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<110> Kyowa Kirin Co., Ltd.

<120> Bispecific antibody binding to TfR

<130> W528470

<150> JP2018-248334

<151> 2018-12-28

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<170> PatentIn version 3.5

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<212> DNA

<213> Homo sapiens

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Ser Thr Asp Phe Thr Gly Thr Ile Lys Leu Leu Asn Glu Asn Ser Tyr
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Val Pro Arg Glu Ala Gly Ser Gln Lys Asp Glu Asn Leu Ala Leu Tyr
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Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp

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

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

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Ser Leu Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe
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Pro Ile Val Asn Ala Glu Leu Ser Phe Phe Gly His Ala His Leu Gly
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Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln
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Phe Pro Pro Ser Arg Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr
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Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp
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Cys Pro Ser Asp Trp Lys Thr Asp Ser Thr Cys Arg Met Val Thr Ser
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Glu Ser Lys Asn Val Lys Leu Thr Val Ser Asn Val Leu Lys Glu Ile
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Lys Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Phe Val Glu Pro Asp
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Tyr Ile Asn Leu Asp Lys Ala Val Leu Gly Thr Ser Asn Phe Lys Val
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Gly Ser His Thr Leu Pro Ala Leu Leu Glu Asn Leu Lys Leu Arg Lys
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Gln Asn Asn Gly Ala Phe Asn Glu Thr Leu Phe Arg Asn Gln Leu Ala
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 <212> PRT
 <213> Cynomolgus monkey

<400> 8

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Asn Ser His Val Glu Met Lys Leu Ala Val Asp Asp Glu Glu Asn Ala
 35 40 45

Asp Asn Asn Thr Lys Ala Asn Gly Thr Lys Pro Lys Arg Cys Gly Gly
 50 55 60

Asn Ile Cys Tyr Gly Thr Ile Ala Val Ile Ile Phe Phe Leu Ile Gly
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Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
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Glu Cys Glu Arg Leu Ala Gly Thr Glu Ser Pro Ala Arg Glu Glu Pro

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105

110

Glu Glu Asp Phe Pro Ala Ala Pro Arg Leu Tyr Trp Asp Asp Leu Lys
 115 120 125

Arg Lys Leu Ser Glu Lys Leu Asp Thr Thr Asp Phe Thr Ser Thr Ile
 130 135 140

Lys Leu Leu Asn Glu Asn Leu Tyr Val Pro Arg Glu Ala Gly Ser Gln
 145 150 155 160

Lys Asp Glu Asn Leu Ala Leu Tyr Ile Glu Asn Gln Phe Arg Glu Phe
 165 170 175

Lys Leu Ser Lys Val Trp Arg Asp Gln His Phe Val Lys Ile Gln Val
 180 185 190

Lys Asp Ser Ala Gln Asn Ser Val Ile Ile Val Asp Lys Asn Gly Gly
 195 200 205

Leu Val Tyr Leu Val Glu Asn Pro Gly Gly Tyr Val Ala Tyr Ser Lys
 210 215 220

Ala Ala Thr Val Thr Gly Lys Leu Val His Ala Asn Phe Gly Thr Lys
 225 230 235 240

Lys Asp Phe Glu Asp Leu Asp Ser Pro Val Asn Gly Ser Ile Val Ile
 245 250 255

Val Arg Ala Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn Ala Glu
 260 265 270

Ser Leu Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe
 275 280 285

Pro Ile Val Lys Ala Asp Leu Ser Phe Phe Gly His Ala His Leu Gly
 290 295 300

Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln
305 310 315 320

Phe Pro Pro Ser Gln Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr
325 330 335

Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp
340 345 350

Cys Pro Ser Asp Trp Lys Thr Asp Ser Thr Cys Lys Met Val Thr Ser
355 360 365

Glu Asn Lys Ser Val Lys Leu Thr Val Ser Asn Val Leu Lys Glu Thr
370 375 380

Lys Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Phe Val Glu Pro Asp
385 390 395 400

His Tyr Val Val Val Gly Ala Gln Arg Asp Ala Trp Gly Pro Gly Ala
405 410 415

Ala Lys Ser Ser Val Gly Thr Ala Leu Leu Leu Lys Leu Ala Gln Met
420 425 430

Phe Ser Asp Met Val Leu Lys Asp Gly Phe Gln Pro Ser Arg Ser Ile
435 440 445

Ile Phe Ala Ser Trp Ser Ala Gly Asp Phe Gly Ser Val Gly Ala Thr
450 455 460

Glu Trp Leu Glu Gly Tyr Leu Ser Ser Leu His Leu Lys Ala Phe Thr
465 470 475 480

Tyr Ile Asn Leu Asp Lys Ala Val Leu Gly Thr Ser Asn Phe Lys Val
485 490 495

Ser Ala Ser Pro Leu Leu Tyr Thr Leu Ile Glu Lys Thr Met Gln Asp

500

505

510

Val Lys His Pro Val Thr Gly Arg Ser Leu Tyr Gln Asp Ser Asn Trp
 515 520 525

Ala Ser Lys Val Glu Lys Leu Thr Leu Asp Asn Ala Ala Phe Pro Phe
 530 535 540

Leu Ala Tyr Ser Gly Ile Pro Ala Val Ser Phe Cys Phe Cys Glu Asp
 545 550 555 560

Thr Asp Tyr Pro Tyr Leu Gly Thr Thr Met Asp Thr Tyr Lys Glu Leu
 565 570 575

Val Glu Arg Ile Pro Glu Leu Asn Lys Val Ala Arg Ala Ala Ala Glu
 580 585 590

Val Ala Gly Gln Phe Val Ile Lys Leu Thr His Asp Thr Glu Leu Asn
 595 600 605

Leu Asp Tyr Glu Arg Tyr Asn Ser Gln Leu Leu Leu Phe Leu Arg Asp
 610 615 620

Leu Asn Gln Tyr Arg Ala Asp Val Lys Glu Met Gly Leu Ser Leu Gln
 625 630 635 640

Trp Leu Tyr Ser Ala Arg Gly Asp Phe Phe Arg Ala Thr Ser Arg Leu
 645 650 655

Thr Thr Asp Phe Arg Asn Ala Glu Lys Arg Asp Lys Phe Val Met Lys
 660 665 670

Lys Leu Asn Asp Arg Val Met Arg Val Glu Tyr Tyr Phe Leu Ser Pro
 675 680 685

Tyr Val Ser Pro Lys Glu Ser Pro Phe Arg His Val Phe Trp Gly Ser
 690 695 700

Gly Ser His Thr Leu Ser Ala Leu Leu Glu Ser Leu Lys Leu Arg Arg
705 710 715 720

Gln Asn Asn Ser Ala Phe Asn Glu Thr Leu Phe Arg Asn Gln Leu Ala
725 730 735

Leu Ala Thr Trp Thr Ile Gln Gly Ala Ala Asn Ala Leu Ser Gly Asp
740 745 750

Val Trp Asp Ile Asp Asn Glu Phe
755 760

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<211> 1914
<212> DNA
<213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

<400> 10

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Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln

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Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

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

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

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
 225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
 245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
 260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
 275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
 290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
 305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
 325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
 340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
 355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
 370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
 385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
 405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln

420

425

430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
 435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
 450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
 465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
 485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
 500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
 515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
 530 535 540

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

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
 565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
 580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
 595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
 610 615 620

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$\langle 211 \rangle$	1914
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Monkey

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<210> 12
 <211> 638
 <212> PRT
 <213> Monkey

<400> 12

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Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
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 35 40 45

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

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
 275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
 290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
 305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
 325 330 335

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

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
 355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
 370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
 385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
 405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
 420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
 435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
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Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu

465 470 475 480

Phe Gly Thr Ser Ser Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
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Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
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Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Gln Asn
 515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Ile Leu Glu Gly
 530 535 540

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

Glu Cys Leu Pro Gln Val Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
 565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
 580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
 595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
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Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Ala Arg
625 630 635

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<211> 3630
<212> DNA
<213> Homo sapiens

<400> 13
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agcgagatct cctccatcct ggagaaagga gaacgcctcc ctcagccacc catatgtacc	2820
atogatgtct acatgatcat ggtcaagtgc tggatgatag acgcagatag tcgcccacaa	2880
ttccgtgagt tgatcatoga attctccaaa atggcccgag acccccagcg ctaccttgc	2940
attcaggggg atgaaagaat gcatttgcca agtcctacag actccaactt ctaccgtgcc	3000
ctgatggatg aagaagacat ggacgacgtg gtggatgccg acgagtacct catcccacag	3060

cagggtttct tcagcagccc ctccacgtca cggactcccc tcctgagctc tctgagtga 3120
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 aaggaagaca gcttcttgca gcgatacagc tcagacccca caggcgcctt gactgaggac 3240
 agcatagacg acaccttcct cccagtgcct gaatacataa accagtccgt tcccaaaagg 3300
 cccgctggct ctgtgcagaa tcctgtctat cacaatcagc ctctgaacct cgcgccagc 3360
 agagaccac actaccagga cccccacagc actgcagtgg gcaaccccgga gtatctcaac 3420
 actgtccagc ccacctgtgt caacagcaca ttgcacagcc ctgcccactg ggcccagaaa 3480
 ggagccacc aaattagcct ggacaaccct gactaccagc aggacttctt tccaaggaa 3540
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 gcgccacaaa gcagtgaatt tattggagca 3630

<210> 14
 <211> 1210
 <212> PRT
 <213> Homo sapiens

<400> 14

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

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

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
 35 40 45

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

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

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val

35

85

90

95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
 290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
 305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
 325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
 340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
 355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
 370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
 385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
 405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
 420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
 435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
 450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
 465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu

485

490

495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
 500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
 515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
 530 535 540

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

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
 565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
 580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
 595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
 610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
 625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
 645 650 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
 660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
 675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
740 745 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
755 760 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
770 775 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785 790 795 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
805 810 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
820 825 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
850 855 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865 870 875 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp

885

890

895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
 900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
 915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
 930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
 945 950 955 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
 965 970 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
 980 985 990

Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
 995 1000 1005

Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
 1010 1015 1020

Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
 1025 1030 1035

Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
 1040 1045 1050

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
 1055 1060 1065

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
 1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
1175 1180 1185

Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln
1190 1195 1200

Ser Ser Glu Phe Ile Gly Ala
1205 1210

<210> 15
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> description of the artificial sequence: the base sequence of A27
VL

<400> 15
gaaatagtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gtcacacctc gtggacgttc 300
ggccaaggga ccaaggtgga aatcaaaa 327

<210> 16
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> description of the artificial sequence: the amino acid sequence
of A27 VL

<400> 16

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 17

<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of A27 LCDR1

<400> 17

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 18
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of A27 LCDR2

<400> 18

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 19
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of A27 LCDR3

<400> 19

Gln Gln Tyr Gly Ser Ser Pro Pro Trp Thr
1 5 10

<210> 20
<211> 366
<212> DNA
<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of
PSM4072 VH

<400> 20
gaggtgcagc tgggtggagac tgggggaggc ttggtgcaac ctggggggtc cctgagactc 60
tcctgtacag cctctggatt cacctttgaa agtcatgccca tgtactgggt ccggcaagct 120
ccaggggaagg ggctggagtg ggtctcgggt attagtaatg gaggtagtag cacagagtac 180
gcagactcgc tgagggggccg gttcaccatt tccagagaca attccaagaa tacgggtgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagaccaaga 300
tctccatata tcttctacga tgctgctggt gtctggggcc aaggggaccct ggtcaccgtc 360
tcctca 366

<210> 21
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> description of the artificial sequence: the amino acid sequence
of PSM4072 VH

<400> 21
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Glu Ser His
20 25 30
Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Asn Gly Gly Ser Ser Thr Glu Tyr Ala Asp Ser Val
50 55 60
Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Arg Ser Pro Tyr Leu Phe Tyr Asp Ala Ala Gly Val Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 22
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> description of the artificial sequence: the amino acid sequence
 of PSM4072 HCDR1

<400> 22

Ser His Ala Met Tyr
 1 5

<210> 23
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> description of the artificial sequence: the amino acid sequence
 of PSM4072 HCDR2

<400> 23

Gly Ile Ser Asn Gly Gly Ser Ser Thr Glu Tyr Ala Asp Ser Val Arg
 1 5 10 15

Gly

<210> 24
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of PSM4072 HCDR3

<400> 24

Pro Arg Ser Pro Tyr Leu Phe Tyr Asp Ala Ala Gly Val
1 5 10

<210> 25

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of R327 VH

<400> 25

gaggtgcagc tggaggagac cgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tctgtgcag cctctggatt cagctttgac aagtatacca tgaactgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagtt atttctaag ggggagtttc tacagactac	180
gcagactccg ttaaggccg gttcaccgtc tccagagaca attccaagaa cacactgtac	240
ctgcaaatga acagcctgag agccgaggat atggccacat attactgtgc gcgtgcgagc	300
cagccgtggc tctataggac cgggtcggat gtgtggggcc aggggacaat ggtcaccgtc	360
tcttca	366

<210> 26

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of R327 VH

<400> 26

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asp Lys Tyr
 20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Val Ile Ser Asn Gly Gly Val Ser Thr Asp Tyr Ala Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Ala Ser Gln Pro Trp Leu Tyr Arg Thr Gly Ala Asp Val Trp
 100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 27

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of R327 HCDR1

<400> 27

Lys Tyr Thr Met Asn
 1 5

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of R327 HCDR2

<400> 28

Val	Ile	Ser	Asn	Gly	Gly	Val	Ser	Thr	Asp	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 29

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of R327 HCDR3

<400> 29

Ala	Ser	Gln	Pro	Trp	Leu	Tyr	Arg	Thr	Gly	Ala	Asp	Val
1				5					10			

<210> 30

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of Tfr1071 VH

<400> 30

tacgtgcagc	tggtggagtc	tgggggaggc	ttggtacagc	ctggggggtc	cctgagactc	60
tactgtgcag	cctctggatt	cagctttgac	aagtatacca	tgaactgggt	ccgccaggct	120
ccagggaagg	ggctggagtg	ggtctcagtt	atttctaattg	ggggagtctc	tacagactac	180
gcagactccg	ttaagggccg	gttcaccgtc	tccagagaca	attccaagaa	cacactgtac	240
ctgcaaatga	acagcctgag	agccgaggat	atggccacat	attactgtgc	gcgtgcgagc	300
cagccgtggc	totataggac	oggtgoggat	gtgtggggcc	aggggaccct	gtcaccgtc	360

tcctca

366

<210> 31
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of TfR1071 VH

<400> 31

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asp Lys Tyr
 20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Val Ile Ser Asn Gly Gly Val Ser Thr Asp Tyr Ala Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Ala Ser Gln Pro Trp Leu Tyr Arg Thr Gly Ala Asp Val Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 32
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of TFR1071 HCDR1

<400> 32

Lys Tyr Thr Met Asn
1 5

<210> 33

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of TFR1071 HCDR2

<400> 33

Val Ile Ser Asn Gly Gly Val Ser Thr Asp Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 34

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of TFR1071 HCDR3

<400> 34

Ala Ser Gln Pro Trp Leu Tyr Arg Thr Gly Ala Asp Val
1 5 10

<210> 35

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of
TfR4016 VH

<400> 35

tacgtgcagc tggtaggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tcctgtgcag cctctggatt cagctttgac aagtatacca tgaactgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagtt atttotaatg ggggagtttc tacagactac	180
gcagactccg ttaagggccg gttcacccgc tccagagaca attccaagaa cacactgtac	240
ctgcaaatga acagcctgag agccgaggat atggccacat attactgtgc gcgtgcgagc	300
cagccgtggc tctataggac cggtagcgat gtgtggggcc aggggaccac ggtcacccgc	360
tcctca	366

<210> 36

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of TfR4016 VH

<400> 36

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

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Asp	Lys	Tyr
			20					25					30		

Thr	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
			35				40					45			

Ser	Val	Ile	Ser	Asn	Gly	Gly	Val	Ser	Thr	Asp	Tyr	Ala	Asp	Ser	Val
						55					60				

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Ala Ser Gln Pro Trp Leu Tyr Arg Thr Gly Ala Asp Val Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 37
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> description of the artificial sequence: the amino acid sequence
 of TFR4016 HCDR1

<400> 37

Lys Tyr Thr Met Asn
 1 5

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

<220>
 <223> description of the artificial sequence: the amino acid sequence
 of TFR4016 HCDR2

<400> 38

Val Ile Ser Asn Gly Gly Val Ser Thr Asp Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 39
 <211> 13
 <212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of Tfr4016 HCDR3

<400> 39

Ala	Ser	Gln	Pro	Trp	Leu	Tyr	Arg	Thr	Gly	Ala	Asp	Val
1				5					10			

<210> 40

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of cyno186 VH

<400> 40

caggtgcagc	tggtggagtc	tgggggagaa	ttcgtacagc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cccctttaaa	ggctatgcca	tgaattgggt	ccgccaggct	120
ccagggaagg	gattggagtg	ggtctcaaga	ataagtaatg	gtggtagcta	catagactac	180
gcagactccg	taaagggccg	gttcaccatc	tcagagaca	attccaagaa	cacgctgtat	240
ttgcaaatag	acagcctgag	aaccgaggac	acggccgtat	attactgtgc	gaaagcgaag	300
gacgcctata	ggtggaacaa	cgctatagac	gaatggggcc	aagggaccct	ggtcaccgto	360
tcctca						366

<210> 41

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of cyno186 VH

<400> 41

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Glu	Phe	Val	Gln	Pro	Gly	Gly
1				5					10					15	

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Lys Gly Tyr
 20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ser Asn Gly Gly Ser Tyr Ile Asp Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

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

Ala Lys Ala Lys Asp Ala Tyr Arg Trp Asn Asn Ala Ile Asp Glu Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 42

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of cyno186 HCDR1

<400> 42

Gly Tyr Ala Met Asn
 1 5

<210> 43

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of cyno186 HCDR2

<400> 43

Arg	Ile	Ser	Asn	Gly	Gly	Ser	Tyr	Ile	Asp	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 44

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of cyno186 HCDR3

<400> 44

Ala	Lys	Asp	Ala	Tyr	Arg	Trp	Asn	Asn	Ala	Ile	Asp	Glu
1				5					10			

<210> 45

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of cyno292 VH

<400> 45

caggtgcagc	tggtgcaatc	tgggggaggc	ctggtcaagc	ctggggggtc	cctgagaatc	60
tcctgtacaa	cctctggatt	cccctttgat	ggctatacca	tgacctgggt	cggccaggct	120
ccaggggaagg	ggctggagtg	ggtctcaagt	attagtaatg	gtggtagcac	cattttcgtc	180
tcagactcag	tgagaggccg	attcaccatc	tccagagaca	acgccaagaa	ttcactgtat	240
ctccaaatga	acaacgtggg	agccgaggac	acggctgtgt	attactgtgc	gagagctcga	300
gatgcgtatg	gctggacgct	tccttctgac	atctggggcc	aagggacaat	ggtcaccgtc	360

tcttca

366

<210> 46

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of cyno292 VH

<400> 46

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

Ser	Leu	Arg	Ile	Ser	Cys	Thr	Thr	Ser	Gly	Phe	Pro	Phe	Asp	Gly	Tyr
			20					25					30		

Thr	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
			35				40					45			

Ser	Ser	Ile	Ser	Asn	Gly	Gly	Ser	Thr	Ile	Phe	Val	Ser	Asp	Ser	Val
	50					55						60			

Arg	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65					70					75				80	

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

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

Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser
			115				120		

<210> 47

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of cyno292 HCDR1

<400> 47

Gly Tyr Thr Met Thr
1 5

<210> 48

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of cyno292 HCDR2

<400> 48

Ser Ile Ser Asn Gly Gly Ser Thr Ile Phe Val Ser Asp Ser Val Arg
1 5 10 15

Gly

<210> 49

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of cyno292 HCDR3

<400> 49

Ala Arg Asp Ala Tyr Gly Trp Thr Leu Pro Ser Asp Ile
1 5 10

<210> 50

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of TfR1007 VH

<400> 50

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

Ser Leu Ser Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Lys Gly Tyr
 20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Leu Ser Asn Gly Gly Gly Ser Ser Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Thr Leu Gly Ala Tyr Tyr Ile Lys Ser Ala Met Asp Val Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 51

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of cyno163 VH

<400> 51

58

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Arg Ser Pro Tyr Leu Phe Tyr Asp Ala Ala Gly Val Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 52

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of 22-30 VH

<400> 52

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Arg Leu Ser Ser Val Thr Thr Ala Asp Thr Ala Leu Tyr Tyr Cys Thr
85 90 95

Arg Glu Ala Gly Tyr Tyr Asp Ser Ser Gly Tyr Tyr Gly Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 53

<211> 107

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> description of the artificial sequence: the amino acid sequence of 22-30 VL

<400> 53

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Tyr Asn Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 54
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> description of the artificial sequence: the amino acid sequence
of T14 VH

<400> 54

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

Ser Leu Arg Leu Ser Cys Val Val Ser Gly Gly Thr Phe Ser Asn Phe
20 25 30

Asn Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Gly Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Ser Ser Ser Trp Tyr Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

61

100

105

110

Ser Ser

<210> 55

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of TfR434 VH

<400> 55

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Lys Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Asn Phe Trp Ser Gly Tyr Tyr Ser Pro Val Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 56
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of TfR435 VH

<400> 56

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Lys Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Ser Asn Phe Trp Ser Gly Tyr Tyr Ser Pro Val Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 57
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence

of TfR434, 435 VL

<400> 57

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
20 25 30

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

Ile Tyr Glu Asp Thr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
85 90 95

Ala Tyr His Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu
100 105 110

<210> 58

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of E08
VH

<400> 58

gaggtgcagc tgggtggagtc tgggggaggc ttgtacagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt cagctttaac aacaatgcc a tgaactgggt ccgtcaggct 120

ccaggaagg ggctggagt ggtctcagg attcgtgcc atggcggtac gacatactac 180

gcagactccg tgaagggcc gttcaccatc tccagagaca attccaagaa cacactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat atttctgtgg aaagacgcct 300
gactgggaaa tcttctacta cgctatggac gcctggggcc aagggaccac ggtcaccgto 360
tcctca 366

<210> 59
<211> 122
<212> PRT
<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of E08 VH

<400> 59

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Asn Asn
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Arg Ala Asp Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Gly Lys Thr Pro Asp Trp Glu Ile Phe Tyr Tyr Ala Met Asp Ala Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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

<220>

<223> description of the artificial sequence: the amino acid sequence
 of E08 HCDR1

<400> 60

Asn Asn Ala Met Asn
 1 5

<210> 61
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of E08 HCDR2

<400> 61

Gly Ile Arg Ala Asp Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 62
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of E08 HCDR3

<400> 62

Thr Pro Asp Trp Glu Ile Phe Tyr Tyr Ala Met Asp Ala
 1 5 10

<210> 63

<211> 363
 <212> DNA
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of E12 VH

<400> 63

```
caggtgcagc tggtagtc tgggggagc ttgtacagc ctggggggtc cctgagactc      60
tcctgtgcag cctctagatt caccttagc gcctatgcca tgggtgggt gcgccaggct      120
ccaggaagg ggctggagt ggtctcaatt attgatagt gtggtgtgta cacatactac      180
gcagactcca tgaagggccg cttcaccatc tccagagaca attccaagaa caogctgtat      240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagatcat      300
tatggtgttg tttggggact tggagattac tggggccagg gaacctggt cactgtctcc      360
tca                                                                    363
```

<210> 64
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of E12 VH

<400> 64

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1           5           10          15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Arg Phe Thr Phe Ser Ala Tyr
          20          25          30
```

```
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
```

```
Ser Ile Ile Asp Ser Gly Gly Val Tyr Thr Tyr Tyr Ala Asp Ser Met
          50          55          60
```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp His Tyr Gly Val Val Trp Gly Leu Gly Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 65
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> description of the artificial sequence: the amino acid sequence
 of E12 HCDR1

<400> 65

Ala Tyr Ala Met Gly
 1 5

<210> 66
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> description of the artificial sequence: the amino acid sequence
 of E12 HCDR2

<400> 66

Ile Ile Asp Ser Gly Gly Val Tyr Thr Tyr Tyr Ala Asp Ser Met Lys
 1 5 10 15

Gly

<210> 67
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of E12 HCDR3

<400> 67

Asp His Tyr Gly Val Val Trp Gly Leu Gly Asp Tyr
 1 5 10

<210> 68
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of E17
 VH

<400> 68
 caggtgcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac tctgtccctc 60
 acctgcgcac tgtacagtgg gtccttcagt gctcaggact ggagctggat ccgccagtcc 120
 ccagagaagg ggctggagtg gattggggaa atctggcaag ggggaaaaac caactacaac 180
 ccgtccctca agagtcgagt tagtatatca agagacaact ccaagaacca gttgtccctg 240
 cagctgagct ctgtgaccgc ogcggacacg gctgtgtatt actgtgcgag ggtggactgg 300
 tttatcgtg tttttgaaat ctggggccaa gggacaatgg tcaccgtctc ttca 354

<210> 69
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of E17 VH

<400> 69

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

Thr Leu Ser Leu Thr Cys Ala Leu Tyr Ser Gly Ser Phe Ser Ala Gln
 20 25 30

Asp Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Glu Ile Trp Gln Gly Gly Lys Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Ser Ile Ser Arg Asp Asn Ser Lys Asn Gln Leu Ser Leu
 65 70 75 80

Gln Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Val Asp Trp Ser Tyr Arg Val Phe Glu Ile Trp Gly Gln Gly Thr
 100 105 110

Met Val Thr Val Ser Ser
 115

<210> 70

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of E17 HCDR1

<400> 70

Ala Gln Asp Trp Ser
 1 5

<210> 71

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of E17 HCDR2

<400> 71

Glu	Ile	Trp	Gln	Gly	Gly	Lys	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 72

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of E17 HCDR3

<400> 72

Val	Asp	Trp	Ser	Tyr	Arg	Val	Phe	Glu	Ile
1				5					10

<210> 73

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of KME07 VH

<400> 73

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

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Phe
			20					25					30		

Ala	Phe	Gly	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			

Gly Glu Val Arg Pro Gly Phe Gly Thr Glu Ile Leu Thr Gln Asn Phe
 50 55 60

Gln Asp Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Thr Tyr
 65 70 75 80

Met Glu Leu Arg Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Leu Leu Arg Gly Gly Tyr Ile Glu Asn Pro Phe Glu Ile
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 74

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of KME09 VH

<400> 74

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Phe
 20 25 30

Ala Trp Gly Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Glu Ile Arg Pro Gly Phe Gly Thr Glu Ile Tyr Ala Gln Asn Phe
 50 55 60

Gln Asp Arg Val Thr Phe Ile Thr Asp Glu Ala Thr Ser Thr Thr Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 75

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of KME11 VH

<400> 75

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Leu Ser Thr Tyr
20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Phe Ala Trp Met
35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Val Thr Tyr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gly Asp Glu Leu Ser Glu Gly His Ser Glu Tyr Tyr His Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 76

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of Cetuximab VH

<400> 76

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

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
 50 55 60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
 65 70 75 80

Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
 85 90 95

Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ala
 115

<210> 77

<211> 107
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of Cetuximab VL

<400> 77

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

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
 20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
 35 40 45

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

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

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
 85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105

<210> 78
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of HN3 VH

<400> 78

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

75

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Tyr Phe Asp Phe Asp Ser Tyr
20 25 30

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

Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Thr Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Arg Val Asn Met Asp Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ser
115

<210> 79

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid of
sequence of linker

<400> 79

Glu Ser

1

<210> 80

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid of
sequence of linker

<400> 80

Glu Ser Lys Tyr Gly
1 5

<210> 81

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid of
sequence of linker

<400> 81

Glu Ser Lys Tyr Gly Pro Pro
1 5

<210> 82

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid of
sequence of linker

<400> 82

Gly Gly Gly Gly Ser
1 5

<210> 83

<211> 981

<212> DNA

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of
IgG4PE R409K constant region

<400> 83
 gctagcacca agggggccatc cgtcttcccc ctggcgccct gctccaggag cacctccgag 60
 agcacagccg cccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 120
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggtgttcct acagtccctca 180
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc 240
 tacactgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 300
 aaatatggtc ccccatgccc accatgccc gcacctgagt tcgagggggg accatcagtc 360
 ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 420
 tgcgtgggtg tggacgtgag ccaggaagac ccgaggtcc agttcaactg gtacgtggat 480
 ggcggtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 540
 cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 600
 tgcaaggtct ccaacaaagg cctcccgctc tccatcgaga aaaccatctc caaagccaaa 660
 gggcagcccc gagagccaca ggtgtacacc ctgcccccat ccaggagga gatgaccaag 720
 aaccaggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag 780
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccggt gctggactcc 840
 gacggctcct tcttctctta cagcaagcta accgtggaca agagcaggtg gcaggagggg 900
 aatgtcttct catgtccgt gatgcatgag gctctgcaca accactacac acagaagagc 960
 ctctccctgt ctctgggtaa a 981

<210> 84
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> description of the artificial sequence: the amino acid sequence
 of IgG4PE R409K constant region

<400> 84

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

210

215

220

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
 325

<210> 85
 <211> 294
 <212> DNA
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the base sequence of
 modified codons of IgG4 CH1

<400> 85
 gctagcacca aaggaccttc tgtatttcct cttgogccat gctctcgctc tacgtcagaa 60
 tcaactgccg ctctgggggtg cctggttaaa gactacttcc cggagcctgt gacagtgagt 120
 tggaactccg gcgccctgac atcaggagtg catacatttc ccgccgtgct tcagagcagc 180
 ggactttata gcctcagcag tgtggtgacc gtgccatctt ccagcctggg gaccaagacc 240
 tacacctgta acgtggacca caaaccagc aacaccaagg ttgataagag ggctc 294

<210> 86
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of IgG4PE constant region

<400> 86

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp

145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270

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

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
 325

<210> 87

<211> 763

<212> PRT

<213> Mus musculus

<400> 87

Met Met Asp Gln Ala Arg Ser Ala Phe Ser Asn Leu Phe Gly Gly Glu
 1 5 10 15

Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
 20 25 30

Asn Ser His Val Glu Met Lys Leu Ala Ala Asp Glu Glu Glu Asn Ala
 35 40 45

Asp Asn Asn Met Lys Ala Ser Val Arg Lys Pro Lys Arg Phe Asn Gly
 50 55 60

Arg Leu Cys Phe Ala Ala Ile Ala Leu Val Ile Phe Phe Leu Ile Gly
 65 70 75 80

Phe Met Ser Gly Tyr Leu Gly Tyr Cys Lys Arg Val Glu Gln Lys Glu
 85 90 95

Glu Cys Val Lys Leu Ala Glu Thr Glu Glu Thr Asp Lys Ser Glu Thr
 100 105 110

Met Glu Thr Glu Asp Val Pro Thr Ser Ser Arg Leu Tyr Trp Ala Asp
 115 120 125

Leu Lys Thr Leu Leu Ser Glu Lys Leu Asn Ser Ile Glu Phe Ala Asp
 130 135 140

Thr Ile Lys Gln Leu Ser Gln Asn Thr Tyr Thr Pro Arg Glu Ala Gly
 145 150 155 160

Ser Gln Lys Asp Glu Ser Leu Ala Tyr Tyr Ile Glu Asn Gln Phe His
 165 170 175

Glu Phe Lys Phe Ser Lys Val Trp Arg Asp Glu His Tyr Val Lys Ile
 180 185 190

Gln Val Lys Ser Ser Ile Gly Gln Asn Met Val Thr Ile Val Gln Ser
 195 200 205

Asn Gly Asn Leu Asp Pro Val Glu Ser Pro Glu Gly Tyr Val Ala Phe
 210 215 220

Ser Lys Pro Thr Glu Val Ser Gly Lys Leu Val His Ala Asn Phe Gly
 225 230 235 240

Thr Lys Lys Asp Phe Glu Glu Leu Ser Tyr Ser Val Asn Gly Ser Leu
 245 250 255

Val Ile Val Arg Ala Gly Glu Ile Thr Phe Ala Glu Lys Val Ala Asn
 260 265 270

Ala Gln Ser Phe Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Lys Asn
 275 280 285

Lys Phe Pro Val Val Glu Ala Asp Leu Ala Leu Phe Gly His Ala His
 290 295 300

Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His
 305 310 315 320

Thr Gln Phe Pro Pro Ser Gln Ser Ser Gly Leu Pro Asn Ile Pro Val
 325 330 335

Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Lys Met Glu
 340 345 350

Gly Ser Cys Pro Ala Arg Trp Asn Ile Asp Ser Ser Cys Lys Leu Glu
 355 360 365

Leu Ser Gln Asn Gln Asn Val Lys Leu Ile Val Lys Asn Val Leu Lys
 370 375 380

Glu Arg Arg Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Tyr Glu Glu
385 390 395 400

Pro Asp Arg Tyr Val Val Val Gly Ala Gln Arg Asp Ala Leu Gly Ala
405 410 415

Gly Val Ala Ala Lys Ser Ser Val Gly Thr Gly Leu Leu Leu Lys Leu
420 425 430

Ala Gln Val Phe Ser Asp Met Ile Ser Lys Asp Gly Phe Arg Pro Ser
435 440 445

Arg Ser Ile Ile Phe Ala Ser Trp Thr Ala Gly Asp Phe Gly Ala Val
450 455 460

Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser Ser Leu His Leu Lys
465 470 475 480

Ala Phe Thr Tyr Ile Asn Leu Asp Lys Val Val Leu Gly Thr Ser Asn
485 490 495

Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr Leu Met Gly Lys Ile
500 505 510

Met Gln Asp Val Lys His Pro Val Asp Gly Lys Ser Leu Tyr Arg Asp
515 520 525

Ser Asn Trp Ile Ser Lys Val Glu Lys Leu Ser Phe Asp Asn Ala Ala
530 535 540

Tyr Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala Val Ser Phe Cys Phe
545 550 555 560

Cys Glu Asp Ala Asp Tyr Pro Tyr Leu Gly Thr Arg Leu Asp Thr Tyr
565 570 575

Glu Ala Leu Thr Gln Lys Val Pro Gln Leu Asn Gln Met Val Arg Thr
580 585 590

Ala Ala Glu Val Ala Gly Gln Leu Ile Ile Lys Leu Thr His Asp Val
 595 600 605

Glu Leu Asn Leu Asp Tyr Glu Met Tyr Asn Ser Lys Leu Leu Ser Phe
 610 615 620

Met Lys Asp Leu Asn Gln Phe Lys Thr Asp Ile Arg Asp Met Gly Leu
 625 630 635 640

Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp Tyr Phe Arg Ala Thr
 645 650 655

Ser Arg Leu Thr Thr Asp Phe His Asn Ala Glu Lys Thr Asn Arg Phe
 660 665 670

Val Met Arg Glu Ile Asn Asp Arg Ile Met Lys Val Glu Tyr His Phe
 675 680 685

Leu Ser Pro Tyr Val Ser Pro Arg Glu Ser Pro Phe Arg His Ile Phe
 690 695 700

Trp Gly Ser Gly Ser His Thr Leu Ser Ala Leu Val Glu Asn Leu Lys
 705 710 715 720

Leu Arg Gln Lys Asn Ile Thr Ala Phe Asn Glu Thr Leu Phe Arg Asn
 725 730 735

Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly Val Ala Asn Ala Leu
 740 745 750

Ser Gly Asp Ile Trp Asn Ile Asp Asn Glu Phe
 755 760

<210> 88

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of Apical domain mouse chimera of human TfR extracellular domain

<400> 88

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Ser Ser Ile Gly Gln Asn Met
100 105 110

Val Thr Ile Val Gln Ser Asn Gly Asn Leu Asp Pro Val Glu Ser Pro
115 120 125

Glu Gly Tyr Val Ala Phe Ser Lys Pro Thr Glu Val Ser Gly Lys Leu
130 135 140

Val His Ala Asn Phe Gly Thr Lys Lys Asp Phe Glu Glu Leu Ser Tyr
145 150 155 160

Ser Val Asn Gly Ser Leu Val Ile Val Arg Ala Gly Glu Ile Thr Phe
165 170 175

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

Ile Tyr Met Asp Lys Asn Lys Phe Pro Val Val Glu Ala Asp Leu Ala
 195 200 205

Leu Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

Phe Pro Ser Phe Asn His Thr Gln Phe Pro Pro Ser Gln Ser Ser Gly
 225 230 235 240

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
 245 250 255

Leu Phe Gly Lys Met Glu Gly Ser Cys Pro Ala Arg Trp Asn Ile Asp
 260 265 270

Ser Ser Cys Lys Leu Glu Leu Ser Gln Asn Gln Asn Val Lys Leu Ile
 275 280 285

Val Lys Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
 290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
 305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
 340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser

370

375

380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
 625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 89

<211> 675

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of Protease-like domain mouse chimera of human TfR extracellular
 domain

<400> 89

Cys Lys Arg Val Glu Gln Lys Glu Glu Cys Val Lys Leu Ala Glu Thr
 1 5 10 15

Glu Glu Thr Asp Lys Ser Glu Thr Met Glu Thr Glu Asp Val Pro Thr
 20 25 30

Ser Ser Arg Leu Tyr Trp Ala Asp Leu Lys Thr Leu Leu Ser Glu Lys
 35 40 45

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

90

50

55

60

Thr Tyr Thr Pro Arg Glu Ala Gly Ser Gln Lys Asp Glu Ser Leu Ala
65 70 75 80

Tyr Tyr Ile Glu Asn Gln Phe His Glu Phe Lys Phe Ser Lys Val Trp
85 90 95

Arg Asp Glu His Tyr Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn
100 105 110

Ser Val Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu
115 120 125

Asn Pro Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly
130 135 140

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

Tyr Thr Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile
165 170 175

Thr Phe Ala Glu Lys Val Ala Asn Ala Glu Ser Leu Asn Ala Ile Gly
180 185 190

Val Leu Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu
195 200 205

Leu Ser Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr
210 215 220

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

Ser Gly Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala
245 250 255

Glu Lys Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys
 260 265 270

Thr Asp Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys
 275 280 285

Leu Thr Val Ser Asn Val Leu Lys Glu Arg Arg Ile Leu Asn Ile Phe
 290 295 300

Gly Val Ile Lys Gly Tyr Glu Glu Pro Asp Arg Tyr Val Val Val Gly
 305 310 315 320

Ala Gln Arg Asp Ala Leu Gly Ala Gly Val Ala Ala Lys Ser Ser Val
 325 330 335

Gly Thr Gly Leu Leu Leu Lys Leu Ala Gln Val Phe Ser Asp Met Ile
 340 345 350

Ser Lys Asp Gly Phe Arg Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp
 355 360 365

Thr Ala Gly Asp Phe Gly Ala Val Gly Ala Thr Glu Trp Leu Glu Gly
 370 375 380

Tyr Leu Ser Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp
 385 390 395 400

Lys Val Val Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu
 405 410 415

Leu Tyr Thr Leu Met Gly Lys Ile Met Gln Asp Val Lys His Pro Val
 420 425 430

Asp Gly Lys Ser Leu Tyr Arg Asp Ser Asn Trp Ile Ser Lys Val Glu
 435 440 445

Lys Leu Ser Phe Asp Asn Ala Ala Tyr Pro Phe Leu Ala Tyr Ser Gly

450

455

460

Ile Pro Ala Val Ser Phe Cys Phe Cys Glu Asp Ala Asp Tyr Pro Tyr
 465 470 475 480

Leu Gly Thr Arg Leu Asp Thr Tyr Glu Ala Leu Thr Gln Lys Val Pro
 485 490 495

Gln Leu Asn Gln Met Val Arg Thr Ala Ala Glu Val Ala Gly Gln Leu
 500 505 510

Ile Ile Lys Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg
 515 520 525

Tyr Asn Ser Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg
 530 535 540

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

Arg Gly Asp Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly
 565 570 575

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

Val Met Arg Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys
 595 600 605

Glu Ser Pro Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu
 610 615 620

Pro Ala Leu Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala
 625 630 635 640

Phe Asn Glu Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr
 645 650 655

Ile Gln Gly Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp
 660 665 670

Asn Glu Phe
 675

<210> 90
 <211> 672
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> description of the artificial sequence: the amino acid sequence
 of A01

<400> 90

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
 1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
 20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
 35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
 85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
 100 105 110

Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
 115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu
 130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
 165 170 175

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

Ile Tyr Met Asp Lys Asn Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
 195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
 245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
 260 265 270

Ser Ser Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr
 275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
 290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
 305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
 340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
 370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
 625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 91

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of A02

<400> 91

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr

97

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

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
 245 250 255

Leu Phe Gly Asn Met Glu Gly Ser Cys Pro Ala Arg Trp Asn Thr Asp
 260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr
 275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
 290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
 305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
 340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
 370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr

405

410

415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
660 665 670

<210> 92

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of A03

<400> 92

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
 100 105 110

Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
 115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu
 130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Glu Ile Thr Phe
 165 170 175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
 195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
 245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
 260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr
 275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
 290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
 305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
 340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
 370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
 625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 93
 <211> 672
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of A04

<400> 93

Cys	Lys	Gly	Val	Glu	Pro	Lys	Thr	Glu	Cys	Glu	Arg	Leu	Ala	Gly	Thr
1				5					10					15	

Glu	Ser	Pro	Val	Arg	Glu	Glu	Pro	Gly	Glu	Asp	Phe	Pro	Ala	Ala	Arg
			20					25					30		

Arg	Leu	Tyr	Trp	Asp	Asp	Leu	Lys	Arg	Lys	Leu	Ser	Glu	Lys	Leu	Asp
		35					40					45			

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

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

Val	Glu	Asn	Gln	Phe	Arg	Glu	Phe	Lys	Leu	Ser	Lys	Val	Trp	Arg	Asp
				85					90					95	

Gln	His	Phe	Val	Lys	Ile	Gln	Val	Lys	Asp	Ser	Ala	Gln	Asn	Ser	Val
			100					105					110		

Ile	Ile	Val	Asp	Lys	Asn	Gly	Arg	Leu	Val	Tyr	Leu	Val	Glu	Asn	Pro
		115					120					125			

Gly	Gly	Tyr	Val	Ala	Tyr	Ser	Lys	Ala	Ala	Thr	Val	Thr	Gly	Lys	Leu
	130						135					140			

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

Pro	Val	Asn	Gly	Ser	Ile	Val	Ile	Val	Arg	Ala	Gly	Glu	Ile	Thr	Phe
				165					170				175		

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
 195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
 245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Arg Trp Lys Thr Asp
 260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr
 275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
 290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
 305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
 340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser

370

375

380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
 625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 94

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of A05

<400> 94

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
 1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
 20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
 35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
100 105 110

Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu
130 135 140

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

Ser Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
165 170 175

Ala Glu Lys Val Ala Asn Ala Glu Ser Phe Asn Ala Ile Gly Val Leu
180 185 190

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
 260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr
 275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
 290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
 305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
 340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
 370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 95

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of A06

<400> 95

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
 1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
 20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
 35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
 85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
 100 105 110

Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
 115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu
 130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
 165 170 175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
 195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
 245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
 260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr
 275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
 290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
 305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp

340

345

350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
 370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
 625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 96

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of A07

<400> 96

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
 1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
 20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
 35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
 85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
 100 105 110

Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
 115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu
 130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
 165 170 175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
 195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
260 265 270

Ser Thr Cys Arg Leu Glu Thr Ser Gln Ser Lys Asn Val Lys Leu Thr
275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
 625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 97

<211> 671

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of A08

<400> 97

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
 1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
 20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
 35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
 85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
 100 105 110

Ile Ile Val Gln Lys Asn Gly Arg Leu Asp Leu Val Glu Asn Pro Gly
 115 120 125

Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu Val
 130 135 140

His Ala Asn Phe Gly Thr Lys Lys Asp Phe Glu Asp Leu Tyr Thr Pro
 145 150 155 160

Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe Ala
 165 170 175

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

Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser Phe
 195 200 205

Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly Phe
 210 215 220

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

Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys Leu
 245 250 255

Phe Gly Lys Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp Ser
 260 265 270

Thr Cys Arg Met Val Thr Ser Glu Ser Gln Asn Val Lys Leu Thr Val
 275 280 285

Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val Ile
 290 295 300

Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln Arg

120

305 310 315 320

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

Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp Gly
 340 345 350

Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly Asp
 355 360 365

Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser Ser
 370 375 380

Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val Leu
385 390 395 400

Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr Leu
 405 410 415

Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln Phe
 420 425 430

Leu Tyr Gln Asp Ser Asn Trp Ala Ser Lys Val Glu Lys Leu Thr Leu
 435 440 445

Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala Val
 450 455 460

Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr Thr
465 470 475 480

Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn Lys
 485 490 495

Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys Leu
 500 505 510

Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser Gln
 515 520 525

Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile Lys
 530 535 540

Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp Phe
 545 550 555 560

Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu Lys
 565 570 575

Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg Val
 580 585 590

Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro Phe
 595 600 605

Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu Leu
 610 615 620

Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu Thr
 625 630 635 640

Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly Ala
 645 650 655

Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 98

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of A09

<400> 98

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
 1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
 20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
 35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
 85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
 100 105 110

Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
 115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Pro Thr Glu Val Ser Gly Lys Leu
 130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
 165 170 175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
 195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
 245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
 260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr
 275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
 290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
 305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
 340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
 370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

125

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
660 665 670

<210> 99

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of A10

<400> 99

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
 85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
 100 105 110

Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
 115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Pro Thr Glu Val Thr Gly Lys Leu
 130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
 165 170 175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
 195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
 245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
 260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr

275

280

285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
 290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
 305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
 340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
 370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
 625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 100

<211> 673

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of A11

<400> 100

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Ser Ser Ile Gly Gln Asn Ser
100 105 110

Val Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu Asn
115 120 125

Pro Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys
130 135 140

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

130

Thr Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr
165 170 175

Phe Ala Glu Lys Val Ala Asn Ala Glu Ser Leu Asn Ala Ile Gly Val
180 185 190

Leu Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu
195 200 205

Ser Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro
210 215 220

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

Gly Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu
245 250 255

Lys Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr
260 265 270

Asp Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu
275 280 285

Thr Val Lys Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly
290 295 300

Val Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala
305 310 315 320

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

Ala Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys
340 345 350

Asp Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala
355 360 365

Gly Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu
 370 375 380

Ser Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala
 385 390 395 400

Val Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr
 405 410 415

Thr Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly
 420 425 430

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

Thr Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro
 450 455 460

Ala Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly
 465 470 475 480

Thr Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu
 485 490 495

Asn Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile
 500 505 510

Lys Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn
 515 520 525

Ser Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp
 530 535 540

Ile Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly
 545 550 555 560

Asp Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala
 565 570 575

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

Arg Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser
 595 600 605

Pro Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala
 610 615 620

Leu Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn
 625 630 635 640

Glu Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln
 645 650 655

Gly Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu
 660 665 670

Phe

<210> 101

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of A12

<400> 101

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
 1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
 20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
 35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
 85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
 100 105 110

Ile Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
 115 120 125

Glu Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu
 130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
 165 170 175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ala
 195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
 210 215 220

Phe Pro Ser Phe Asn His Thr Gln Phe Pro Pro Ser Arg Ser Ser Gly

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

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu

136

625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 102

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of A13

<400> 102

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
100 105 110

137

Ile Ile Val Gln Ser Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu
130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
165 170 175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr
275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
 325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
 340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
 355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
 370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
 625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 103

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of A14

<400> 103

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
35 40 45

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

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

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Ser Val
100 105 110

Ile Ile Val Gln Ser Asn Gly Arg Leu Val Tyr Leu Val Glu Asn Pro
115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu
130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
165 170 175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser

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

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro

143

595

600

605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
660 665 670

<210> 104

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of A15

<400> 104

Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu Ala Gly Thr
1 5 10 15

Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro Ala Ala Arg
20 25 30

Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu Lys Leu Asp
35 40 45

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

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

144

Val Glu Asn Gln Phe Arg Glu Phe Lys Leu Ser Lys Val Trp Arg Asp
85 90 95

Gln His Phe Val Lys Ile Gln Val Lys Asp Ser Ala Gln Asn Met Val
100 105 110

Thr Ile Val Asp Lys Asn Gly Arg Leu Val Tyr Pro Val Glu Ser Pro
115 120 125

Gly Gly Tyr Val Ala Tyr Ser Lys Ala Ala Thr Val Thr Gly Lys Leu
130 135 140

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

Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala Gly Lys Ile Thr Phe
165 170 175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Thr
275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu
 565 570 575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
 580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
 595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
 610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
 625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
 645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
 660 665 670

<210> 105

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of A16

<400> 105

Cys	Lys	Gly	Val	Glu	Pro	Lys	Thr	Glu	Cys	Glu	Arg	Leu	Ala	Gly	Thr
1				5				10						15	

Glu	Ser	Pro	Val	Arg	Glu	Glu	Pro	Gly	Glu	Asp	Phe	Pro	Ala	Ala	Arg
			20					25					30		

Arg	Leu	Tyr	Trp	Asp	Asp	Leu	Lys	Arg	Lys	Leu	Ser	Glu	Lys	Leu	Asp
		35					40					45			

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

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

Val	Glu	Asn	Gln	Phe	Arg	Glu	Phe	Lys	Leu	Ser	Lys	Val	Trp	Arg	Asp
			85						90					95	

Gln	His	Phe	Val	Lys	Ile	Gln	Val	Lys	Asp	Ser	Ala	Gln	Asn	Met	Val
			100					105					110		

Ile	Ile	Val	Asp	Lys	Asn	Gly	Arg	Leu	Val	Tyr	Leu	Val	Glu	Asn	Pro
		115					120					125			

Gly	Gly	Tyr	Val	Ala	Tyr	Ser	Lys	Ala	Ala	Glu	Val	Thr	Gly	Lys	Leu
		130					135				140				

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

Pro	Val	Asn	Gly	Ser	Ile	Val	Ile	Val	Arg	Ala	Gly	Lys	Ile	Thr	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

148

165

170

175

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

Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val Asn Ala Glu Leu Ser
195 200 205

Phe Phe Gly His Ala His Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly
210 215 220

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

Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys
245 250 255

Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp
260 265 270

Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys Asn Val Lys Leu Ile
275 280 285

Val Ser Asn Val Leu Lys Glu Ile Lys Ile Leu Asn Ile Phe Gly Val
290 295 300

Ile Lys Gly Phe Val Glu Pro Asp His Tyr Val Val Val Gly Ala Gln
305 310 315 320

Arg Asp Ala Trp Gly Pro Gly Ala Ala Lys Ser Gly Val Gly Thr Ala
325 330 335

Leu Leu Leu Lys Leu Ala Gln Met Phe Ser Asp Met Val Leu Lys Asp
340 345 350

Gly Phe Gln Pro Ser Arg Ser Ile Ile Phe Ala Ser Trp Ser Ala Gly
355 360 365

Asp Phe Gly Ser Val Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser
 370 375 380

Ser Leu His Leu Lys Ala Phe Thr Tyr Ile Asn Leu Asp Lys Ala Val
 385 390 395 400

Leu Gly Thr Ser Asn Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr
 405 410 415

Leu Ile Glu Lys Thr Met Gln Asn Val Lys His Pro Val Thr Gly Gln
 420 425 430

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

Leu Asp Asn Ala Ala Phe Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala
 450 455 460

Val Ser Phe Cys Phe Cys Glu Asp Thr Asp Tyr Pro Tyr Leu Gly Thr
 465 470 475 480

Thr Met Asp Thr Tyr Lys Glu Leu Ile Glu Arg Ile Pro Glu Leu Asn
 485 490 495

Lys Val Ala Arg Ala Ala Ala Glu Val Ala Gly Gln Phe Val Ile Lys
 500 505 510

Leu Thr His Asp Val Glu Leu Asn Leu Asp Tyr Glu Arg Tyr Asn Ser
 515 520 525

Gln Leu Leu Ser Phe Val Arg Asp Leu Asn Gln Tyr Arg Ala Asp Ile
 530 535 540

Lys Glu Met Gly Leu Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp
 545 550 555 560

Phe Phe Arg Ala Thr Ser Arg Leu Thr Thr Asp Phe Gly Asn Ala Glu

150

565

570

575

Lys Thr Asp Arg Phe Val Met Lys Lys Leu Asn Asp Arg Val Met Arg
580 585 590

Val Glu Tyr His Phe Leu Ser Pro Tyr Val Ser Pro Lys Glu Ser Pro
595 600 605

Phe Arg His Val Phe Trp Gly Ser Gly Ser His Thr Leu Pro Ala Leu
610 615 620

Leu Glu Asn Leu Lys Leu Arg Lys Gln Asn Asn Gly Ala Phe Asn Glu
625 630 635 640

Thr Leu Phe Arg Asn Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly
645 650 655

Ala Ala Asn Ala Leu Ser Gly Asp Val Trp Asp Ile Asp Asn Glu Phe
660 665 670

<210> 106

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of VH starting with Tfr1071 EVQL

<400> 106

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asp Lys Tyr
20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

151

Ser Val Ile Ser Asn Gly Gly Val Ser Thr Asp Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Ala Ser Gln Pro Trp Leu Tyr Arg Thr Gly Ala Asp Val Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 107

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of Tfr1007 HCDR1

<400> 107

Gly Tyr Ser Met Ser
1 5

<210> 108

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of Tfr1007 HCDR2

<400> 108

Ser Leu Ser Asn Gly Gly Gly Ser Ser Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 109

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of Tfr1007 HCDR3

<400> 109

Thr	Leu	Gly	Ala	Tyr	Tyr	Ile	Lys	Ser	Ala	Met	Asp	Val
1				5					10			

<210> 110

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of Cetuximab VH

<400> 110

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

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

Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu
		35					40					45			

Gly	Val	Ile	Trp	Ser	Gly	Gly	Asn	Thr	Asp	Tyr	Asn	Thr	Pro	Phe	Thr
		50				55					60				

Ser	Arg	Leu	Ser	Ile	Asn	Lys	Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Phe
65					70					75				80	

153

Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 111

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of Cetuximab VL

<400> 111

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

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

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

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

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 112
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of Panitumumab VH

<400> 112

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
 20 25 30

Asp Tyr Tyr Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Ile Gly His Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Ile Asp Thr Ser Lys Thr Gln Phe
 65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr
 85 90 95

Cys Val Arg Asp Arg Val Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110

Thr Met Val Thr Val Ser Ser
 115

<210> 113
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of Panitumumab VL

<400> 113

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

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

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

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

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

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

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 114

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence of Necitumumab VH

<400> 114

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe
 65 70 75 80

Ser Leu Lys Val Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala Arg Val Ser Ile Phe Gly Val Gly Thr Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 115

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
 of Necitumumab VL

<400> 115

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Tyr Gly Ser Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Ala Glu Ile Lys
100 105

<210> 116

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of Nimotuzumab VH

<400> 116

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Tyr Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
50 55 60

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

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

158

Thr Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
100 105 110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 117

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> description of the artificial sequence: the amino acid sequence
of Nimotuzumab VL

<400> 117

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

Asp Arg Phe Arg Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Tyr
85 90 95

Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110