu Gly Gly Ser Ser Leu Gly Gly Ser Ser
1 5 10

<210> 128
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 128

Gly Leu Gly Ser Ser Gly Leu Gly Ser Ser
1 5 10

<210> 129
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 129

Gly Gly Leu Ser Ser Gly Gly Leu Ser Ser
1 5 10

<210> 130
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 130

Gly Ser Gly Gly Gly Ala
1 5

<210> 131
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 131

Gly Ser Gly Gly Gly Ala Gly Ser Gly Gly Gly Ala
1 5 10

<210> 132
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 132

Gly Ser Gly Gly Gly Ala Gly Ser Gly Gly Gly Ala Gly Ser Gly Gly
1 5 10 15

Gly Ala

<210> 133
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 133

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> 134
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 134

Gly Glu Asn Leu Tyr Phe Gln Ser Gly Gly
1 5 10

<210> 135
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 135

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser
1 5 10

<210> 136
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 136

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
1 5 10

<210> 137

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 137

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10

<210> 138

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 138

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> 139

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 139

Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly
1 5 10

<210> 140

<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 140

Gly Gly Gly Ser Ser Ser
1 5

<210> 141
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 141

Gly Leu Gly Gly Leu Ala Ala Ala
1 5

<210> 142
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 142

Lys Pro Glu Pro Lys Pro Ala Pro Ala Pro Lys Pro
1 5 10

<210> 143
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 143

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
1 5 10

<210> 144
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 144

Glu Ala Ala Ala Lys
1 5

<210> 145
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 145

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10

<210> 146
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 146

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

<210> 147
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 147

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
1 5 10 15

Ala Ala Ala Lys
20

<210> 148
<211> 25
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 148

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
1 5 10 15

Ala Ala Ala Lys Glu Ala Ala Ala Lys
20 25

<210> 149
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 149

Pro Ser Arg Leu Glu Glu Glu Leu Arg Arg Arg Leu Thr Glu Pro
1 5 10 15

<210> 150
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 150

Ser Ala Cys Tyr Cys Glu Leu Ser
1 5

<210> 151
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 151

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

<210> 152
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 152

Ser Leu Ser Leu Ser Pro Gly Lys Gly Leu Gly Gly Leu
1 5 10

<210> 153
<211> 5
<212> PRT
<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 153

Gly Pro Gly Pro Gly

1 5

<210> 154

<211> 36

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 154

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> 155

<211> 36

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Linker

<400> 155

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> 156
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Dimerization unit

<400> 156

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

<210> 157
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 157

His Cys Leu Gly Lys Trp Leu Gly His Pro Asp Lys Phe
1 5 10

<210> 158
<211> 29
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 158

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> 159
<211> 14

<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 159

Asn Thr Trp Thr Thr Cys Gln Ser Ile Ala Phe Pro Ser Lys
1 5 10

<210> 160
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 160

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> 161
<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<400> 161

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> 162
<211> 36
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 162

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> 163
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 163

Gly Leu Ser Gly Leu
1 5

<210> 164
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker, REPEAT: m is 1 or more

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> The sequence can be repeated m times, where m is an integer greater than or equal to 1

<400> 164

Gly Gly Gly Gly Ser
1 5

<210> 165
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker, REPEAT: m is 1 or more

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> The sequence can be repeated m times, where m is an integer greater than or equal to 1

<400> 165

Glu Ala Ala Ala Lys
1 5

<210> 166
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker, REPEAT: m is 1 or more

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> The sequence can be repeated m times, where m is an integer greater than or equal to 1

<400> 166

Glu Ala Ala Ala Lys Gly Ser
1 5

<210> 167
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 167

Gly Pro Ser Arg Leu Glu Glu Glu Leu Arg Arg Arg Leu Thr Glu Pro
1 5 10 15

Gly

<210> 168
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Linker

<400> 168

His Glu Tyr Gly Ala Glu Ala Leu Glu Arg Ala Gly
1 5 10

<210> 169
<211> 160
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Murine IL-10

<400> 169

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> 170
<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Natural leader sequence murine SG3A2

<400> 170

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> 171
<211> 70
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Murine SG3A2

<400> 171

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> 172
 <211> 22
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> Natural leader sequence murine VSIG-3

<400> 172

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> 173
 <211> 218
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> Murine VSIG-3 Extracellular domain

<400> 173

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> 174
<211> 35
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Natural leader sequence murine CTLA4

<400> 174

Met Ala Cys Leu Gly Leu Arg Arg Tyr Lys Ala Gln Leu Gln Leu Pro
1 5 10 15

Ser Arg Thr Trp Pro Phe Val Ala Leu Leu Thr Leu Leu Phe Ile Pro
20 25 30

Val Phe Ser
35

<210> 175
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Murine CTLA-4 Extracellular domain

<400> 175

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

Gly Val Ala Ser Phe Pro Cys Glu Tyr Ser Pro Ser His Asn Thr Asp
20 25 30

Glu Val Arg Val Thr Val Leu Arg Gln Thr Asn Asp Gln Met Thr Glu
35 40 45

Val Cys Ala Thr Thr Phe Thr Glu Lys Asn Thr Val Gly Phe Leu Asp
50 55 60

Tyr Pro Phe Cys Ser Gly Thr Phe Asn Glu Ser Arg Val Asn Leu Thr
65 70 75 80

Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Leu Cys Lys Val
85 90 95

Glu Leu Met Tyr Pro Pro Pro Tyr Phe Val Gly Met Gly Asn Gly Thr
100 105 110

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

<210> 176
<211> 29
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Natural leader sequence murine TGF(beta)1

<400> 176

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro 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> 177
 <211> 361
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Artificial Sequence

 <220>
 <221> MISC_FEATURE
 <223> Murine TGF(beta)1 proprotein

 <400> 177

 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> 178
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Natural leader sequence murine PD-1

<400> 178

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> 179
<211> 145
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Murine PD-1 Extracellular domain

<400> 179

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> 180
<211> 21
<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> MOG(35-55)

<400> 180

Met Glu Val Gly Trp Tyr Arg Ser Pro Phe Ser Arg Val Val His Leu
1 5 10 15

Tyr Arg Asn Gly Lys
20

<210> 181

<211> 37

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> MOG(27-63)

<400> 181

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> 182

<211> 37

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> MOG(27-63) with A/Q switch

<400> 182

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> 183
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> GAD65(202-221)

<400> 183

Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val Leu Leu Glu
1 5 10 15

Tyr Val Thr Leu
20

<210> 184
<211> 274
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Met e 1

<400> 184

Met Lys Leu Glu Lys Asp Asn Ala Met Asp Arg Ala Asp Thr Leu Glu
1 5 10 15

Gln Gln Asn Lys Glu Ala Asn Asn Arg Ala Glu Lys Ser Glu Glu Glu
20 25 30

Val His Asn Leu Gln Lys Arg Met Gln Gln Leu Glu Asn Asp Leu Asp
35 40 45

Gln Val Gln Glu Ser Leu Leu Lys Ala Asn Asn Gln Leu Val Glu Lys
50 55 60

Asp Lys Ala Leu Ser Asn Ala Glu Gly Glu Val Ala Ala Leu Asn Arg
65 70 75 80

Arg Ile Gln Leu Leu Glu Glu Asp Leu Glu Arg Ser Glu Glu Arg Leu
85 90 95

Asn Thr Ala Thr Thr Lys Leu Ala Glu Ala Ser Gln Ala Ala Asp Glu
100 105 110

Ser Glu Arg Met Arg Lys Val Leu Glu Asn Arg Ser Leu Ser Asp Glu
115 120 125

Glu Arg Met Asp Ala Leu Glu Asn Gln Leu Lys Glu Ala Arg Phe Leu
130 135 140

Ala Glu Glu Ala Asp Arg Lys Tyr Asp Glu Val Ala Arg Lys Leu Ala
145 150 155 160

Met Val Glu Ala Asp Leu Glu Arg Ala Glu Glu Arg Ala Glu Thr Gly
165 170 175

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

Asn Leu Lys Ser Leu Glu Val Ser Glu Glu Lys Ala Asn Gln Arg Glu
195 200 205

Glu Ala Tyr Lys Glu Gln Ile Lys Thr Leu Thr Asn Lys Leu Lys Ala
210 215 220

Ala Glu Ala Arg Ala Glu Phe Ala Glu Arg Ser Val Gln Lys Leu Gln
225 230 235 240

Lys Glu Val Asp Arg Leu Glu Asp Glu Leu Val Asn Glu Lys Glu Lys
245 250 255

Tyr Lys Ser Ile Thr Asp Glu Leu Asp Gln Thr Phe Ser Glu Leu Ser
260 265 270

Gly Tyr

<210> 185
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE

<223> Met e 1 (16-35)

<400> 185

Glu Gln Gln Asn Lys Glu Ala Asn Asn Arg Ala Glu Lys Ser Glu Glu
1 5 10 15

Glu Val His Asn
20

<210> 186

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Met e 1 (46-65)

<400> 186

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

Val Glu Lys Asp
20

<210> 187

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Met e 1 (76-95)

<400> 187

Ala Ala Leu Asn Arg Arg Ile Gln Leu Leu Glu Glu Asp Leu Glu Arg
1 5 10 15

Ser Glu Glu Arg
20

<210> 188

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Met e 1 (136-155)

<400> 188

Asn Gln Leu Lys Glu Ala Arg Phe Leu Ala Glu Glu Ala Asp Arg Lys
1 5 10 15

Tyr Asp Glu Val
20

<210> 189
<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Met e 1 (210-230)

<400> 189

Ala Tyr Lys Glu Gln Ile Lys Thr Leu Thr Asn Lys Leu Lys Ala Ala
1 5 10 15

Glu Ala Arg Ala Glu
20

<210> 190
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Met e 1 (241-260)

<400> 190

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

Tyr Lys Ser Ile
20

<210> 191
<211> 284
<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Pan b 1

<400> 191

Met Asp Ala Ile Lys Lys Lys Met Gln Ala Met Lys Leu Glu Lys Asp
1 5 10 15

Asn Ala Met Asp Arg Ala Asp Thr Leu Glu Gln Gln Asn Lys Glu Ala
20 25 30

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

Lys Leu Gln Gln Leu Glu Asn Asp Leu Asp Ser Val Gln Glu Ala Leu
50 55 60

Leu Lys Ala Asn Gln His Leu Glu Glu Lys Asp Lys Ala Leu Ser Asn
65 70 75 80

Ala Glu Gly Glu Val Ala Ala Leu Asn Arg Arg Ile Gln Leu Leu Glu
85 90 95

Glu Asp Leu Glu Arg Ser Glu Glu Arg Leu Asn Thr Ala Thr Thr Lys
100 105 110

Leu Ala Glu Ala Ser Gln Ala Ala Asp Glu Ser Glu Arg Met Arg Lys
115 120 125

Val Leu Glu Asn Arg Ser Leu Ser Asp Glu Glu Arg Met Asp Ala Leu
130 135 140

Glu Asn Gln Leu Lys Glu Ala Arg Phe Leu Ala Glu Glu Ala Asp Arg
145 150 155 160

Lys Tyr Asp Glu Val Ala Arg Lys Leu Ala Met Val Glu Ala Asp Leu
165 170 175

Glu Arg Ala Glu Glu Arg Ala Glu Thr Gly Glu Ser Lys Ile Val Glu
180 185 190

Leu Glu Glu Glu Leu Arg Val Val Gly Asn Asn Leu Lys Ser Leu Glu
195 200 205

Val Ser Glu Glu Lys Ala Asn Gln Arg Glu Glu Ala Tyr Lys Glu Gln

210

215

220

Ile Lys Thr Leu Thr Asn Lys Leu Lys Ala Ala Glu Ala Arg Ala Glu
 225 230 235 240

Phe Ala Glu Arg Ser Val Gln Lys Leu Gln Lys Glu Val Asp Arg Leu
 245 250 255

Glu Asp Glu Leu Val Asn Glu Lys Glu Lys Tyr Lys Ser Ile Thr Asp
 260 265 270

Glu Leu Asp Gln Thr Phe Ser Glu Leu Ser Gly Tyr
 275 280

<210> 192
 <211> 20
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> Pan b 1 (26-45)

<400> 192

Glu Gln Gln Asn Lys Glu Ala Asn Asn Arg Ala Glu Lys Ser Glu Glu
 1 5 10 15

Glu Val Phe Gly
 20

<210> 193
 <211> 20
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> Pan b 1 (56-75)

<400> 193

Asp Leu Asp Ser Val Gln Glu Ala Leu Leu Lys Ala Asn Gln His Leu
 1 5 10 15

Glu Glu Lys Asp
 20

<210> 194
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Pan b 1 (86-105)

<400> 194

Ala Ala Leu Asn Arg Arg Ile Gln Leu Leu Glu Glu Asp Leu Glu Arg
1 5 10 15

Ser Glu Glu Arg
20

<210> 195
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Pan b 1 (146-165)

<400> 195

Asn Gln Leu Lys Glu Ala Arg Phe Leu Ala Glu Glu Ala Asp Arg Lys
1 5 10 15

Tyr Asp Glu Val
20

<210> 196
<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Pan b 1 (220-240)

<400> 196

Ala Tyr Lys Glu Gln Ile Lys Thr Leu Thr Asn Lys Leu Lys Ala Ala
1 5 10 15

Glu Ala Arg Ala Glu
20

<210> 197
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Pan b 1 (251-270)

<400> 197

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

Tyr Lys Ser Ile
20

<210> 198
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Natural leader sequence humane CCL3L1

<400> 198

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> 199
<211> 70
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> humane CCL3L1

<400> 199

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> 200
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> misc_feature
<223> Hinge-region 1 from human IgG3

<400> 200
gagctcaaaa cccacttgg tgacacaact cacaca 36

<210> 201
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> misc_feature
<223> Hinge-region 4 from human IgG3

<400> 201
ggcgggtgga gcagcggagg tggaagtgga 30

<210> 202
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE

<223> Human IgG3 CH3 domain

<400> 202

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
50 55 60

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

Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 203

<211> 321

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> misc_feature

<223> Human IgG3 CH3 domain

<400> 203

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> 204

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> misc_feature

<223> Linker

<400> 204

ggcctcgggtg gcctg

15

<210> 205

<211> 390

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Human transforming growth factor beta-1

<400> 205

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro 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> 206

<211> 442

<212> PRT

<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Human Transforming growth factor beta-2

<400> 206

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> 207
<211> 309
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Human transforming growth factor beta-3

<400> 207

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
305

<210> 208
<211> 1173
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> misc_feature
<223> Human transforming growth factor beta-1

<400> 208
atgccgccct ccgggctgcg gctgctgccg ctgctgctac cgctgctgtg gctactggtg 60
ctgacgcctg gccggccggc cgcgggacta tccacctgca agactatcga catggagctg 120
gtgaagcgga agcgcacatga ggccatccgc ggccagatcc tgtccaagct gcggctcgcc 180
agcccccca gccaggggga 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 ggcaccagc gactcgccag agtggttatc ttttgatgtc 600
accggagttg tgcggcagtg gttgagccgt ggaggggaaa ttgagggtt tgccttagc 660
gcccactgct cctgtgacag cagggataac aactgcaag tggacatcaa cgggttcact 720
accggccgcc gaggtgacct ggccaccatt catggcatga accggcctt cctgcttctc 780
atggccaccc cgctggagag ggcccagcat ctgcaaagct cccggcaccg ccgagccctg 840

gacaccaact attgcttcag ctccacggag aagaactgct gcgtgcggca gctgtacatt	900
gacttccgca aggacctcgg ctggaagtgg atccacgagc ccaagggcta ccatgccaac	960
ttctgcctcg ggccctgccc ctacatttgg agcctggaca cgcagtacag caaggtcctg	1020
gccctgtaca accagcataa cccggggccc tcggggcgcc cgtgctgcgt gccgcaggcg	1080
ctggagccgc tgcccatcgt gtactacgtg ggccgcaagc ccaagggtga gcagctgtcc	1140
aacatgatcg tgcgctcctg caagtgcagc tga	1173

<210> 209
 <211> 1329
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> misc_feature
 <223> Human transforming growth factor beta 2

<400> 209	
atgcactact gtgtgctgag cgcttttctg atcctgcatac tggtcacggt cgcgctcagc	60
ctgtctacct gcagcacact cgatatggac cagttcatgc gcaagaggat cgaggcgatc	120
cgcgggcaga tcctgagcaa gctgaagctc accagtcccc cagaagacta tcctgagccc	180
gaggaagtcc ccccgagggt 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 aatttggatga 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 agcttacct gtccctgctg cacttttgta	780
ccatctaata attacatcat cccaaataaa agtgaagaac tagaagcaag atttgcaggt	840
attgatggca cctccacata taccagtggg gatcagaaaa ctataaagtc cactaggaaa	900
aaaaacagtg ggaagacccc acatctcctg ctaatgttat tgccctccta cagacttgag	960
tcacaacaga ccaaccggcg gaagaagcgt gctttggatg cggcctattg ctttagaaat	1020
gtgcaggata attgctgcct acgtccactt tacattgatt tcaagaggga tctagggtgg	1080
aatggatac acgaaccaa aggggtacaat gccaaacttct gtgctggagc atgcccgtat	1140

ttatggagtt cagacactca gcacagcagg gtcctgagct tatataatac cataaatcca	1200
gaagcatctg cttctccttg ctgcgtgtcc caagatttag aacctctaac cattctctac	1260
tacattggca aaacacccaa gattgaacag ctttctaata tgattgtaaa gtcttgcaaa	1320
tgcagctaa	1329

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

<220>
 <223> Artificial Sequence

<220>
 <221> misc_feature
 <223> Human transforming growth factor beta 3

<400> 210	
atgaagatgc acttgcaaag ggctctgggtg gtcctggccc tgctgaactt tgccacggtc	60
agcctctctc tgtccacttg caccaccttg gacttcggcc acatcaagaa gaagagggtg	120
gaagccatta ggggacagat cttgagcaag ctcaggctca ccagcccccc tgagccaacg	180
gtgatgacct acgtccccta tcaggctctg gccctttaca acagcaccgc ggagctgctg	240
gaggagatgc atggggagag ggaggaaggc tgcaccaggg aaaacaccga gtcggaatac	300
tatgccaag aaatccataa attcgacatg atccaggggc tggcggagca caacgaactg	360
gctgtctgcc ctaaaggaat tacctccaag gttttccgct tcaatgtgtc ctgagtgag	420
aaaaatagaa ccaacctatt ccgagcagaa ttccgggtct tgcgggtgcc caaccccagc	480
tctaagcgga atgagcagag gatcgagctc ttccagatcc ttcggccaga tgagcacatt	540
gccaaacagc gctatatcgg tggcaagaat ctgcccacac ggggcactgc cgagtggctg	600
tcctttgatg tcaactgacac tgtgcgtgag tggctgttga gaagagagtc caacttaggt	660
ctagaaatca gcattcactg tccatgtcac acctttcagc ccaatggaga tatcctggaa	720
aacattcacg aggtgatgga aatcaaattc aaaggcgtgg acaatgagga tgaccatggc	780
cgtggagatc tggggcgcct caagaagcag aaggatcacc acaaccctca tctaatactc	840
atgatgattc cccacaccg gctcgacaac ccgggccagg ggggtcagag gaagaagcgg	900
gctttggaca ccaattactg cttccggtga	930

<210> 211
 <211> 178
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Human interleukin-10 isoform 1

<400> 211

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> 212
<211> 537
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> misc_feature

<223> Human interleukin 10 (IL10)

<400> 212

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atgcacagct cagcactgct ctgttcctg gtcctcctga ctggggtag gccagccca      60
ggccaggcca cccagtctga gaacagctgc acccacttcc caggcaacct gcctaacatg    120
cttcgagatc tccgagatgc cttcagcaga gtgaagactt tctttcaaat gaaggatcag    180
ctggacaact tgttggttaa ggagtccttg ctggaggact ttaagggtta cctgggttgc    240
caagccttgt ctgagatgat ccagttttac ctggaggagg tgatgccccca agctgagaac    300
caagaccag acatcaaggc gcatgtgaac tccctggggg agaacctgaa gaccctcagg    360
ctgaggctac ggcgctgtca tcgatttctt ccctgtgaaa acaagagcaa gcccgtaggag   420
caggtgaaga atgcctttaa taagctccaa gagaaaggca tctacaaagc catgagttag   480
tttgacatct tcatcaacta catagaagcc tacatgacaa tgaagatacg aaactga     537
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<210> 213

<211> 93

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial Sequence

<220>

<221> MISC_FEATURE

<223> Human secretoglobin family 3A member 2 precursor (SCGB3A2)

<400> 213

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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> 214

<211> 282

<212> DNA

<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> misc_feature
<223> Human secretoglobin family 3A member 2 (SCGB3A2)

<400> 214
atgaagctgg taactatctt cctgctgggtg accatcagcc tttgtagtta ctctgctact 60
gccttcctca tcaacaaagt gcccttcct gttgacaagt tggcaccttt acctctggac 120
aacattcttc cttttatgga tccattaaag cttcttctga aaactctggg catttctgtt 180
gagcaccttg tggaggggct aaggaagtgt gtaaatgagc tgggaccaga ggcttctgaa 240
gctgtgaaga aactgctgga ggcgctatca cacttggtgt ga 282

<210> 215
<211> 241
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> IGSF11 (VSIG3) (ECD)

<400> 215

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> 216
 <211> 723
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> misc_feature
 <223> IGSF11 (VSIG3) (ECD)

<400> 216
 atgacttctc agcgttcccc tctggcgcct ttgctgctcc tctctctgca cggtgttgca 60
 gcatccctgg aagtgtcaga gagccctggg agtatccagg tggcccgggg tcagccagca 120
 gtcctgccct gcactttcac taccagcgct gccctcatta acctcaatgt catttgatg 180
 gtcactcctc tctccaatgc caaccaacct gaacagggtca tcctgtatca ggggtggacag 240
 atgtttgatg gtgcccccg gttccacggg agggtaggat ttacaggcac catgccagct 300
 accaatgtct ctatcttcat taataacact cagttatcag aactggcac ctaccagtgc 360
 ctgggtcaaca accttcaga catagggggc aggaacattg gggtcaccgg tctcacagtg 420
 ttagttcccc cttctgcccc aactgcca atccaaggat cccaggatat tggcagcgat 480

gtcatcctgc tctgtagctc agaggaaggc attcctcgac caacttacct ttgggagaag 540
 ttagacaata ccctcaaact acctccaaca gctactcagg accaggtcca gggaacagtc 600
 accatccgga acatcagtgc cctgtcttca ggtttgtacc agtgcgtggc ttctaattgct 660
 attggaacca gcacctgtct tctggatctc caggttatit caccagcc caggaacatt 720
 gga 723

<210> 217
 <211> 161
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial Sequence

<220>
 <221> MISC_FEATURE
 <223> CTLA4_HUMAN Cytotoxic T-lymphocyte protein 4 (ECD)

<400> 217

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> 218
<211> 483
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> misc_feature
<223> Human cytotoxic T-lymphocyte associated protein 4 (CTLA4) (ECD)

<400> 218
atggcttgcc ttggatttca gcggcacaaag gctcagctga acctggctac caggacctgg 60
ccctgcactc tcctgttttt tcttctcttc atccctgtct tctgcaaagc aatgcacgtg 120
gcccagcctg ctgtggtact ggccagcagc cgaggcatcg ccagctttgt gtgtgagtat 180
gcatctccag gcaaagccac tgagggtccgg gtgacagtgc ttcggcaggc tgacagccag 240
gtgactgaag tctgtgcggc aacctacatg atggggaatg agttgacctt cctagatgat 300
tccatctgca cgggcacctc cagtggaaat caagtgaacc tcactatcca aggactgagg 360
gccatggaca cgggactcta catctgcaag gtggagctca tgtaccacc gccatactac 420
ctgggcatag gcaacggaac ccagatttat gtaattgatc cagaaccgtg cccagattct 480
gac 483

<210> 219
<211> 170
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> MISC_FEATURE
<223> Human programmed cell death protein 1 PDCD1 (PD-1) (ECD)

<400> 219

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 80

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
145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val
165 170

<210> 220
<211> 510
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial Sequence

<220>
<221> misc_feature
<223> Human programmed cell death 1 PDCD1 (PD-1) (ECD)

<400> 220
atgcagatcc cacaggcgcc ctggccagtc gtctgggcgg tgctacaact gggctggcgg 60
ccaggatggt tcttagactc ccagacagg ccctggaacc ccccccactt ctccccagcc 120
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg 180
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc 240
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttcctgtg cacacaactg 300
cccaacgggc gtgacttcca catgagcgtg gtcaggggcc ggcgcaatga cagcggcacc 360
tacctctgtg gggccatctc cctggcccc aaggcgcaga tcaaagagag cctgcgggca 420
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc 480
aggccagccg gccagttcca aaccctggtg 510