

SEQUENCE LISTING

<110> JCR PHARMACEUTICALS CO., LTD.

<120> NOVEL ANTI-HUMAN TRANSFERRIN RECEPTOR ANTIBODY THAT PASSES THROUGH

<130> FP17-0782-00

<150> JP2016-252148

<151> 2016-12-26

<160> 189

<170> PatentIn version 3.5

<210> 1

<211> 760

<212> PRT

<213> Homo sapiens

<400> 1

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

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

Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
65 70 75 80

Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
85 90 95

Glu Cys Glu Arg Leu Ala Gly Thr Glu Ser Pro Val Arg Glu Glu Pro
100 105 110

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

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

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

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

Glu Ser Lys Asn Val Lys Leu Thr Val Ser Asn Val Leu Lys Glu Ile
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 Gly 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 Asn
500 505 510

Val Lys His Pro Val Thr Gly Gln Phe 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

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

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

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

Leu Asn Gln Tyr Arg Ala Asp Ile 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 Gly Asn Ala Glu Lys Thr Asp Arg Phe Val Met Lys
660 665 670

Lys Leu Asn Asp Arg Val Met Arg Val Glu Tyr His 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 Pro Ala Leu Leu Glu Asn Leu Lys Leu Arg Lys
705 710 715 720

Gln Asn Asn Gly 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

<210> 2

<211> 760

<212> PRT

<213> Macaca fascicularis

<400> 2

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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 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
65 70 75 80

Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
85 90 95

Glu Cys Glu Arg Leu Ala Gly Thr Glu Ser Pro Ala Arg Glu Glu Pro
100 105 110

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 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

<210> 3
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of an exemplified linker 1

<400> 3

Gly Gly Gly Gly Ser
1 5

<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of an exemplified linker 2

<400> 4

Gly Gly Gly Gly Gly Ser
1 5

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

<220>
<223> Amino acid sequence of an exemplified linker 3

<400> 5

Ser Gly Gly Gly Gly
1 5

<210> 6
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence 1 of CDR 1 in the light chain of mouse
anti-hTfR antibody No.3

<400> 6

Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 7
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence 2 of CDR 1 in the light chain of mouse
anti-hTfR antibody No.3

<400> 7

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 8
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence 1 of CDR 2 in the light chain of mouse anti-hTfR antibody No.3

<400> 8

Lys Val Ser Asn Arg Phe
1 5

<210> 9

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 2 of CDR 2 in the light chain of mouse anti-hTfR antibody No.3

<400> 9

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 10

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of CDR 3 in the light chain of mouse anti-hTfR antibody No. 3

<400> 10

Ser Gln Ser Thr His Val Pro Trp Thr
1 5

<210> 11

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 1 of CDR 1 in the heavy chain of mouse anti-hTfR antibody No.3

<400> 11

Asn Tyr Trp Leu Gly
1 5

<210> 12

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 2 of CDR 1 in the heavy chain of mouse
anti-hTfR antibody No.3

<400> 12

Gly Tyr Ser Phe Thr Asn Tyr Trp
1 5

<210> 13

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 1 of CDR 2 in the heavy chain of mouse
anti-hTfR antibody No.3

<400> 13

Ile Tyr Pro Gly Gly Asp Tyr Pro
1 5

<210> 14

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 2 of CDR 2 in the heavy chain of mouse
anti-hTfR antibody No.3

<400> 14

Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe Lys

1 5 10 15

Val

<210> 15
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence 1 of CDR 3 in the heavy chain of mouse
anti-hTfR antibody No.3

<400> 15

Ser Gly Asn Tyr Asp Glu Val Ala Tyr
1 5

<210> 16
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence 2 of CDR 3 in the heavy chain of mouse
anti-hTfR antibody No.3

<400> 16

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

<210> 17
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence 1 of the variable region of the light chain
of humanized anti-hTfR antibody No.3

<400> 17

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly

1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asn Gly Asn Thr Tyr Leu His Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45
 Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
 85 90 95
 Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 18
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence 2 of the variable region of the light chain
 of humanized anti-hTfR antibody No.3

<400> 18

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30

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

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

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

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

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 19

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 3 of the variable region of the light chain
of humanized anti-hTfR antibody No.3

<400> 19

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser

85

90

95

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 20

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 4 of the variable region of the light chain
 of humanized anti-hTfR antibody No.3

<400> 20

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

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

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

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

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

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

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 21

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 5 of the variable region of the light chain of humanized anti-hTfR antibody No.3

<400> 21

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

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

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

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

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

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

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 22

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 6 of the variable region of the light chain of humanized anti-hTfR antibody No.3

<400> 22

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 23

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the light chain of humanized anti-hTfR
antibody No.3 containing amino acid sequence 2 as the variable
region

<400> 23

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 24
<211> 740
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding the amino acid sequence of the light chain of humanized anti-hTfR antibody No.3 containing amino acid sequence 2 as the variable region, synthetic sequence

<400> 24

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acgctgccc ccaccatggg ctggagctgg attctgctgt tcctcctgag cgtgacagca      60
ggagtgcaca gcgacatcgt gatgaccag actcccctga gcctgagcgt gacacctggc      120
cagcctgccca gcatcagctg cagaagctct cagagcctgg tgcacagcaa cggcaacacc      180
tacctgcact ggtatctgca gaagcccggc cagagccctc agctgctgat ctacaagggtg      240
tccaacagat tcagcggcgt gcccgcagaga ttctccggca gcggctctgg caccgacttc      300
accctgaaga tttccagagt ggaagccgag gacgtgggagc tgtactactg cagccagagc      360
acccacgtgc cctggacatt cggccagggc accaagggtgg aaatcaagag aaccgtggcc      420
gctcccagcg tgttcatctt cccacctagc gacgagcagc tgaagtccgg cacagcctct      480
gtcgtgtgcc tgctgaacaa cttctacccc cgcgaggcca aggtgcagtg gaagggtggac      540
aacgccctgc agagcggcaa cagccaggaa agcgtgaccg agcaggactc caaggacagc      600
acctacagcc tgagcagcac cctgaccctg agcaaggccg actacgagaa gcacaagggtg      660
tacgcctgcg aagtgaacca ccagggcctg tctagccccg tgaccaagag cttcaacaga      720
ggcgagtgtt aagcggccgc                                     740
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<210> 25

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the light chain of humanized anti-hTfR antibody No.3 containing amino acid sequence 4 as the variable region

<400> 25

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Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1           5           10          15
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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 26
 <211> 740
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence encoding the amino acid sequence of the light chain of humanized anti-hTfR antibody No.3 containing amino acid sequence 4 as the variable region, synthetic sequence

<400> 26
 acgcgtgccg ccaccatggg ctggagctgg attctgctgt tcctcctgag cgtgacagca 60
 ggagtgcaca gcgacatcgt gatgaccag agccccctga gcctgcctgt gacacctggc 120
 gagcctgcca gcatcagctg cagatctagc cagagcctgg tgcacagcaa cggcaacacc 180
 tacctgcact ggtatctgca gaagcccggc cagagccctc agctgctgat ctacaaggtg 240
 tccaacagat tcagcggcgt gcccagacaga ttctccggca gcggctctgg caccgacttc 300
 accctgaaga tctccagagt ggaagccgag gacgtgggcg tgtactactg cagccagagc 360
 acccacgtgc cctggacatt cggccagggc accaaggtgg aaatcaagag aaccgtggcc 420
 gctcccagcg tgttcatctt cccacctagc gacgagcagc tgaagtccgg cacagcctct 480
 gtcgtgtgcc tgctgaacaa cttctacccc cgcgaggcca aggtgcagtg gaaggtggac 540
 aacgccctgc agagcggcaa cagccaggaa agcgtgaccg agcaggactc caaggacagc 600
 acctacagcc tgagcagcac cctgaccctg agcaaggccg actacgagaa gcacaaggtg 660
 tacgcctgcg aagtgacca ccagggcctg tctagccccg tgaccaagag cttcaacaga 720
 ggcgagtgt aagcggccgc 740

<210> 27
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of the light chain of humanized anti-hTfR

antibody No.3 containing amino acid sequence 5 as the variable region

<400> 27

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

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

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

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

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

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

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 28
<211> 740
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding the amino acid sequence of the light chain of humanized anti-hTfR antibody No.3 containing amino acid sequence 5 as the variable region, synthetic sequence

<400> 28
acgcgtgccg ccaccatggg ctggagctgg attctgctgt tcctcctgag cgtgacagca 60
ggagtgcaca gcgacatcgt gatgacccag acaccctga gcctgcctgt gacacctggc 120
gagcctgcca gcatcagctg cagatctagc cagagcctgg tgcacagcaa cggcaacacc 180
tacctgcact ggtatctgca gaagcccggc cagagccctc agctgctgat ctacaaggctg 240
tccaacagat tcagcggcgt gcccgcagaga ttctccggca gcggctcttg caccgacttc 300
accctgaaga tctccagagt ggaagccgag gacgtgggcg tgtactactg cagccagagc 360
accacgtgc cctggacatt cggccagggc accaggctgg aaatcaagag aaccgtggcc 420
gctcccagcg tgttcatctt cccacctagc gacgagcagc tgaagtccgg cacagcctct 480
gtcgtgtgcc tgctgaacaa cttctacccc cgcgaggcca aggtgcagtg gaaggtggac 540
aacgccctgc agagcggcaa cagccaggaa agcgtgaccg agcaggactc caaggacagc 600
acctacagcc tgagcagcac cctgaccctg agcaaggccg actacgagaa gcacaaggctg 660
tacgcctgcg aagtgaccca ccagggcctg tctagccccg tgaccaagag cttcaacaga 720
ggcgagtgtc aagcggccgc 740

<210> 29
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of the light chain of humanized anti-hTfR antibody No.3 containing amino acid sequence 6 as the variable region

<400> 29

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 30
 <211> 740
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence encoding the amino acid sequence of the light chain of humanized anti-hTfR antibody No.3 containing amino acid sequence 6 as the variable region, synthetic sequence

<400> 30
 acgcgtgccg ccaccatggg ctggagctgg attctgctgt tcctcctgag cgtgacagca 60
 ggagtgcaca gcgacatcgt gatgaccag actcccctga gcctgagcgt gacacctggc 120
 cagcctgcca gcatcagctg cagatccagc cagagcctgg tgcacagcaa cggcaacacc 180
 tacctgcact ggtatctgca gaagcccggc cagagccctc agctgctgat ctacaagggtg 240
 tccaacagat tcagcggcgt gcccagacaga ttctccggca gcggctctgg caccgacttc 300
 accctgaaga tttccagagt ggaagccgag gacgtgggcg tggtcttctg cagccagagc 360
 acccagctgc cctggacatt cggccagggc accaagggtg aaatcaagag aaccgtggcc 420
 gctcccagcg tgttcatctt cccacctagc gacgagcagc tgaagtccgg cacagcctct 480
 gtcgtgtgcc tgctgaacaa cttctacccc cgcgaggcca aggtgcagtg gaagggtggac 540

aacgccctgc agagcggcaa cagccaggaa agcgtgaccg agcaggactc caaggacagc 600
acctacagcc tgagcagcac cctgaccctg agcaaggccg actacgagaa gcacaaggtg 660
tacgcctgcg aagtgaccca ccagggcctg tctagccccg tgaccaagag cttcaacaga 720
ggcgagtgtc aagcggccgc 740

<210> 31
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence 1 of the variable region of the heavy chain
of humanized anti-hTfR antibody No.3

<400> 31

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

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

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

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

Lys Val Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser

115

<210> 32
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence 2 of the variable region of the heavy chain
of humanized anti-hTfR antibody No.3

<400> 32

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

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

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 33
<211> 118
<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 3 of the variable region of the heavy chain of humanized anti-hTfR antibody No.3

<400> 33

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

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

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

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

Lys Val Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 34

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 4 of the variable region of the heavy chain of humanized anti-hTfR antibody No.3

<400> 34

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

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

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 35

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 5 of the variable region of the heavy chain
of humanized anti-hTfR antibody No.3

<400> 35

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 Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Val Val Thr Val Ser Ser
115

<210> 36

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence 6 of the variable region of the heavy chain
of humanized anti-hTfR antibody No.3

<400> 36

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

Lys Val Lys Ala Ile Ile Ser Ala Asp Thr Ser Ile Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 37
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of the heavy chain of humanized anti-hTfR
antibody No.3 containing amino acid sequence 2 as the variable
region

<400> 37

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

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

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 38

<211> 1427
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding the amino acid sequence of the heavychain of humanized anti-hTfR antibody No.3 containing amino acid sequence 2 as the variable region, synthetic sequence

<400> 38

```
acgcgtgccg ccaccatggg ctggagctgg attctgctgt tcctcctgag cgtgacagca      60
ggagtgcaca gcgagggtgca actagtgcag tctggagcag aggtgaaaaa gcccggggag      120
tctctgaaga tttcctgtaa gggttctgga tacagcttta ccaactactg gctgggatgg      180
gtgcgccaga tgcccgggaa aggcttgag tggatggggg acatctaccc cggcggagac      240
taccctacat acagcgagaa gttcaaggct caggtcacca tctcagccga caagtccatc      300
agcaccgcct acctgcagtg gagcagcctg aaggcctcgg acaccgcat gtattactgt      360
gcgagatcag gcaattacga cgaagtggcc tactggggcc aaggaaccct ggtcaccgtc      420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc      480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg      540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag      600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc      660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagaaagtt      720
gagcccaa at cttgtgacaa aactcacacg tgcccaccgt gcccagcacc tgaactcctg      780
ggagggtccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      840
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      900
aactggtacg tggacggcgt ggagggtgcat aatgccaaga caaagccgcg ggaggagcag      960
tacaacagca cgtaccgggt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat     1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc     1080
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg     1140
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc     1200
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gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc 1320
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380
tacacgcaga agagcctctc cctgtctccg ggtaaataag cggccgc 1427

<210> 39
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of the heavy chain (IgG4) of humanized anti-hTfR antibody No.3 containing amino acid sequence 2 as the variable region

<400> 39

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

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

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

<210> 40
 <211> 1418
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence encoding the amino acid sequence of the heavy
 chain (IgG4) of humanized anti-hTfR antibody No.3 containing
 amino acid sequence 2 as the variable region, synthetic sequence

<400> 40
 acgcgtgccg ccaccatggg ctggagctgg attctgctgt tcctcctgag cgtgacagca 60

ggagtgcaca gcgagggtgca actagtgcag tctggagcag aggtgaaaaa gccccggggag	120
tctctgaaga tttcctgtaa gggttctgga tacagcttta ccaactactg gctgggatgg	180
gtgcgccaga tgccccgggaa aggcctggag tggatggggg acatctaccc cggcggagac	240
taccctacat acagcgagaa gttcaaggct caggtcacca tctcagccga caagtccatc	300
agcaccgcct acctgcagtg gagcagcctg aaggcctcgg acaccgcat gtattactgt	360
gcgagatcag gcaattacga cgaagtggcc tactggggcc aaggaaccct ggtcaccgtc	420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg cgccctgctc caggagcacc	480
tccgagagca cagccgccct gggctgcctg gtcaaggact acttccccga accggtgacg	540
gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca ctttcccggc tgtcctacag	600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacg	660
aagacctaca cctgcaacgt agatcacaag cccagcaaca ccaagggtgga caagagagtt	720
gagtccaaat atggtcccc atgcccacca tgcccagcac ctgagttcct ggggggtcca	780
tcagtcttcc tgttcccccc aaaacccaag gacacttca tgatctcccg gaccctgag	840
gtcacgtgcg tgggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac	900
gtggatggcg tggagggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc	960
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa cggcaaggag	1020
tacaagtgca aggtctccaa caaaggcctc ccgtcctcca tcgagaaaac catctccaaa	1080
gccaaagggc agccccgaga gccacagggtg tacaccctgc ccccatccca ggaggagatg	1140
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc	1200
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1260
gactccgacg gctccttctt cctctacagc aggctcaccg tggacaagag cagggtggcag	1320
gaggggaatg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag	1380
aagagcctct ccctgtctcc gggtaaataa gcggccgc	1418

<210> 41

<211> 43

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer hTfR5', synthetic sequence

 <400> 41
 ccgacgcgtc gccaccatga tggatcaagc tagatcagca ttc 43

 <210> 42
 <211> 59
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer hTfR3', synthetic sequence

 <400> 42
 ataatgcggc cgcttaatga tgatgatgat gatgaaactc attgtcaatg tcccaaacg 59

 <210> 43
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer Hyg-Sfi5', synthetic sequence

 <400> 43
 gaggccgcct cggcctctga 20

 <210> 44
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer Hyg-BstX3', synthetic sequence

 <400> 44
 aaccatcgtg atgggtgcta ttcctttgc 29

 <210> 45
 <211> 4460
 <212> DNA

<213> Artificial Sequence

<220>

<223> "Nucleotide sequence of the DNA formed of a cDNA encoding chimeric hTfR and a loxP-flanked neomycin resistance gene placed on the cDNA's 3' side, synthetic sequence "

<400> 45

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ttgtttggtg gggaaccatt gtcatacacc cggttttagcc ttgctcggca agtagatgga	120
gataacagtc atgtggagat gaaactggct gcagatgaag aagaaaatgc cgacaataac	180
atgaaggcta gtgtcagaaa acccaagagg tttaatggaa gactctgctt tgcagctatt	240
gcactagtca ttttcttctt gattggattc atgagtggct acctgggcta ttgtaaaggg	300
gtagaaccaa aaactgagtg tgagagactg gcaggaaccg agtctccagt gagggaggag	360
ccaggagagg acttcctgc agcacgtcgc ttatattggg atgacctgaa gagaaagttg	420
tcggagaaac tggacagcac agacttcacc ggcaccatca agctgctgaa tgaaaattca	480
tatgtccctc gtgaggctgg atctcaaaaa gatgaaaatc ttgcgttgta tgttgaaaat	540
caatttcgtg aatttaaact cagcaaagtc tggcgtgatc aacattttgt taagattcag	600
gtcaaagaca gcgctcaaaa ctcggtgatc atagttgata agaacggtag acttgtttac	660
ctggtggaga atcctggggg ttatgtggcg tatagtaagg ctgcaacagt tactggtaaa	720
ctggtccatg ctaattttgg tactaaaaaa gattttgagg atttatacac tcctgtgaat	780
ggatctatag tgattgtcag agcagggaaa atcacctttg cagaaaagggt tgcaaatgct	840
gaaagcttaa atgcaattgg tgtgttgata tacatggacc agactaaatt tcccattgtt	900
aacgcagaac tttcattctt tggacatgct catctgggga caggtgaccc ttacacacct	960
ggattccctt cttcaatca cactcagttt ccaccatctc ggtcatcagg attgcctaata	1020
atacctgtcc agacaatctc cagagctgct gcagaaaagc tgtttgggaa tatggaagga	1080
gactgtccct ctgactggaa aacagactct acatgtagga tggtaacctc agaaagcaag	1140
aatgtgaagc tcaactgtgag caatgtgctg aaagagataa aaattcttaa catctttgga	1200
gttattaaag gctttgtaga accagatcac tatgtttag ttggggccca gagagatgca	1260

tggggccctg gagctgcaaa atccggtgta ggcacagctc tcctattgaa acttgcccag	1320
atgttctcag atatggtctt aaaagatggg tttcagccca gcagaagcat tatctttgcc	1380
agttggagtg ctggagactt tggatcgggtt ggtgccactg aatggctaga gggatacctt	1440
tcgtccctgc atttaaaggc tttcacttat attaactctgg ataaagcggg tcttggtacc	1500
agcaacttca aggtttctgc cagcccactg ttgtatacgc ttattgagaa aacaatgcaa	1560
aatgtgaagc atccggttac tgggcaattt ctatatcagg acagcaactg ggccagcaaa	1620
gttgagaaac tcactttaga caatgctgct ttccctttcc ttgcatattc tggaatccca	1680
gcagtttctt tctgtttttg cgaggacaca gattatcctt atttgggtac caccatggac	1740
acctataagg aactgattga gaggattcct gagtngaaca aagtggcacg agcagctgca	1800
gaggtcgctg gtcagttcgt gattaaacta acccatgatg ttgaattgaa cctggactat	1860
gagaggtaca acagccaact gctttcattt gtgagggatc tgaaccaata cagagcagac	1920
ataaaggaaa tgggcctgag tttacagtgg ctgtattctg ctcgtggaga cttcttccgt	1980
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<210> 46
 <211> 5003
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of the 5'-arm of targeting vector, synthetic sequence

<400> 46	
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gtaaaggctg atactttcga acttgcaccg cagggttggg tgcggtgag aaagcgagcc	540
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<210> 47
 <211> 2604
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Nucleotide sequence of the 3'-arm of targeting vector, synthetic sequence

<400> 47

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tcagatgggt gtgagccacc atgtgggtgc tgggacttga aactggacc tttggaaaag	240
cagttgggta ctcttacc caagctatc acaccagccc caatacccca aattttgacc	300
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<210> 48
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Amino acid sequence of the variable region of the light chain of mouse anti-hTfR antibody No.3

<400> 48

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

Asp Arg Phe Ser 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 Phe Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg

<210> 49

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the variable region of the heavy chain of mouse anti-hTfR antibody No.3

<400> 49

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

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

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Thr
115

<210> 50
<211> 525
<212> PRT
<213> Homo sapiens

<400> 50

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

Ile Ile Val Asp Asp Leu Arg Pro Ser Leu Gly Cys Tyr Gly Asp Lys
20 25 30

Leu Val Arg Ser Pro Asn Ile Asp Gln Leu Ala Ser His Ser Leu Leu

35

40

45

Phe Gln Asn Ala Phe Ala Gln Gln Ala Val Cys Ala Pro Ser Arg Val
 50 55 60

Ser Phe Leu Thr Gly Arg Arg Pro Asp Thr Thr Arg Leu Tyr Asp Phe
 65 70 75 80

Asn Ser Tyr Trp Arg Val His Ala Gly Asn Phe Ser Thr Ile Pro Gln
 85 90 95

Tyr Phe Lys Glu Asn Gly Tyr Val Thr Met Ser Val Gly Lys Val Phe
 100 105 110

His Pro Gly Ile Ser Ser Asn His Thr Asp Asp Ser Pro Tyr Ser Trp
 115 120 125

Ser Phe Pro Pro Tyr His Pro Ser Ser Glu Lys Tyr Glu Asn Thr Lys
 130 135 140

Thr Cys Arg Gly Pro Asp Gly Glu Leu His Ala Asn Leu Leu Cys Pro
 145 150 155 160

Val Asp Val Leu Asp Val Pro Glu Gly Thr Leu Pro Asp Lys Gln Ser
 165 170 175

Thr Glu Gln Ala Ile Gln Leu Leu Glu Lys Met Lys Thr Ser Ala Ser
 180 185 190

Pro Phe Phe Leu Ala Val Gly Tyr His Lys Pro His Ile Pro Phe Arg
 195 200 205

Tyr Pro Lys Glu Phe Gln Lys Leu Tyr Pro Leu Glu Asn Ile Thr Leu
 210 215 220

Ala Pro Asp Pro Glu Val Pro Asp Gly Leu Pro Pro Val Ala Tyr Asn
 225 230 235 240

Pro Trp Met Asp Ile Arg Gln Arg Glu Asp Val Gln Ala Leu Asn Ile
245 250 255

Ser Val Pro Tyr Gly Pro Ile Pro Val Asp Phe Gln Arg Lys Ile Arg
260 265 270

Gln Ser Tyr Phe Ala Ser Val Ser Tyr Leu Asp Thr Gln Val Gly Arg
275 280 285

Leu Leu Ser Ala Leu Asp Asp Leu Gln Leu Ala Asn Ser Thr Ile Ile
290 295 300

Ala Phe Thr Ser Asp His Gly Trp Ala Leu Gly Glu His Gly Glu Trp
305 310 315 320

Ala Lys Tyr Ser Asn Phe Asp Val Ala Thr His Val Pro Leu Ile Phe
325 330 335

Tyr Val Pro Gly Arg Thr Ala Ser Leu Pro Glu Ala Gly Glu Lys Leu
340 345 350

Phe Pro Tyr Leu Asp Pro Phe Asp Ser Ala Ser Gln Leu Met Glu Pro
355 360 365

Gly Arg Gln Ser Met Asp Leu Val Glu Leu Val Ser Leu Phe Pro Thr
370 375 380

Leu Ala Gly Leu Ala Gly Leu Gln Val Pro Pro Arg Cys Pro Val Pro
385 390 395 400

Ser Phe His Val Glu Leu Cys Arg Glu Gly Lys Asn Leu Leu Lys His
405 410 415

Phe Arg Phe Arg Asp Leu Glu Glu Asp Pro Tyr Leu Pro Gly Asn Pro
420 425 430

Arg Glu Leu Ile Ala Tyr Ser Gln Tyr Pro Arg Pro Ser Asp Ile Pro
435 440 445

Gln Trp Asn Ser Asp Lys Pro Ser Leu Lys Asp Ile Lys Ile Met Gly
450 455 460

Tyr Ser Ile Arg Thr Ile Asp Tyr Arg Tyr Thr Val Trp Val Gly Phe
465 470 475 480

Asn Pro Asp Glu Phe Leu Ala Asn Phe Ser Asp Ile His Ala Gly Glu
485 490 495

Leu Tyr Phe Val Asp Ser Asp Pro Leu Gln Asp His Asn Met Tyr Asn
500 505 510

Asp Ser Gln Gly Gly Asp Leu Phe Gln Leu Leu Met Pro
515 520 525

<210> 51

<211> 975

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
anti-hTfR antibody No.3 (humanized 2) and hI2S

<400> 51

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

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

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

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe

50

55

60

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

Gly Ser Ser Glu Thr Gln Ala Asn Ser Thr Thr Asp Ala Leu Asn Val
450 455 460

Leu Leu Ile Ile Val Asp Asp Leu Arg Pro Ser Leu Gly Cys Tyr Gly
465 470 475 480

Asp Lys Leu Val Arg Ser Pro Asn Ile Asp Gln Leu Ala Ser His Ser
485 490 495

Leu Leu Phe Gln Asn Ala Phe Ala Gln Gln Ala Val Cys Ala Pro Ser
500 505 510

Arg Val Ser Phe Leu Thr Gly Arg Arg Pro Asp Thr Thr Arg Leu Tyr
515 520 525

Asp Phe Asn Ser Tyr Trp Arg Val His Ala Gly Asn Phe Ser Thr Ile
530 535 540

Pro Gln Tyr Phe Lys Glu Asn Gly Tyr Val Thr Met Ser Val Gly Lys
545 550 555 560

Val Phe His Pro Gly Ile Ser Ser Asn His Thr Asp Asp Ser Pro Tyr
565 570 575

Ser Trp Ser Phe Pro Pro Tyr His Pro Ser Ser Glu Lys Tyr Glu Asn
580 585 590

Thr Lys Thr Cys Arg Gly Pro Asp Gly Glu Leu His Ala Asn Leu Leu
595 600 605

Cys Pro Val Asp Val Leu Asp Val Pro Glu Gly Thr Leu Pro Asp Lys
610 615 620

Gln Ser Thr Glu Gln Ala Ile Gln Leu Leu Glu Lys Met Lys Thr Ser
625 630 635 640

Ala Ser Pro Phe Phe Leu Ala Val Gly Tyr His Lys Pro His Ile Pro
645 650 655

Phe Arg Tyr Pro Lys Glu Phe Gln Lys Leu Tyr Pro Leu Glu Asn Ile
660 665 670

Thr Leu Ala Pro Asp Pro Glu Val Pro Asp Gly Leu Pro Pro Val Ala
675 680 685

Tyr Asn Pro Trp Met Asp Ile Arg Gln Arg Glu Asp Val Gln Ala Leu
690 695 700

Asn Ile Ser Val Pro Tyr Gly Pro Ile Pro Val Asp Phe Gln Arg Lys
705 710 715 720

Ile Arg Gln Ser Tyr Phe Ala Ser Val Ser Tyr Leu Asp Thr Gln Val
725 730 735

Gly Arg Leu Leu Ser Ala Leu Asp Asp Leu Gln Leu Ala Asn Ser Thr
740 745 750

Ile Ile Ala Phe Thr Ser Asp His Gly Trp Ala Leu Gly Glu His Gly
755 760 765

Glu Trp Ala Lys Tyr Ser Asn Phe Asp Val Ala Thr His Val Pro Leu
770 775 780

Ile Phe Tyr Val Pro Gly Arg Thr Ala Ser Leu Pro Glu Ala Gly Glu
785 790 795 800

Lys Leu Phe Pro Tyr Leu Asp Pro Phe Asp Ser Ala Ser Gln Leu Met
805 810 815

Glu Pro Gly Arg Gln Ser Met Asp Leu Val Glu Leu Val Ser Leu Phe
820 825 830

Pro Thr Leu Ala Gly Leu Ala Gly Leu Gln Val Pro Pro Arg Cys Pro

835

840

845

Val Pro Ser Phe His Val Glu Leu Cys Arg Glu Gly Lys Asn Leu Leu
 850 855 860

Lys His Phe Arg Phe Arg Asp Leu Glu Glu Asp Pro Tyr Leu Pro Gly
 865 870 875 880

Asn Pro Arg Glu Leu Ile Ala Tyr Ser Gln Tyr Pro Arg Pro Ser Asp
 885 890 895

Ile Pro Gln Trp Asn Ser Asp Lys Pro Ser Leu Lys Asp Ile Lys Ile
 900 905 910

Met Gly Tyr Ser Ile Arg Thr Ile Asp Tyr Arg Tyr Thr Val Trp Val
 915 920 925

Gly Phe Asn Pro Asp Glu Phe Leu Ala Asn Phe Ser Asp Ile His Ala
 930 935 940

Gly Glu Leu Tyr Phe Val Asp Ser Asp Pro Leu Gln Asp His Asn Met
 945 950 955 960

Tyr Asn Asp Ser Gln Gly Gly Asp Leu Phe Gln Leu Leu Met Pro
 965 970 975

<210> 52

<211> 3011

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding the amino acid sequence of fusion protein of the heavy chain of anti-hTfR antibody No.3 (humanized 2) and hI2S, synthetic sequence

<400> 52

acgcgtgccg ccaccatggg ctggagctgg attctgctgt tcctcctgag cgtgacagca 60

ggagtgcaca gcgaggtgca actagtgcag tctggagcag aggtgaaaaa gcccggggag 120

tctctgaaga tttcctgtaa gggttctgga tacagcttta ccaactactg gctgggatgg	180
gtgcgccaga tgcccgggaa aggcttgag tggatggggg acatctaccc cggcggagac	240
taccctacat acagcgagaa gttcaaggct caggtcacca tctcagccga caagtccatc	300
agcaccgcct acctgcagtg gagcagcctg aaggcctcgg acaccgcat gtattactgt	360
gcgagatcag gcaattacga cgaagtggcc tactggggcc aaggaaccct ggtcaccgtc	420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc	480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag	600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	720
gagcccaa at cttgtgacaa aactcacacg tgcccaccgt gcccagcacc tgaactcctg	780
ggagggtccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg	840
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	900
aactggtacg tggacggcgt ggagggtgcat aatgccaaga caaagccgcg ggaggagcag	960
tacaacagca cgtaccgggt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1080
atctccaaag ccaaagggca gccccgagaa ccacagggtgt acaccctgcc cccatcccgg	1140
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1260
cccgtgctgg actccgacgg ctcttcttc ctctacagca agctcaccgt ggacaagagc	1320
agggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1380
tacacgcaga agagcctctc cctgtctccg ggtaaaggat cttccgaaac gcaggccaac	1440
tcgaccacag atgctctgaa cgttcttctc atcatcgtgg atgacctgcg cccctccctg	1500
ggctgttatg gggataagct ggtgagggtcc ccaaattattg accaactggc atcccacagc	1560

ctcctcttcc agaatgcctt tgcgcagcaa gcagtgtgcg ccccgagccg cgtttctttc	1620
ctcactggca ggagacctga caccacccgc ctgtacgact tcaactccta ctggagggtg	1680
cacgctggaa acttctccac catccccag tacttcaagg agaatggcta tgtgaccatg	1740
tcggtgggaa aagtctttca ccctgggata tcttctaacc ataccgatga ttctccgtat	1800
agctggtctt ttccacctta tcatccttcc tctgagaagt atgaaaacac taagacatgt	1860
cgagggccag atggagaact ccatgccaac ctgctttgcc ctgtggatgt gctggatgtt	1920
cccgagggca ccttgcctga caaacagagc actgagcaag ccatacagtt gttggaaaag	1980
atgaaaacgt cagccagtcc tttcttcctg gccgttgggt atcataagcc acacatcccc	2040
ttcagatacc ccaaggaatt tcagaagttg tatcccttgg agaacatcac cctggcccc	2100
gatcccgagg tccctgatgg cctaccccc tgggcctaca acccctggat ggacatcagg	2160
caacgggaag acgtccaagc cttaaaccatc agtgtgccgt atgggtccaat tcctgtggac	2220
tttcagcgga aaatccgcca gagctacttt gcctctgtgt catatttgga tacacaggtc	2280
ggccgcctct tgagtgcttt ggacgatctt cagctggcca acagcaccat cattgcattt	2340
acctcggatc atgggtgggc tctaggtgaa catggagaat gggccaaata cagcaatttt	2400
gatgttgcta cccatgttcc cctgatattc tatgttcctg gaaggacggc ttcacttccg	2460
gaggcaggcg agaagctttt cccttacctc gacccttttg attccgcctc acagttgatg	2520
gagccaggca ggcaatccat ggaccttgtg gaacttgtgt ctctttttcc cacgctggct	2580
ggacttgacg gactgcaggt tccacctcgc tgccccgttc cttcatttca cgttgagctg	2640
tgcagagaag gcaagaacct tctgaagcat tttcgattcc gtgacttgga agaagatccg	2700
tacctccctg gtaatccccg tgaactgatt gcctatagcc agtatccccg gccttcagac	2760
atccctcagt ggaattctga caagccgagt ttaaaagata taaagatcat gggctattcc	2820
atacgacca tagactatag gtatactgtg tgggttggct tcaatcctga tgaatttcta	2880
gctaactttt ctgacatcca tgcaggggaa ctgtattttg tggattctga cccattgcag	2940
gatcacaata tgtataatga ttcccaaggt ggagacctt tccagttgtt gatgccttaa	3000
taagcggccg c	3011

<210> 53
<211> 975
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No.3N and hI2S

<400> 53

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu

340

345

350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

Gly Ser Ser Glu Thr Gln Ala Asn Ser Thr Thr Asp Ala Leu Asn Val
 450 455 460

Leu Leu Ile Ile Val Asp Asp Leu Arg Pro Ser Leu Gly Cys Tyr Gly
 465 470 475 480

Asp Lys Leu Val Arg Ser Pro Asn Ile Asp Gln Leu Ala Ser His Ser
 485 490 495

Leu Leu Phe Gln Asn Ala Phe Ala Gln Gln Ala Val Cys Ala Pro Ser
 500 505 510

Arg Val Ser Phe Leu Thr Gly Arg Arg Pro Asp Thr Thr Arg Leu Tyr
 515 520 525

Asp Phe Asn Ser Tyr Trp Arg Val His Ala Gly Asn Phe Ser Thr Ile
 530 535 540

Pro Gln Tyr Phe Lys Glu Asn Gly Tyr Val Thr Met Ser Val Gly Lys
545 550 555 560

Val Phe His Pro Gly Ile Ser Ser Asn His Thr Asp Asp Ser Pro Tyr
565 570 575

Ser Trp Ser Phe Pro Pro Tyr His Pro Ser Ser Glu Lys Tyr Glu Asn
580 585 590

Thr Lys Thr Cys Arg Gly Pro Asp Gly Glu Leu His Ala Asn Leu Leu
595 600 605

Cys Pro Val Asp Val Leu Asp Val Pro Glu Gly Thr Leu Pro Asp Lys
610 615 620

Gln Ser Thr Glu Gln Ala Ile Gln Leu Leu Glu Lys Met Lys Thr Ser
625 630 635 640

Ala Ser Pro Phe Phe Leu Ala Val Gly Tyr His Lys Pro His Ile Pro
645 650 655

Phe Arg Tyr Pro Lys Glu Phe Gln Lys Leu Tyr Pro Leu Glu Asn Ile
660 665 670

Thr Leu Ala Pro Asp Pro Glu Val Pro Asp Gly Leu Pro Pro Val Ala
675 680 685

Tyr Asn Pro Trp Met Asp Ile Arg Gln Arg Glu Asp Val Gln Ala Leu
690 695 700

Asn Ile Ser Val Pro Tyr Gly Pro Ile Pro Val Asp Phe Gln Arg Lys
705 710 715 720

Ile Arg Gln Ser Tyr Phe Ala Ser Val Ser Tyr Leu Asp Thr Gln Val
725 730 735

Gly Arg Leu Leu Ser Ala Leu Asp Asp Leu Gln Leu Ala Asn Ser Thr
740 745 750

Ile Ile Ala Phe Thr Ser Asp His Gly Trp Ala Leu Gly Glu His Gly
755 760 765

Glu Trp Ala Lys Tyr Ser Asn Phe Asp Val Ala Thr His Val Pro Leu
770 775 780

Ile Phe Tyr Val Pro Gly Arg Thr Ala Ser Leu Pro Glu Ala Gly Glu
785 790 795 800

Lys Leu Phe Pro Tyr Leu Asp Pro Phe Asp Ser Ala Ser Gln Leu Met
805 810 815

Glu Pro Gly Arg Gln Ser Met Asp Leu Val Glu Leu Val Ser Leu Phe
820 825 830

Pro Thr Leu Ala Gly Leu Ala Gly Leu Gln Val Pro Pro Arg Cys Pro
835 840 845

Val Pro Ser Phe His Val Glu Leu Cys Arg Glu Gly Lys Asn Leu Leu
850 855 860

Lys His Phe Arg Phe Arg Asp Leu Glu Glu Asp Pro Tyr Leu Pro Gly
865 870 875 880

Asn Pro Arg Glu Leu Ile Ala Tyr Ser Gln Tyr Pro Arg Pro Ser Asp
885 890 895

Ile Pro Gln Trp Asn Ser Asp Lys Pro Ser Leu Lys Asp Ile Lys Ile
900 905 910

Met Gly Tyr Ser Ile Arg Thr Ile Asp Tyr Arg Tyr Thr Val Trp Val
915 920 925

Gly Phe Asn Pro Asp Glu Phe Leu Ala Asn Phe Ser Asp Ile His Ala
 930 935 940

Gly Glu Leu Tyr Phe Val Asp Ser Asp Pro Leu Gln Asp His Asn Met
 945 950 955 960

Tyr Asn Asp Ser Gln Gly Gly Asp Leu Phe Gln Leu Leu Met Pro
 965 970 975

<210> 54
 <211> 3011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence encoding the amino acid sequence of fusion
 protein of the heavy chain of humanized anti-hTfR antibody No.3N
 and hI2S, synthetic sequence

<400> 54
 acgcgtgccg ccaccatggg ctggagctgg attctgctgt tcctcctgag cgtgacagca 60
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 tctctgaaga tttcctgtaa gggttctgga tacagcttta tgaactactg gctgggatgg 180
 gtgcgccaga tgcccgggaa aggcttgag tggatggggg acatctaccc cggcggagac 240
 taccctacat acagcgagaa gttcaaggct caggtcacca tctcagccga caagtccatc 300
 agcaccgcct acctgcagtt gagcagcctg aaggcctcgg acaccgcat gtattactgt 360
 gcgagatcag gcaattacga cgaagtggcc tactggggcc aaggaaccct ggtcaccgtc 420
 tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttccccggc tgtcctacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
 cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaaggtgga caagaaagtt 720
 gagcccaaatt cttgtgacaa aactcacacg tgcccaccgt gcccagcacc tgaactcctg 780

ggagggtccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg	840
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	900
aactggtacg tggacggcgt ggagggtgcat aatgccaaga caaagccgcg ggaggagcag	960
tacaacagca cgtaccgggt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1080
atctccaaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1140
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1260
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cacgtggaa acttctccac catccccag tacttcaagg agaatggcta tgtgaccatg	1740
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cgagggccag atggagaact ccatgccaac ctgctttgcc ctgtggatgt gctggatgtt	1920
cccgagggca ccttgcctga caaacagagc actgagcaag ccatacagtt gttggaaaag	1980
atgaaaacgt cagccagtcc tttcttcctg gccgttgggt atcataagcc acacatcccc	2040
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gatcccgagg tccctgatgg cctacccctt gtggcctaca acccctggat ggacatcagg	2160
caacgggaag acgtccaagc cttaaaccatc agtgtgccgt atgggtccaat tcctgtggac	2220
tttcagcgga aaatccgcca gagctacttt gcctctgtgt catatttgga tacacaggtc	2280

ggccgcctct tgagtgcttt ggacgatctt cagctggcca acagcaccat cattgcattt 2340
 acctcggatc atgggtgggc tctaggtgaa catggagaat gggccaaata cagcaatttt 2400
 gatgttgcta cccatgttcc cctgatattc tatgttcctg gaaggacggc ttcacttccg 2460
 gaggcaggcg agaagctttt cccttacctc gacccttttg attccgcctc acagttgatg 2520
 gagccaggca ggcaatccat ggaccttggt gaacttgtgt ctctttttcc cacgctggct 2580
 ggacttgtag gactgcaggt tccacctcgc tgccccgttc cttcatttca cgttgagctg 2640
 tgcagagaag gcaagaacct tctgaagcat tttcgattcc gtgacttgga agaagatccg 2700
 tacctccctg gtaatccccg tgaactgatt gcctatagcc agtatccccg gccttcagac 2760
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 gctaactttt ctgacatcca tgcaggggaa ctgtattttg tggattctga cccattgcag 2940
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 taagcggccg c 3011

<210> 55
 <211> 883
 <212> PRT
 <213> Homo sapiens

<400> 55

Ala His Pro Gly Arg Pro Arg Ala Val Pro Thr Gln Cys Asp Val Pro
 1 5 10 15

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

Gln Cys Glu Ala Arg Gly Cys Cys Tyr Ile Pro Ala Lys Gln Gly Leu
 35 40 45

Gln Gly Ala Gln Met Gly Gln Pro Trp Cys Phe Phe Pro Pro Ser Tyr
 50 55 60

Pro Ser Tyr Lys Leu Glu Asn Leu Ser Ser Ser Glu Met Gly Tyr Thr
65 70 75 80

Ala Thr Leu Thr Arg Thr Thr Pro Thr Phe Phe Pro Lys Asp Ile Leu
85 90 95

Thr Leu Arg Leu Asp Val Met Met Glu Thr Glu Asn Arg Leu His Phe
100 105 110

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

Pro Arg Val His Ser Arg Ala Pro Ser Pro Leu Tyr Ser Val Glu Phe
130 135 140

Ser Glu Glu Pro Phe Gly Val Ile Val His Arg Gln Leu Asp Gly Arg
145 150 155 160

Val Leu Leu Asn Thr Thr Val Ala Pro Leu Phe Phe Ala Asp Gln Phe
165 170 175

Leu Gln Leu Ser Thr Ser Leu Pro Ser Gln Tyr Ile Thr Gly Leu Ala
180 185 190

Glu His Leu Ser Pro Leu Met Leu Ser Thr Ser Trp Thr Arg Ile Thr
195 200 205

Leu Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly Ala Asn Leu Tyr Gly
210 215 220

Ser His Pro Phe Tyr Leu Ala Leu Glu Asp Gly Gly Ser Ala His Gly
225 230 235 240

Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val Val Leu Gln Pro Ser
245 250 255

Pro Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile Leu Asp Val Tyr Ile
260 265 270

Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln Gln Tyr Leu Asp Val
275 280 285

Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly Leu Gly Phe His Leu
290 295 300

Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr Arg Gln Val Val Glu
305 310 315 320

Asn Met Thr Arg Ala His Phe Pro Leu Asp Val Gln Trp Asn Asp Leu
325 330 335

Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe Asn Lys Asp Gly Phe
340 345 350

Arg Asp Phe Pro Ala Met Val Gln Glu Leu His Gln Gly Gly Arg Arg
355 360 365

Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser Ser Gly Pro Ala Gly
370 375 380

Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg Gly Val Phe Ile Thr
385 390 395 400

Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val Trp Pro Gly Ser Thr
405 410 415

Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu Ala Trp Trp Glu Asp
420 425 430

Met Val Ala Glu Phe His Asp Gln Val Pro Phe Asp Gly Met Trp Ile
435 440 445

Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly Ser Glu Asp Gly Cys
450 455 460

Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val Pro Gly Val Val Gly
465 470 475 480

Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser Ser His Gln Phe Leu
485 490 495

Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly Leu Thr Glu Ala Ile
500 505 510

Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly Thr Arg Pro Phe Val
515 520 525

Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg Tyr Ala Gly His Trp
530 535 540

Thr Gly Asp Val Trp Ser Ser Trp Glu Gln Leu Ala Ser Ser Val Pro
545 550 555 560

Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro Leu Val Gly Ala Asp
565 570 575

Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu Leu Cys Val Arg Trp
580 585 590

Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg Asn His Asn Ser Leu
595 600 605

Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe Ser Glu Pro Ala Gln Gln
610 615 620

Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala Leu Leu Pro His Leu
625 630 635 640

Tyr Thr Leu Phe His Gln Ala His Val Ala Gly Glu Thr Val Ala Arg

645

650

655

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

His Gln Leu Leu Trp Gly Glu Ala Leu Leu Ile Thr Pro Val Leu Gln
 675 680 685

Ala Gly Lys Ala Glu Val Thr Gly Tyr Phe Pro Leu Gly Thr Trp Tyr
 690 695 700

Asp Leu Gln Thr Val Pro Ile Glu Ala Leu Gly Ser Leu Pro Pro Pro
 705 710 715 720

Pro Ala Ala Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln Trp Val
 725 730 735

Thr Leu Pro Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg Ala Gly
 740 745 750

Tyr Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu Ser Arg
 755 760 765

Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly Glu Ala
 770 775 780

Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu Val Leu Glu
 785 790 795 800

Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala Arg Asn Asn Thr Ile
 805 810 815

Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly Ala Gly Leu Gln Leu
 820 825 830

Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala Pro Gln Gln Val Leu
 835 840 845

Ser Asn Gly Val Pro Val Ser Asn Phe Thr Tyr Ser Pro Asp Thr Lys
850 855 860

Val Leu Asp Ile Cys Val Ser Leu Leu Met Gly Glu Gln Phe Leu Val
865 870 875 880

Ser Trp Cys

<210> 56
<211> 896
<212> PRT
<213> Homo sapiens

<400> 56

Gln Gln Gly Ala Ser Arg Pro Gly Pro Arg Asp Ala Gln Ala His Pro
1 5 10 15

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

Arg Phe Asp Cys Ala Pro Asp Lys Ala Ile Thr Gln Glu Gln Cys Glu
35 40 45

Ala Arg Gly Cys Cys Tyr Ile Pro Ala Lys Gln Gly Leu Gln Gly Ala
50 55 60

Gln Met Gly Gln Pro Trp Cys Phe Phe Pro Pro Ser Tyr Pro Ser Tyr
65 70 75 80

Lys Leu Glu Asn Leu Ser Ser Ser Glu Met Gly Tyr Thr Ala Thr Leu
85 90 95

Thr Arg Thr Thr Pro Thr Phe Phe Pro Lys Asp Ile Leu Thr Leu Arg
100 105 110

Leu Asp Val Met Met Glu Thr Glu Asn Arg Leu His Phe Thr Ile Lys
115 120 125

Asp Pro Ala Asn Arg Arg Tyr Glu Val Pro Leu Glu Thr Pro Arg Val
130 135 140

His Ser Arg Ala Pro Ser Pro Leu Tyr Ser Val Glu Phe Ser Glu Glu
145 150 155 160

Pro Phe Gly Val Ile Val His Arg Gln Leu Asp Gly Arg Val Leu Leu
165 170 175

Asn Thr Thr Val Ala Pro Leu Phe Phe Ala Asp Gln Phe Leu Gln Leu
180 185 190

Ser Thr Ser Leu Pro Ser Gln Tyr Ile Thr Gly Leu Ala Glu His Leu
195 200 205

Ser Pro Leu Met Leu Ser Thr Ser Trp Thr Arg Ile Thr Leu Trp Asn
210 215 220

Arg Asp Leu Ala Pro Thr Pro Gly Ala Asn Leu Tyr Gly Ser His Pro
225 230 235 240

Phe Tyr Leu Ala Leu Glu Asp Gly Gly Ser Ala His Gly Val Phe Leu
245 250 255

Leu Asn Ser Asn Ala Met Asp Val Val Leu Gln Pro Ser Pro Ala Leu
260 265 270

Ser Trp Arg Ser Thr Gly Gly Ile Leu Asp Val Tyr Ile Phe Leu Gly
275 280 285

Pro Glu Pro Lys Ser Val Val Gln Gln Tyr Leu Asp Val Val Gly Tyr
290 295 300

Pro Phe Met Pro Pro Tyr Trp Gly Leu Gly Phe His Leu Cys Arg Trp

305		310		315		320
Gly Tyr Ser Ser Thr Ala Ile Thr Arg Gln Val Val Glu Asn Met Thr						
		325		330		335
Arg Ala His Phe Pro Leu Asp Val Gln Trp Asn Asp Leu Asp Tyr Met						
		340		345		350
Asp Ser Arg Arg Asp Phe Thr Phe Asn Lys Asp Gly Phe Arg Asp Phe						
		355		360		365
Pro Ala Met Val Gln Glu Leu His Gln Gly Gly Arg Arg Tyr Met Met						
		370		375		380
Ile Val Asp Pro Ala Ile Ser Ser Ser Gly Pro Ala Gly Ser Tyr Arg						
385		390		395		400
Pro Tyr Asp Glu Gly Leu Arg Arg Gly Val Phe Ile Thr Asn Glu Thr						
		405		410		415
Gly Gln Pro Leu Ile Gly Lys Val Trp Pro Gly Ser Thr Ala Phe Pro						
		420		425		430
Asp Phe Thr Asn Pro Thr Ala Leu Ala Trp Trp Glu Asp Met Val Ala						
		435		440		445
Glu Phe His Asp Gln Val Pro Phe Asp Gly Met Trp Ile Asp Met Asn						
		450		455		460
Glu Pro Ser Asn Phe Ile Arg Gly Ser Glu Asp Gly Cys Pro Asn Asn						
465		470		475		480
Glu Leu Glu Asn Pro Pro Tyr Val Pro Gly Val Val Gly Gly Thr Leu						
		485		490		495
Gln Ala Ala Thr Ile Cys Ala Ser Ser His Gln Phe Leu Ser Thr His						
		500		505		510

Tyr Asn Leu His Asn Leu Tyr Gly Leu Thr Glu Ala Ile Ala Ser His
515 520 525

Arg Ala Leu Val Lys Ala Arg Gly Thr Arg Pro Phe Val Ile Ser Arg
530 535 540

Ser Thr Phe Ala Gly His Gly Arg Tyr Ala Gly His Trp Thr Gly Asp
545 550 555 560

Val Trp Ser Ser Trp Glu Gln Leu Ala Ser Ser Val Pro Glu Ile Leu
565 570 575

Gln Phe Asn Leu Leu Gly Val Pro Leu Val Gly Ala Asp Val Cys Gly
580 585 590

Phe Leu Gly Asn Thr Ser Glu Glu Leu Cys Val Arg Trp Thr Gln Leu
595 600 605

Gly Ala Phe Tyr Pro Phe Met Arg Asn His Asn Ser Leu Leu Ser Leu
610 615 620

Pro Gln Glu Pro Tyr Ser Phe Ser Glu Pro Ala Gln Gln Ala Met Arg
625 630 635 640

Lys Ala Leu Thr Leu Arg Tyr Ala Leu Leu Pro His Leu Tyr Thr Leu
645 650 655

Phe His Gln Ala His Val Ala Gly Glu Thr Val Ala Arg Pro Leu Phe
660 665 670

Leu Glu Phe Pro Lys Asp Ser Ser Thr Trp Thr Val Asp His Gln Leu
675 680 685

Leu Trp Gly Glu Ala Leu Leu Ile Thr Pro Val Leu Gln Ala Gly Lys
690 695 700

Ala Glu Val Thr Gly Tyr Phe Pro Leu Gly Thr Trp Tyr Asp Leu Gln
705 710 715 720

Thr Val Pro Ile Glu Ala Leu Gly Ser Leu Pro Pro Pro Pro Ala Ala
725 730 735

Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln Trp Val Thr Leu Pro
740 745 750

Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg Ala Gly Tyr Ile Ile
755 760 765

Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu Ser Arg Gln Gln Pro
770 775 780

Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly Glu Ala Arg Gly Glu
785 790 795 800

Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu Val Leu Glu Arg Gly Ala
805 810 815

Tyr Thr Gln Val Ile Phe Leu Ala Arg Asn Asn Thr Ile Val Asn Glu
820 825 830

Leu Val Arg Val Thr Ser Glu Gly Ala Gly Leu Gln Leu Gln Lys Val
835 840 845

Thr Val Leu Gly Val Ala Thr Ala Pro Gln Gln Val Leu Ser Asn Gly
850 855 860

Val Pro Val Ser Asn Phe Thr Tyr Ser Pro Asp Thr Lys Val Leu Asp
865 870 875 880

Ile Cys Val Ser Leu Leu Met Gly Glu Gln Phe Leu Val Ser Trp Cys
885 890 895

<210> 57
<211> 1333
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N and hGAA

<400> 57

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

Gly Ser Ala His Pro Gly Arg Pro Arg Ala Val Pro Thr Gln Cys Asp
450 455 460

Val Pro Pro Asn Ser Arg Phe Asp Cys Ala Pro Asp Lys Ala Ile Thr
465 470 475 480

Gln Glu Gln Cys Glu Ala Arg Gly Cys Cys Tyr Ile Pro Ala Lys Gln
485 490 495

Gly Leu Gln Gly Ala Gln Met Gly Gln Pro Trp Cys Phe Phe Pro Pro
500 505 510

Ser Tyr Pro Ser Tyr Lys Leu Glu Asn Leu Ser Ser Ser Glu Met Gly
515 520 525

Tyr Thr Ala Thr Leu Thr Arg Thr Thr Pro Thr Phe Phe Pro Lys Asp
530 535 540

Ile Leu Thr Leu Arg Leu Asp Val Met Met Glu Thr Glu Asn Arg Leu
545 550 555 560

His Phe Thr Ile Lys Asp Pro Ala Asn Arg Arg Tyr Glu Val Pro Leu
565 570 575

Glu Thr Pro Arg Val His Ser Arg Ala Pro Ser Pro Leu Tyr Ser Val
580 585 590

Glu Phe Ser Glu Glu Pro Phe Gly Val Ile Val His Arg Gln Leu Asp
595 600 605

Gly Arg Val Leu Leu Asn Thr Thr Val Ala Pro Leu Phe Phe Ala Asp
610 615 620

Gln Phe Leu Gln Leu Ser Thr Ser Leu Pro Ser Gln Tyr Ile Thr Gly
625 630 635 640

Leu Ala Glu His Leu Ser Pro Leu Met Leu Ser Thr Ser Trp Thr Arg
645 650 655

Ile Thr Leu Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly Ala Asn Leu
660 665 670

Tyr Gly Ser His Pro Phe Tyr Leu Ala Leu Glu Asp Gly Gly Ser Ala
675 680 685

His Gly Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val Val Leu Gln
690 695 700

Pro Ser Pro Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile Leu Asp Val
705 710 715 720

Tyr Ile Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln Gln Tyr Leu
725 730 735

Asp Val Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly Leu Gly Phe

740

745

750

His Leu Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr Arg Gln Val
 755 760 765

Val Glu Asn Met Thr Arg Ala His Phe Pro Leu Asp Val Gln Trp Asn
 770 775 780

Asp Leu Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe Asn Lys Asp
 785 790 795 800

Gly Phe Arg Asp Phe Pro Ala Met Val Gln Glu Leu His Gln Gly Gly
 805 810 815

Arg Arg Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser Ser Gly Pro
 820 825 830

Ala Gly Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg Gly Val Phe
 835 840 845

Ile Thr Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val Trp Pro Gly
 850 855 860

Ser Thr Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu Ala Trp Trp
 865 870 875 880

Glu Asp Met Val Ala Glu Phe His Asp Gln Val Pro Phe Asp Gly Met
 885 890 895

Trp Ile Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly Ser Glu Asp
 900 905 910

Gly Cys Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val Pro Gly Val
 915 920 925

Val Gly Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser Ser His Gln
 930 935 940

Phe Leu Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly Leu Thr Glu
 945 950 955 960

Ala Ile Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly Thr Arg Pro
 965 970 975

Phe Val Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg Tyr Ala Gly
 980 985 990

His Trp Thr Gly Asp Val Trp Ser Ser Trp Glu Gln Leu Ala Ser Ser
 995 1000 1005

Val Pro Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro Leu Val
 1010 1015 1020

Gly Ala Asp Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu Leu
 1025 1030 1035

Cys Val Arg Trp Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg
 1040 1045 1050

Asn His Asn Ser Leu Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe
 1055 1060 1065

Ser Glu Pro Ala Gln Gln Ala Met Arg Lys Ala Leu Thr Leu Arg
 1070 1075 1080

Tyr Ala Leu Leu Pro His Leu Tyr Thr Leu Phe His Gln Ala His
 1085 1090 1095

Val Ala Gly Glu Thr Val Ala Arg Pro Leu Phe Leu Glu Phe Pro
 1100 1105 1110

Lys Asp Ser Ser Thr Trp Thr Val Asp His Gln Leu Leu Trp Gly
 1115 1120 1125

Glu	Ala	Leu	Leu	Ile	Thr	Pro	Val	Leu	Gln	Ala	Gly	Lys	Ala	Glu
1130						1135					1140			
Val	Thr	Gly	Tyr	Phe	Pro	Leu	Gly	Thr	Trp	Tyr	Asp	Leu	Gln	Thr
1145						1150					1155			
Val	Pro	Ile	Glu	Ala	Leu	Gly	Ser	Leu	Pro	Pro	Pro	Pro	Ala	Ala
1160						1165					1170			
Pro	Arg	Glu	Pro	Ala	Ile	His	Ser	Glu	Gly	Gln	Trp	Val	Thr	Leu
1175						1180					1185			
Pro	Ala	Pro	Leu	Asp	Thr	Ile	Asn	Val	His	Leu	Arg	Ala	Gly	Tyr
1190						1195					1200			
Ile	Ile	Pro	Leu	Gln	Gly	Pro	Gly	Leu	Thr	Thr	Thr	Glu	Ser	Arg
1205						1210					1215			
Gln	Gln	Pro	Met	Ala	Leu	Ala	Val	Ala	Leu	Thr	Lys	Gly	Gly	Glu
1220						1225					1230			
Ala	Arg	Gly	Glu	Leu	Phe	Trp	Asp	Asp	Gly	Glu	Ser	Leu	Glu	Val
1235						1240					1245			
Leu	Glu	Arg	Gly	Ala	Tyr	Thr	Gln	Val	Ile	Phe	Leu	Ala	Arg	Asn
1250						1255					1260			
Asn	Thr	Ile	Val	Asn	Glu	Leu	Val	Arg	Val	Thr	Ser	Glu	Gly	Ala
1265						1270					1275			
Gly	Leu	Gln	Leu	Gln	Lys	Val	Thr	Val	Leu	Gly	Val	Ala	Thr	Ala
1280						1285					1290			
Pro	Gln	Gln	Val	Leu	Ser	Asn	Gly	Val	Pro	Val	Ser	Asn	Phe	Thr
1295						1300					1305			

Tyr Ser Pro Asp Thr Lys Val Leu Asp Ile Cys Val Ser Leu Leu
1310 1315 1320

Met Gly Glu Gln Phe Leu Val Ser Trp Cys
1325 1330

<210> 58
<211> 1330
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hGAA

<400> 58

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Ala
435 440 445

His Pro Gly Arg Pro Arg Ala Val Pro Thr Gln Cys Asp Val Pro Pro
450 455 460

Asn Ser Arg Phe Asp Cys Ala Pro Asp Lys Ala Ile Thr Gln Glu Gln
465 470 475 480

Cys Glu Ala Arg Gly Cys Cys Tyr Ile Pro Ala Lys Gln Gly Leu Gln
485 490 495

Gly Ala Gln Met Gly Gln Pro Trp Cys Phe Phe Pro Pro Ser Tyr Pro
500 505 510

Ser Tyr Lys Leu Glu Asn Leu Ser Ser Ser Glu Met Gly Tyr Thr Ala
515 520 525

Thr Leu Thr Arg Thr Thr Pro Thr Phe Phe Pro Lys Asp Ile Leu Thr
530 535 540

Leu Arg Leu Asp Val Met Met Glu Thr Glu Asn Arg Leu His Phe Thr
545 550 555 560

Ile Lys Asp Pro Ala Asn Arg Arg Tyr Glu Val Pro Leu Glu Thr Pro
565 570 575

Arg Val His Ser Arg Ala Pro Ser Pro Leu Tyr Ser Val Glu Phe Ser
580 585 590

Glu Glu Pro Phe Gly Val Ile Val His Arg Gln Leu Asp Gly Arg Val
595 600 605

Leu Leu Asn Thr Thr Val Ala Pro Leu Phe Phe Ala Asp Gln Phe Leu
610 615 620

Gln Leu Ser Thr Ser Leu Pro Ser Gln Tyr Ile Thr Gly Leu Ala Glu
625 630 635 640

His Leu Ser Pro Leu Met Leu Ser Thr Ser Trp Thr Arg Ile Thr Leu
645 650 655

Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly Ala Asn Leu Tyr Gly Ser
660 665 670

His Pro Phe Tyr Leu Ala Leu Glu Asp Gly Gly Ser Ala His Gly Val
675 680 685

Phe Leu Leu Asn Ser Asn Ala Met Asp Val Val Leu Gln Pro Ser Pro
690 695 700

Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile Leu Asp Val Tyr Ile Phe

705		710		715		720
Leu Gly Pro Glu Pro Lys Ser Val Val Gln Gln Tyr Leu Asp Val Val						
		725		730		735
Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly Leu Gly Phe His Leu Cys						
		740		745		750
Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr Arg Gln Val Val Glu Asn						
		755		760		765
Met Thr Arg Ala His Phe Pro Leu Asp Val Gln Trp Asn Asp Leu Asp						
		770		775		780
Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe Asn Lys Asp Gly Phe Arg						
785		790		795		800
Asp Phe Pro Ala Met Val Gln Glu Leu His Gln Gly Gly Arg Arg Tyr						
		805		810		815
Met Met Ile Val Asp Pro Ala Ile Ser Ser Ser Gly Pro Ala Gly Ser						
		820		825		830
Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg Gly Val Phe Ile Thr Asn						
		835		840		845
Glu Thr Gly Gln Pro Leu Ile Gly Lys Val Trp Pro Gly Ser Thr Ala						
		850		855		860
Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu Ala Trp Trp Glu Asp Met						
865		870		875		880
Val Ala Glu Phe His Asp Gln Val Pro Phe Asp Gly Met Trp Ile Asp						
		885		890		895
Met Asn Glu Pro Ser Asn Phe Ile Arg Gly Ser Glu Asp Gly Cys Pro						
		900		905		910

Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val Pro Gly Val Val Gly Gly
915 920 925

Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser Ser His Gln Phe Leu Ser
930 935 940

Thr His Tyr Asn Leu His Asn Leu Tyr Gly Leu Thr Glu Ala Ile Ala
945 950 955 960

Ser His Arg Ala Leu Val Lys Ala Arg Gly Thr Arg Pro Phe Val Ile
965 970 975

Ser Arg Ser Thr Phe Ala Gly His Gly Arg Tyr Ala Gly His Trp Thr
980 985 990

Gly Asp Val Trp Ser Ser Trp Glu Gln Leu Ala Ser Ser Val Pro Glu
995 1000 1005

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

Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu Leu Cys Val Arg
1025 1030 1035

Trp Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg Asn His Asn
1040 1045 1050

Ser Leu Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe Ser Glu Pro
1055 1060 1065

Ala Gln Gln Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala Leu
1070 1075 1080

Leu Pro His Leu Tyr Thr Leu Phe His Gln Ala His Val Ala Gly
1085 1090 1095

Glu Thr	Val Ala Arg Pro	Leu Phe Leu Glu Phe Pro	Lys Asp Ser
1100		1105	1110
Ser Thr	Trp Thr Val Asp His	Gln Leu Leu Trp Gly	Glu Ala Leu
1115		1120	1125
Leu Ile	Thr Pro Val Leu Gln	Ala Gly Lys Ala Glu	Val Thr Gly
1130		1135	1140
Tyr Phe	Pro Leu Gly Thr Trp	Tyr Asp Leu Gln Thr	Val Pro Ile
1145		1150	1155
Glu Ala	Leu Gly Ser Leu Pro	Pro Pro Pro Ala Ala	Pro Arg Glu
1160		1165	1170
Pro Ala	Ile His Ser Glu Gly	Gln Trp Val Thr Leu	Pro Ala Pro
1175		1180	1185
Leu Asp	Thr Ile Asn Val His	Leu Arg Ala Gly Tyr	Ile Ile Pro
1190		1195	1200
Leu Gln	Gly Pro Gly Leu Thr	Thr Thr Glu Ser Arg	Gln Gln Pro
1205		1210	1215
Met Ala	Leu Ala Val Ala Leu	Thr Lys Gly Gly Glu	Ala Arg Gly
1220		1225	1230
Glu Leu	Phe Trp Asp Asp Gly	Glu Ser Leu Glu Val	Leu Glu Arg
1235		1240	1245
Gly Ala	Tyr Thr Gln Val Ile	Phe Leu Ala Arg Asn	Asn Thr Ile
1250		1255	1260
Val Asn	Glu Leu Val Arg Val	Thr Ser Glu Gly Ala	Gly Leu Gln
1265		1270	1275

Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala Pro Gln Gln
 1280 1285 1290

Val Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr Tyr Ser Pro
 1295 1300 1305

Asp Thr Lys Val Leu Asp Ile Cys Val Ser Leu Leu Met Gly Glu
 1310 1315 1320

Gln Phe Leu Val Ser Trp Cys
 1325 1330

<210> 59
 <211> 4076
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide seuquence encoding the amino acid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hGAA, synthetic sequence

<400> 59
 acgcgtgccg ccaccatggg ttggagcctc atcttgctct tccttgctgc tgttgctacg 60
 cgagtcggca gcgaggtgca actagtcag tctggagcag aggtgaaaaa gcccggggag 120
 tctctgaaga tttcctgtaa gggttctgga tacagcttta tgaactactg gctgggatgg 180
 gtgcgccaga tgccccgggaa aggcctggag tggatggggg acatctaccc cggcggagac 240
 taccctacat acagcgagaa gttcaaggct caggtcacca tctcagccga caagtccatc 300
 agcaccgcct acctgcagtt gagcagcctg aaggcctcgg acaccgcat gtattactgt 360
 gcgagatcag gcaattacga cgaagtggcc tactggggcc aaggaaccct ggtcaccgtc 420
 tcctcagcta gcaccaaggg cccatcggtc ttccccctgg cgccctgctc caggagcacc 480
 tccgagagca cagccgccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca ctttcccggc tgtcctacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacg 660

aagacctaca cctgcaacgt agatcacaag cccagcaaca ccaaggtgga caagagagtt	720
gagtccaaat atggtccccc atgcccacca tgcccagcac ctgagttcct ggggggtcca	780
tcagtcttcc tgttcccccc aaaacccaag gacactctca tgatctcccg gacccctgag	840
gtcacgtgcg tgggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac	900
gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc	960
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa cggcaaggag	1020
tacaagtgca aggtctccaa caaaggcctc ccgctcctca tcgagaaaac catctccaaa	1080
gccaaagggc agccccgaga gccacaggtg tacaccctgc ccccatccca ggaggagatg	1140
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc	1200
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1260
gactccgacg gctccttctt cctctacagc aggtcaccg tggacaagag caggtggcag	1320
gaggggaatg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag	1380
aagagcctct ccctgtctcc gggtaaagga tctgctcacc ctggacggcc tagggccgtg	1440
cctacccagt gcgacgtgcc tcctaattcc aggttcgact gcgccccga taaagccatc	1500
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cgggtgcact ccagggtcc ttccccctctg tatagcgtgg agtttagcga ggagcccttc	1860
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ctggccctcg aagatggagg cagcgctcat ggcgtgttcc tgctgaattc caacgctatg	2160

gacgtggtgc tccaaccctc ccctgccctg tcctggagga gcacaggcgg cattctggac	2220
gtctacattt tcctcggccc cgagcctaaa tccgtcgtcc agcagtacct ggacgtggtg	2280
ggctaccctt ttatgcctcc ttactggggc ctgggctttc acctgtgtag gtggggctat	2340
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atgatgattg tggaccctgc tatttccagc tccggacctg ctggctccta ccggccctac	2580
gacgagggac tgcggagggg cgtcttcac acaaacgaaa ccggtcagcc cctgattgga	2640
aaggtgtggc ccggttctac agctttcccc gactttacaa accccacagc cctggcttgg	2700
tgggaggaca tgggtggccga gtttcacgac cagggtgcctt tcgacggcat gtggatcgat	2760
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gagaatcccc cctacgtccc cggagtcgtg ggaggcacac tccaggctgc cacaatctgc	2880
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tccaggagca catttgccgg ccacggcagg tacgctggcc actggacagg cgatgtctgg	3060
tcctcctggg agcaactggc ttccagcgtc cccgagatcc tccagttcaa cctgctgggc	3120
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cccattgagg ccctgggttc tctccctcct cctcctgccg ctcccaggga acctgctatc	3600

85

90

95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu
 130 135 140

Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln
 145 150 155 160

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
 165 170 175

Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg
 180 185 190

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 195 200 205

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
 210 215 220

Tyr Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr
 225 230 235 240

Lys Val Glu Ile Lys
 245

<210> 61

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of Fab heavy chain of humanized anti-hTfR antibody No. 3N

<400> 61

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr
225

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence 1 of CDR1 in the heavy chain of humanized
anti-hTfR antibody No. 3N

<400> 62

Gly Tyr Ser Phe Met Asn Tyr Trp
1 5

<210> 63
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence 2 of CDR1 in the heavy chain of humanized
anti-hTfR antibody No. 3N

<400> 63

Gly Tyr Ser Phe Met Asn Tyr Trp Leu Gly
1 5 10

<210> 64
<211> 30
<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of framework region 3 in the heavy chain of humanized anti-hTfR antibody No. 3N

<400> 64

Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1 5 10 15

Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
20 25 30

<210> 65

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the variable region of the heavy chain of humanized anti-hTfR antibody No. 3N

<400> 65

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 66
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of the heavy chain of humanized anti-hTfR
antibody No. 3N

<400> 66

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr

tctctgaaga tttcctgtaa gggttctgga tacagcttta tgaactactg gctgggatgg	180
gtgcgccaga tgccccgggaa aggccctggag tggatggggg acatctaccc cggcggagac	240
taccctacat acagcgagaa gttcaaggctc caggtcacca tctcagccga caagtccatc	300
agcaccgcct acctgcagtt gagcagcctg aaggcctcgg acaccgcat gtattactgt	360
gcgagatcag gcaattacga cgaagtggcc tactggggcc aaggaaccct ggtcaccgtc	420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc	480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag	600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	720
gagcccaa at cttgtgacaa aactcacacg tgccccaccgt gcccagcacc tgaactcctg	780
ggagggtccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg	840
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	900
aactggtacg tggacggcgt ggagggtgcat aatgccaaga caaagccgcg ggaggagcag	960
tacaacagca cgtaccgggt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1080
atctccaaag ccaaagggca gccccgagaa ccacagggtgt acaccctgcc cccatcccgg	1140
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1260
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc	1320
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1380
tacacgcaga agagcctctc cctgtctccg ggtaaataag cggccgc	1427

<210> 68
 <211> 445
 <212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4)

<400> 68

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165

170

175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

<210> 69
 <211> 1418
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide seuquence encoding the amino acid sequence of the
 heavy chain of humanized anti-hTfR antibody No. 3N (IgG4),
 synthetic sequence

<400> 69
 acgcgtgccg ccaccatggg ctggagctgg attctgctgt tcctcctgag cgtgacagca 60
 ggagtgcaca gcgaggtgca actagtgcag tctggagcag aggtgaaaaa gcccggggag 120
 tctctgaaga tttcctgtaa gggttctgga tacagcttta tgaactactg gctgggatgg 180
 gtgcgccaga tgcccgggaa aggcctggag tggatggggg acatctaccc cggcggagac 240
 taccctacat acagcgagaa gttcaaggct caggtcacca tctcagccga caagtccatc 300
 agcaccgcct acctgcagtt gagcagcctg aaggcctcgg acaccgccat gtattactgt 360
 gcgagatcag gcaattacga cgaagtggcc tactggggcc aaggaaccct ggtcaccgtc 420
 tcctcagcta gcaccaaggg cccatcggtc ttccccctgg cgccctgctc caggagcacc 480

tccgagagca cagccgccct gggctgcctg gtcaaggact acttccccga accggtgacg	540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag	600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacg	660
aagacctaca cctgcaacgt agatcacaag cccagcaaca ccaaggtgga caagagagtt	720
gagtccaaat atggtcccc atgcccacca tgcccagcac ctgagttcct ggggggtcca	780
tcagtcttcc tgttcccccc aaaacccaag gacacttca tgatctcccg gaccctgag	840
gtcacgtgcg tgggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac	900
gtggatggcg tggagggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc	960
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa cggcaaggag	1020
tacaagtgca aggtctccaa caaaggcctc ccgtcctcca tcgagaaaac catctccaaa	1080
gccaaagggc agccccgaga gccacagggtg tacaccctgc ccccatcca ggaggagatg	1140
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc	1200
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1260
gactccgacg gctccttctt cctctacagc aggctcaccg tggacaagag caggtggcag	1320
gaggggaatg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag	1380
aagagcctct ccctgtctcc gggtaaataa gcggccgc	1418

<210> 70
 <211> 218
 <212> PRT
 <213> Homo sapiens

<400> 70

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

Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
			20					25					30		

Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 50 55 60

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 85 90 95

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 100 105 110

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 115 120 125

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 130 135 140

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 145 150 155 160

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 165 170 175

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 180 185 190

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 195 200 205

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 210 215

<210> 71
 <211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the Fab heavy chain of humanized anti-hTfR antibody 3N, further introduced with Fc region of human IgG

<400> 71

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

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
20 25 30

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
35 40 45

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
50 55 60

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
85 90 95

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
100 105 110

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
115 120 125

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
130 135 140

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
145 150 155 160

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
165 170 175

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
180 185 190

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
195 200 205

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
225 230 235 240

Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
245 250 255

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
260 265 270

Met Asn Tyr Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
275 280 285

Glu Trp Met Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser
290 295 300

Glu Lys Phe Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
305 310 315 320

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
325 330 335

Tyr Tyr Cys Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly
340 345 350

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

355

360

365

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 370 375 380

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 385 390 395 400

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 420 425 430

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

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 450 455 460

Asp Lys Thr His Thr
 465

<210> 72
 <211> 1491
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide seuquence encoding the amino acid sequence of the Fab heavy chain of humanized anti-hTfR antibody 3N, further introduced with Fc region of human IgG

<400> 72
 acgcgtcgcc accatggggtt ggagcctcat cttgctcttc cttgtcgctg ttgctacgcg 60
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 acccaaggac accctcatga tctcccgac ccctgaggtc acatgcgtgg tgggtggacgt 180
 gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa 240

tgccaagaca aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct	300
caccgtcctg caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa	360
agccctccca gccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc	420
acaggtgtac accctgcccc catcccgga ggagatgacc aagaaccagg tcagcctgac	480
ctgcctggtc aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca	540
gccggagaac aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct	600
ctacagcaag ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc	660
cgtgatgcac gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg	720
taaaggtggc ggagggctctg gaggaggcgg tagcggcgga ggaggttccg ggggcgggtg	780
aagcggaggc ggtggatccg aggtgcaact agtgcagtct ggagcagagg tgaaaaagcc	840
cggggagtct ctgaagattt cctgtaaggg ttctggatac agctttatga actactggct	900
gggatgggtg cgccagatgc ccgggaaagg cctggagtgg atgggggaca tctaccccg	960
cggagactac cctacatata gcgagaagtt caaggtccag gtcaccatct cagccgacaa	1020
gtccatcagc accgcctacc tgcagttgag cagcctgaag gcctcggaca ccgcatgta	1080
ttactgtgcg agatcaggca attacgacga agtggcctac tggggccaag gaaccctggt	1140
caccgtctcc tcagctagca ccaagggccc atcggctctt cccctggcac cctcctcaa	1200
gagcacctct gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc	1260
ggtgacggtg tcgtggaact caggcgcct gaccagcggc gtgcacacct tcccggctgt	1320
cctacagtcc tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt	1380
gggcacccag acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa	1440
gaaagttgag ccgaagagct gtgataagac gcatacgtaa taagcggccg c	1491

<210> 73
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Amino acid sequence of framework region 3 in the heavy chain of humanized anti-hTfR antibody No. 3

<400> 73

Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1 5 10 15

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
20 25 30

<210> 74

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of albumin binding domain

<400> 74

Leu Ala Glu Ala Lys Val Leu Ala Leu Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

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

Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
35 40 45

<210> 75

<211> 628

<212> PRT

<213> Homo sapiens

<400> 75

Ala Glu Ala Pro His Leu Val His Val Asp Ala Ala Arg Ala Leu Trp
1 5 10 15

Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu Pro
20 25 30

His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn
35 40 45

Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg
50 55 60

Thr His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg
65 70 75 80

Gly Leu Ser Tyr Asn Phe Thr His Leu Asp Gly Tyr Leu Asp Leu Leu
85 90 95

Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu Leu Met Gly Ser Ala Ser
100 105 110

Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val Phe Glu Trp Lys
115 120 125

Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly Leu
130 135 140

Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His
145 150 155 160

His Asp Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr
165 170 175

Tyr Asp Ala Cys Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg
180 185 190

Leu Gly Gly Pro Gly Asp Ser Phe His Thr Pro Pro Arg Ser Pro Leu
195 200 205

Ser Trp Gly Leu Leu Arg His Cys His Asp Gly Thr Asn Phe Phe Thr
210 215 220

Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His Arg Lys Gly
225 230 235 240

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

Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn
260 265 270

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

Ala Asp Val Thr Tyr Ala Ala Met Val Val Lys Val Ile Ala Gln His
290 295 300

Gln Asn Leu Leu Leu Ala Asn Thr Thr Ser Ala Phe Pro Tyr Ala Leu
305 310 315 320

Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro His Pro Phe Ala
325 330 335

Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg Pro Pro
340 345 350

His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu
355 360 365

Ala Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly
370 375 380

Thr Val Leu Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His
385 390 395 400

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

Ala Ser Asp Asp Thr Arg Ala His Pro Asn Arg Ser Val Ala Val Thr
420 425 430

Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val Tyr Val Thr
435 440 445

Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg Arg
450 455 460

Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg
465 470 475 480

Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly
485 490 495

Gly Arg Leu Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu
500 505 510

Val His Val Cys Ala Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg
515 520 525

Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln Leu Val Leu Val Trp Ser
530 535 540

Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr Tyr Glu Ile Gln Phe
545 550 555 560

Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro Ser Thr
565 570 575

Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser
580 585 590

Tyr Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser
595 600 605

Asp Pro Val Pro Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser

610

615

620

Pro Gly Asn Pro
625

<210> 76
<211> 626
<212> PRT
<213> Homo sapiens

<400> 76

Ala Pro His Leu Val His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu
1 5 10 15

Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser
20 25 30

Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala
35 40 45

Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His
50 55 60

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

Ser Tyr Asn Phe Thr His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu
85 90 95

Asn Gln Leu Leu Pro Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His
100 105 110

Phe Thr Asp Phe Glu Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu
115 120 125

Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His
130 135 140

Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp
 145 150 155 160

Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp
 165 170 175

Ala Cys Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly
 180 185 190

Gly Pro Gly Asp Ser Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp
 195 200 205

Gly Leu Leu Arg His Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu
 210 215 220

Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg
 225 230 235 240

Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile
 245 250 255

Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu
 260 265 270

Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp
 275 280 285

Val Thr Tyr Ala Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn
 290 295 300

Leu Leu Leu Ala Asn Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser
 305 310 315 320

Asn Asp Asn Ala Phe Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg
 325 330 335

Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg Pro Pro His Val
340 345 350

Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu
355 360 365

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

Leu Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro
385 390 395 400

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

Asp Asp Thr Arg Ala His Pro Asn Arg Ser Val Ala Val Thr Leu Arg
420 425 430

Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr
435 440 445

Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly
450 455 460

Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala
465 470 475 480

Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg
485 490 495

Leu Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His
500 505 510

Val Cys Ala Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg
515 520 525

Ala Leu Pro Leu Thr Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu

530

535

540

His Val Gly Ser Lys Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln
 545 550 555 560

Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn
 565 570 575

Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg
 580 585 590

Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro
 595 600 605

Val Pro Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly
 610 615 620

Asn Pro
 625

<210> 77
 <211> 279
 <212> PRT
 <213> Homo sapiens

<400> 77

Asp Pro Pro Ala Pro Leu Pro Leu Val Ile Trp His Gly Met Gly Asp
 1 5 10 15

Ser Cys Cys Asn Pro Leu Ser Met Gly Ala Ile Lys Lys Met Val Glu
 20 25 30

Lys Lys Ile Pro Gly Ile Tyr Val Leu Ser Leu Glu Ile Gly Lys Thr
 35 40 45

Leu Met Glu Asp Val Glu Asn Ser Phe Phe Leu Asn Val Asn Ser Gln
 50 55 60

Val Thr Thr Val Cys Gln Ala Leu Ala Lys Asp Pro Lys Leu Gln Gln
65 70 75 80

Gly Tyr Asn Ala Met Gly Phe Ser Gln Gly Gly Gln Phe Leu Arg Ala
85 90 95

Val Ala Gln Arg Cys Pro Ser Pro Pro Met Ile Asn Leu Ile Ser Val
100 105 110

Gly Gly Gln His Gln Gly Val Phe Gly Leu Pro Arg Cys Pro Gly Glu
115 120 125

Ser Ser His Ile Cys Asp Phe Ile Arg Lys Thr Leu Asn Ala Gly Ala
130 135 140

Tyr Ser Lys Val Val Gln Glu Arg Leu Val Gln Ala Glu Tyr Trp His
145 150 155 160

Asp Pro Ile Lys Glu Asp Val Tyr Arg Asn His Ser Ile Phe Leu Ala
165 170 175

Asp Ile Asn Gln Glu Arg Gly Ile Asn Glu Ser Tyr Lys Lys Asn Leu
180 185 190

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

Val Asp Pro Val Asp Ser Glu Trp Phe Gly Phe Tyr Arg Ser Gly Gln
210 215 220

Ala Lys Glu Thr Ile Pro Leu Gln Glu Thr Ser Leu Tyr Thr Gln Asp
225 230 235 240

Arg Leu Gly Leu Lys Glu Met Asp Asn Ala Gly Gln Leu Val Phe Leu
245 250 255

Ala Thr Glu Gly Asp His Leu Gln Leu Ser Glu Glu Trp Phe Tyr Ala
260 265 270

His Ile Ile Pro Phe Leu Gly
275

<210> 78
<211> 583
<212> PRT
<213> Homo sapiens

<400> 78

Leu Ser Asp Ser Arg Val Leu Trp Ala Pro Ala Glu Ala His Pro Leu
1 5 10 15

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

Arg Asp Val Phe Gly Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys Gly
35 40 45

Leu Phe Thr Ala Ile Asn Leu Gly Leu Lys Lys Glu Pro Asn Val Ala
50 55 60

Arg Val Gly Ser Val Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile Ala
65 70 75 80

Pro Pro Ala Val Cys Gln Ser Ile Val His Leu Phe Glu Asp Asp Met
85 90 95

Val Glu Val Trp Arg Arg Ser Val Leu Ser Pro Ser Glu Ala Cys Gly
100 105 110

Leu Leu Leu Gly Ser Thr Cys Gly His Trp Asp Ile Phe Ser Ser Trp
115 120 125

Asn Ile Ser Leu Pro Thr Val Pro Lys Pro Pro Pro Lys Pro Pro Ser
130 135 140

Pro Pro Ala Pro Gly Ala Pro Val Ser Arg Ile Leu Phe Leu Thr Asp
145 150 155 160

Leu His Trp Asp His Asp Tyr Leu Glu Gly Thr Asp Pro Asp Cys Ala
165 170 175

Asp Pro Leu Cys Cys Arg Arg Gly Ser Gly Leu Pro Pro Ala Ser Arg
180 185 190

Pro Gly Ala Gly Tyr Trp Gly Glu Tyr Ser Lys Cys Asp Leu Pro Leu
195 200 205

Arg Thr Leu Glu Ser Leu Leu Ser Gly Leu Gly Pro Ala Gly Pro Phe
210 215 220

Asp Met Val Tyr Trp Thr Gly Asp Ile Pro Ala His Asp Val Trp His
225 230 235 240

Gln Thr Arg Gln Asp Gln Leu Arg Ala Leu Thr Thr Val Thr Ala Leu
245 250 255

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

His Glu Ser Thr Pro Val Asn Ser Phe Pro Pro Pro Phe Ile Glu Gly
275 280 285

Asn His Ser Ser Arg Trp Leu Tyr Glu Ala Met Ala Lys Ala Trp Glu
290 295 300

Pro Trp Leu Pro Ala Glu Ala Leu Arg Thr Leu Arg Ile Gly Gly Phe
305 310 315 320

Tyr Ala Leu Ser Pro Tyr Pro Gly Leu Arg Leu Ile Ser Leu Asn Met
325 330 335

Asn Phe Cys Ser Arg Glu Asn Phe Trp Leu Leu Ile Asn Ser Thr Asp
340 345 350

Pro Ala Gly Gln Leu Gln Trp Leu Val Gly Glu Leu Gln Ala Ala Glu
355 360 365

Asp Arg Gly Asp Lys Val His Ile Ile Gly His Ile Pro Pro Gly His
370 375 380

Cys Leu Lys Ser Trp Ser Trp Asn Tyr Tyr Arg Ile Val Ala Arg Tyr
385 390 395 400

Glu Asn Thr Leu Ala Ala Gln Phe Phe Gly His Thr His Val Asp Glu
405 410 415

Phe Glu Val Phe Tyr Asp Glu Glu Thr Leu Ser Arg Pro Leu Ala Val
420 425 430

Ala Phe Leu Ala Pro Ser Ala Thr Thr Tyr Ile Gly Leu Asn Pro Gly
435 440 445

Tyr Arg Val Tyr Gln Ile Asp Gly Asn Tyr Ser Gly Ser Ser His Val
450 455 460

Val Leu Asp His Glu Thr Tyr Ile Leu Asn Leu Thr Gln Ala Asn Ile
465 470 475 480

Pro Gly Ala Ile Pro His Trp Gln Leu Leu Tyr Arg Ala Arg Glu Thr
485 490 495

Tyr Gly Leu Pro Asn Thr Leu Pro Thr Ala Trp His Asn Leu Val Tyr
500 505 510

Arg Met Arg Gly Asp Met Gln Leu Phe Gln Thr Phe Trp Phe Leu Tyr
515 520 525

His Lys Gly His Pro Pro Ser Glu Pro Cys Gly Thr Pro Cys Arg Leu
 530 535 540

Ala Thr Leu Cys Ala Gln Leu Ser Ala Arg Ala Asp Ser Pro Ala Leu
 545 550 555 560

Cys Arg His Leu Met Pro Asp Gly Ser Leu Pro Glu Ala Gln Ser Leu
 565 570 575

Trp Pro Arg Pro Leu Phe Cys
 580

<210> 79
 <211> 489
 <212> PRT
 <213> Homo sapiens

<400> 79

Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp Leu Gly Tyr Gly
 1 5 10 15

Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr Pro Asn Leu Asp
 20 25 30

Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe Tyr Val Pro Val
 35 40 45

Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu Pro
 50 55 60

Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser Arg Gly
 65 70 75 80

Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala Ala Arg
 85 90 95

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

Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe Leu Gly
115 120 125

Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn Leu Thr Cys Phe
130 135 140

Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu Val Pro
145 150 155 160

Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro Trp Leu
165 170 175

Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu Met Ala
180 185 190

Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala Ser His
195 200 205

His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu Arg Ser
210 215 220

Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala Ala Val
225 230 235 240

Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu Glu Thr
245 250 255

Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg Met Ser
260 265 270

Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr Thr Tyr
275 280 285

Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly His Ile
290 295 300

Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu Leu Pro
305 310 315 320

Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr Leu Asp
325 330 335

Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser Pro Arg
340 345 350

Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu Val Arg Gly Val
355 360 365

Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr Gln Gly
370 375 380

Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala Ser Ser
385 390 395 400

Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser Lys Asp
405 410 415

Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala Thr Pro
420 425 430

Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala Gln Leu
435 440 445

Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly Glu Asp
450 455 460

Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg Pro Ala
465 470 475 480

Cys Cys His Cys Pro Asp Pro His Ala
485

<210> 80
<211> 482
<212> PRT
<213> Homo sapiens

<400> 80

Arg Pro Arg Asn Ala Leu Leu Leu Leu Ala Asp Asp Gly Gly Phe Glu
1 5 10 15

Ser Gly Ala Tyr Asn Asn Ser Ala Ile Ala Thr Pro His Leu Asp Ala
20 25 30

Leu Ala Arg Arg Ser Leu Leu Phe Arg Asn Ala Phe Thr Ser Val Ser
35 40 45

Ser Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Leu Pro Gln His
50 55 60

Gln Asn Gly Met Tyr Gly Leu His Gln Asp Val His His Phe Asn Ser
65 70 75 80

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

Arg Thr Gly Ile Ile Gly Lys Lys His Val Gly Pro Glu Thr Val Tyr
100 105 110

Pro Phe Asp Phe Ala Tyr Thr Glu Glu Asn Gly Ser Val Leu Gln Val
115 120 125

Gly Arg Asn Ile Thr Arg Ile Lys Leu Leu Val Arg Lys Phe Leu Gln
130 135 140

Thr Gln Asp Asp Arg Pro Phe Phe Leu Tyr Val Ala Phe His Asp Pro
145 150 155 160

His Arg Cys Gly His Ser Gln Pro Gln Tyr Gly Thr Phe Cys Glu Lys
165 170 175

Phe Gly Asn Gly Glu Ser Gly Met Gly Arg Ile Pro Asp Trp Thr Pro
180 185 190

Gln Ala Tyr Asp Pro Leu Asp Val Leu Val Pro Tyr Phe Val Pro Asn
195 200 205

Thr Pro Ala Ala Arg Ala Asp Leu Ala Ala Gln Tyr Thr Thr Val Gly
210 215 220

Arg Met Asp Gln Gly Val Gly Leu Val Leu Gln Glu Leu Arg Asp Ala
225 230 235 240

Gly Val Leu Asn Asp Thr Leu Val Ile Phe Thr Ser Asp Asn Gly Ile
245 250 255

Pro Phe Pro Ser Gly Arg Thr Asn Leu Tyr Trp Pro Gly Thr Ala Glu
260 265 270

Pro Leu Leu Val Ser Ser Pro Glu His Pro Lys Arg Trp Gly Gln Val
275 280 285

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

Trp Phe Ser Ile Pro Tyr Pro Ser Tyr Ala Ile Phe Gly Ser Lys Thr
305 310 315 320

Ile His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu Glu Ala Glu Pro
325 330 335

Leu Trp Ala Thr Val Phe Gly Ser Gln Ser His His Glu Val Thr Met
340 345 350

Ser Tyr Pro Met Arg Ser Val Gln His Arg His Phe Arg Leu Val His
355 360 365

Asn Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln Asp Phe Tyr Val
370 375 380

Ser Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr Ala Gly Gln Pro
385 390 395 400

Thr Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr Arg Ala Arg Trp
405 410 415

Glu Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr Gln Asn Leu Ala
420 425 430

Thr Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu Arg Asp Gln Leu
435 440 445

Ala Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val Cys Ala Pro Asp
450 455 460

Gly Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln Pro Leu His Asn
465 470 475 480

Glu Leu

<210> 81

<211> 497

<212> PRT

<213> Homo sapiens

<400> 81

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys
1 5 10 15

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

Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg

35

40

45

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
 50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
 65 70 75 80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
 85 90 95

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
 100 105 110

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
 115 120 125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu
 130 135 140

His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu
 145 150 155 160

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala
 165 170 175

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

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
 195 200 205

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
 210 215 220

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
 225 230 235 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
275 280 285

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

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala
305 310 315 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
325 330 335

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
405 410 415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
420 425 430

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

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
450 455 460

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu
465 470 475 480

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg
485 490 495

Gln

<210> 82
<211> 544
<212> PRT
<213> Homo sapiens

<400> 82

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

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

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

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

Asn Val Ala Asp Leu Val Arg Pro Ser Pro Leu Thr Leu His Thr Val
65 70 75 80

Gln Lys Trp Leu Leu Ala Ala Gly Ala Gln Lys Cys His Ser Val Ile

85

90

95

Thr Gln Asp Phe Leu Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu
 100 105 110

Leu Leu Pro Gly Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu
 115 120 125

Thr His Val Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu
 130 135 140

Ala Pro His Val Asp Phe Val Gly Gly Leu His His Phe Pro Pro Thr
 145 150 155 160

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

Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn Leu
 180 185 190

Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln Ala Cys
 195 200 205

Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu Ala Gln Phe
 210 215 220

Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala Ser Val Ala Arg
 225 230 235 240

Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly Ile Glu Ala Ser Leu
 245 250 255

Asp Val Gln Tyr Leu Met Ser Ala Gly Ala Asn Ile Ser Thr Trp Val
 260 265 270

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

Leu Met Leu Leu Ser Asn Glu Ser Ala Leu Pro His Val His Thr Val
290 295 300

Ser Tyr Gly Asp Asp Glu Asp Ser Leu Ser Ser Ala Tyr Ile Gln Arg
305 310 315 320

Val Asn Thr Glu Leu Met Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu
325 330 335

Phe Ala Ser Gly Asp Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg
340 345 350

His Gln Phe Arg Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr
355 360 365

Val Gly Gly Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile
370 375 380

Val Asp Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro
385 390 395 400

Ser Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His
405 410 415

Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro Asp
420 425 430

Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg Val Pro
435 440 445

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

Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser Gly Arg Pro Pro
465 470 475 480

Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln His Gly Ala Gly Leu
485 490 495

Phe Asp Val Thr Arg Gly Cys His Glu Ser Cys Leu Asp Glu Glu Val
500 505 510

Glu Gly Gln Gly Phe Cys Ser Gly Pro Gly Trp Asp Pro Val Thr Gly
515 520 525

Trp Gly Thr Pro Asn Phe Pro Ala Leu Leu Lys Thr Leu Leu Asn Pro
530 535 540

<210> 83
<211> 720
<212> PRT
<213> Homo sapiens

<400> 83

Asp Glu Ala Arg Glu Ala Ala Ala Val Arg Ala Leu Val Ala Arg Leu
1 5 10 15

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

Leu Ala Ala Lys Pro Gly Leu Asp Thr Tyr Ser Leu Gly Gly Gly Gly
35 40 45

Ala Ala Arg Val Arg Val Arg Gly Ser Thr Gly Val Ala Ala Ala Ala
50 55 60

Gly Leu His Arg Tyr Leu Arg Asp Phe Cys Gly Cys His Val Ala Trp
65 70 75 80

Ser Gly Ser Gln Leu Arg Leu Pro Arg Pro Leu Pro Ala Val Pro Gly
85 90 95

Glu Leu Thr Glu Ala Thr Pro Asn Arg Tyr Arg Tyr Tyr Gln Asn Val

100	105	110
Cys Thr Gln Ser Tyr Ser Phe Val Trp Trp Asp Trp Ala Arg Trp Glu		
115	120	125
Arg Glu Ile Asp Trp Met Ala Leu Asn Gly Ile Asn Leu Ala Leu Ala		
130	135	140
Trp Ser Gly Gln Glu Ala Ile Trp Gln Arg Val Tyr Leu Ala Leu Gly		
145	150	155
160		
Leu Thr Gln Ala Glu Ile Asn Glu Phe Phe Thr Gly Pro Ala Phe Leu		
165	170	175
Ala Trp Gly Arg Met Gly Asn Leu His Thr Trp Asp Gly Pro Leu Pro		
180	185	190
Pro Ser Trp His Ile Lys Gln Leu Tyr Leu Gln His Arg Val Leu Asp		
195	200	205
Gln Met Arg Ser Phe Gly Met Thr Pro Val Leu Pro Ala Phe Ala Gly		
210	215	220
His Val Pro Glu Ala Val Thr Arg Val Phe Pro Gln Val Asn Val Thr		
225	230	235
240		
Lys Met Gly Ser Trp Gly His Phe Asn Cys Ser Tyr Ser Cys Ser Phe		
245	250	255
Leu Leu Ala Pro Glu Asp Pro Ile Phe Pro Ile Ile Gly Ser Leu Phe		
260	265	270
Leu Arg Glu Leu Ile Lys Glu Phe Gly Thr Asp His Ile Tyr Gly Ala		
275	280	285
Asp Thr Phe Asn Glu Met Gln Pro Pro Ser Ser Glu Pro Ser Tyr Leu		
290	295	300

Ala Ala Ala Thr Thr Ala Val Tyr Glu Ala Met Thr Ala Val Asp Thr
305 310 315 320

Glu Ala Val Trp Leu Leu Gln Gly Trp Leu Phe Gln His Gln Pro Gln
325 330 335

Phe Trp Gly Pro Ala Gln Ile Arg Ala Val Leu Gly Ala Val Pro Arg
340 345 350

Gly Arg Leu Leu Val Leu Asp Leu Phe Ala Glu Ser Gln Pro Val Tyr
355 360 365

Thr Arg Thr Ala Ser Phe Gln Gly Gln Pro Phe Ile Trp Cys Met Leu
370 375 380

His Asn Phe Gly Gly Asn His Gly Leu Phe Gly Ala Leu Glu Ala Val
385 390 395 400

Asn Gly Gly Pro Glu Ala Ala Arg Leu Phe Pro Asn Ser Thr Met Val
405 410 415

Gly Thr Gly Met Ala Pro Glu Gly Ile Ser Gln Asn Glu Val Val Tyr
420 425 430

Ser Leu Met Ala Glu Leu Gly Trp Arg Lys Asp Pro Val Pro Asp Leu
435 440 445

Ala Ala Trp Val Thr Ser Phe Ala Ala Arg Arg Tyr Gly Val Ser His
450 455 460

Pro Asp Ala Gly Ala Ala Trp Arg Leu Leu Leu Arg Ser Val Tyr Asn
465 470 475 480

Cys Ser Gly Glu Ala Cys Arg Gly His Asn Arg Ser Pro Leu Val Arg
485 490 495

Arg Pro Ser Leu Gln Met Asn Thr Ser Ile Trp Tyr Asn Arg Ser Asp
500 505 510

Val Phe Glu Ala Trp Arg Leu Leu Leu Thr Ser Ala Pro Ser Leu Ala
515 520 525

Thr Ser Pro Ala Phe Arg Tyr Asp Leu Leu Asp Leu Thr Arg Gln Ala
530 535 540

Val Gln Glu Leu Val Ser Leu Tyr Tyr Glu Glu Ala Arg Ser Ala Tyr
545 550 555 560

Leu Ser Lys Glu Leu Ala Ser Leu Leu Arg Ala Gly Gly Val Leu Ala
565 570 575

Tyr Glu Leu Leu Pro Ala Leu Asp Glu Val Leu Ala Ser Asp Ser Arg
580 585 590

Phe Leu Leu Gly Ser Trp Leu Glu Gln Ala Arg Ala Ala Ala Val Ser
595 600 605

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

Leu Trp Gly Pro Glu Gly Asn Ile Leu Asp Tyr Ala Asn Lys Gln Leu
625 630 635 640

Ala Gly Leu Val Ala Asn Tyr Tyr Thr Pro Arg Trp Arg Leu Phe Leu
645 650 655

Glu Ala Leu Val Asp Ser Val Ala Gln Gly Ile Pro Phe Gln Gln His
660 665 670

Gln Phe Asp Lys Asn Val Phe Gln Leu Glu Gln Ala Phe Val Leu Ser
675 680 685

Lys Gln Arg Tyr Pro Ser Gln Pro Arg Gly Asp Thr Val Asp Leu Ala
690 695 700

Lys Lys Ile Phe Leu Lys Tyr Tyr Pro Arg Trp Val Ala Gly Ser Trp
705 710 715 720

<210> 84
<211> 629
<212> PRT
<213> Homo sapiens

<400> 84

Leu Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser Arg Glu Cys
1 5 10 15

Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe Ser Asp Asn
20 25 30

Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro Leu Trp Glu
35 40 45

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

Ser Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val Trp Tyr Glu
65 70 75 80

Arg Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu Arg Thr Arg
85 90 95

Val Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala Ile Val Trp Val
100 105 110

Asn Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr Leu Pro Phe Glu
115 120 125

Ala Asp Ile Ser Asn Leu Val Gln Val Gly Pro Leu Pro Ser Arg Leu
130 135 140

Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro Thr Thr Leu Pro
145 150 155 160

Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys Tyr Pro Lys Gly
165 170 175

Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr Ala Gly Leu
180 185 190

Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr Ile Asp Asp
195 200 205

Ile Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu Val Asn Tyr
210 215 220

Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu Val Arg Leu
225 230 235 240

Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr Gln Gly
245 250 255

Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr Leu Met His
260 265 270

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

Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu Pro Val Gly Ile
290 295 300

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

Phe Tyr Phe His Gly Val Asn Lys His Glu Asp Ala Asp Ile Arg Gly
325 330 335

Lys Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe Asn Leu Leu Arg
340 345 350

Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser His Tyr Pro Tyr Ala Glu
355 360 365

Glu Val Met Gln Met Cys Asp Arg Tyr Gly Ile Val Val Ile Asp Glu
370 375 380

Cys Pro Gly Val Gly Leu Ala Leu Pro Gln Phe Phe Asn Asn Val Ser
385 390 395 400

Leu His His His Met Gln Val Met Glu Glu Val Val Arg Arg Asp Lys
405 410 415

Asn His Pro Ala Val Val Met Trp Ser Val Ala Asn Glu Pro Ala Ser
420 425 430

His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala His Thr
435 440 445

Lys Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn Ser Asn
450 455 460

Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys Leu Asn
465 470 475 480

Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu Ile Gln
485 490 495

Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys Tyr Gln Lys
500 505 510

Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile Ala Gly Phe His
515 520 525

Gln Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr Gln Lys Ser Leu Leu
530 535 540

Glu Gln Tyr His Leu Gly Leu Asp Gln Lys Arg Arg Lys Tyr Val Val
545 550 555 560

Gly Glu Leu Ile Trp Asn Phe Ala Asp Phe Met Thr Glu Gln Ser Pro
565 570 575

Thr Arg Val Leu Gly Asn Lys Lys Gly Ile Phe Thr Arg Gln Arg Gln
580 585 590

Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu Arg Tyr Trp Lys Ile Ala
595 600 605

Asn Glu Thr Arg Tyr Pro His Ser Val Ala Lys Ser Gln Cys Leu Glu
610 615 620

Asn Ser Leu Phe Thr
625

<210> 85
<211> 643
<212> PRT
<213> Homo sapiens

<400> 85

Tyr Val Leu Asp Asp Ser Asp Gly Leu Gly Arg Glu Phe Asp Gly Ile
1 5 10 15

Gly Ala Val Ser Gly Gly Gly Ala Thr Ser Arg Leu Leu Val Asn Tyr
20 25 30

Pro Glu Pro Tyr Arg Ser Gln Ile Leu Asp Tyr Leu Phe Lys Pro Asn
35 40 45

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

Gln Thr Thr Asp Gly Thr Glu Pro Ser His Met His Tyr Ala Leu Asp
65 70 75 80

Glu Asn Tyr Phe Arg Gly Tyr Glu Trp Trp Leu Met Lys Glu Ala Lys
85 90 95

Lys Arg Asn Pro Asn Ile Thr Leu Ile Gly Leu Pro Trp Ser Phe Pro
100 105 110

Gly Trp Leu Gly Lys Gly Phe Asp Trp Pro Tyr Val Asn Leu Gln Leu
115 120 125

Thr Ala Tyr Tyr Val Val Thr Trp Ile Val Gly Ala Lys Arg Tyr His
130 135 140

Asp Leu Asp Ile Asp Tyr Ile Gly Ile Trp Asn Glu Arg Ser Tyr Asn
145 150 155 160

Ala Asn Tyr Ile Lys Ile Leu Arg Lys Met Leu Asn Tyr Gln Gly Leu
165 170 175

Gln Arg Val Lys Ile Ile Ala Ser Asp Asn Leu Trp Glu Ser Ile Ser
180 185 190

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

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

Gly Lys Lys Leu Trp Ser Ser Glu Asp Phe Ser Thr Leu Asn Ser Asp
225 230 235 240

Met Gly Ala Gly Cys Trp Gly Arg Ile Leu Asn Gln Asn Tyr Ile Asn
245 250 255

Gly Tyr Met Thr Ser Thr Ile Ala Trp Asn Leu Val Ala Ser Tyr Tyr
260 265 270

Glu Gln Leu Pro Tyr Gly Arg Cys Gly Leu Met Thr Ala Gln Glu Pro
275 280 285

Trp Ser Gly His Tyr Val Val Glu Ser Pro Val Trp Val Ser Ala His
290 295 300

Thr Thr Gln Phe Thr Gln Pro Gly Trp Tyr Tyr Leu Lys Thr Val Gly
305 310 315 320

His Leu Glu Lys Gly Gly Ser Tyr Val Ala Leu Thr Asp Gly Leu Gly
325 330 335

Asn Leu Thr Ile Ile Ile Glu Thr Met Ser His Lys His Ser Lys Cys
340 345 350

Ile Arg Pro Phe Leu Pro Tyr Phe Asn Val Ser Gln Gln Phe Ala Thr
355 360 365

Phe Val Leu Lys Gly Ser Phe Ser Glu Ile Pro Glu Leu Gln Val Trp
370 375 380

Tyr Thr Lys Leu Gly Lys Thr Ser Glu Arg Phe Leu Phe Lys Gln Leu
385 390 395 400

Asp Ser Leu Trp Leu Leu Asp Ser Asp Gly Ser Phe Thr Leu Ser Leu
405 410 415

His Glu Asp Glu Leu Phe Thr Leu Thr Thr Leu Thr Thr Gly Arg Lys
420 425 430

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

Lys Asp Asp Phe Asn Val Asp Tyr Pro Phe Phe Ser Glu Ala Pro Asn
450 455 460

Phe Ala Asp Gln Thr Gly Val Phe Glu Tyr Phe Thr Asn Ile Glu Asp
465 470 475 480

Pro Gly Glu His His Phe Thr Leu Arg Gln Val Leu Asn Gln Arg Pro
485 490 495

Ile Thr Trp Ala Ala Asp Ala Ser Asn Thr Ile Ser Ile Ile Gly Asp
500 505 510

Tyr Asn Trp Thr Asn Leu Thr Ile Lys Cys Asp Val Tyr Ile Glu Thr
515 520 525

Pro Asp Thr Gly Gly Val Phe Ile Ala Gly Arg Val Asn Lys Gly Gly
530 535 540

Ile Leu Ile Arg Ser Ala Arg Gly Ile Phe Phe Trp Ile Phe Ala Asn
545 550 555 560

Gly Ser Tyr Arg Val Thr Gly Asp Leu Ala Gly Trp Ile Ile Tyr Ala
565 570 575

Leu Gly Arg Val Glu Val Thr Ala Lys Lys Trp Tyr Thr Leu Thr Leu
580 585 590

Thr Ile Lys Gly His Phe Thr Ser Gly Met Leu Asn Asp Lys Ser Leu
595 600 605

Trp Thr Asp Ile Pro Val Asn Phe Pro Lys Asn Gly Trp Ala Ala Ile
610 615 620

Gly Thr His Ser Phe Glu Phe Ala Gln Phe Asp Asn Phe Leu Val Glu
625 630 635 640

Ala Thr Arg

<210> 86
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 86

Gln His Ala Pro Pro Trp Thr Glu Asp Cys Arg Lys Ser Thr Tyr Pro
 1 5 10 15

Pro Ser Gly Pro Thr Tyr Arg Gly Ala Val Pro Trp Tyr Thr Ile Asn
 20 25 30

Leu Asp Leu Pro Pro Tyr Lys Arg Trp His Glu Leu Met Leu Asp Lys
 35 40 45

Ala Pro Val Leu Lys Val Ile Val Asn Ser Leu Lys Asn Met Ile Asn
 50 55 60

Thr Phe Val Pro Ser Gly Lys Ile Met Gln Val Val Asp Glu Lys Leu
 65 70 75 80

Pro Gly Leu Leu Gly Asn Phe Pro Gly Pro Phe Glu Glu Glu Met Lys
 85 90 95

Gly Ile Ala Ala Val Thr Asp Ile Pro Leu Gly Glu Ile Ile Ser Phe
 100 105 110

Asn Ile Phe Tyr Glu Leu Phe Thr Ile Cys Thr Ser Ile Val Ala Glu
 115 120 125

Asp Lys Lys Gly His Leu Ile His Gly Arg Asn Met Asp Phe Gly Val
 130 135 140

Phe Leu Gly Trp Asn Ile Asn Asn Asp Thr Trp Val Ile Thr Glu Gln
 145 150 155 160

Leu Lys Pro Leu Thr Val Asn Leu Asp Phe Gln Arg Asn Asn Lys Thr
165 170 175

Val Phe Lys Ala Ser Ser Phe Ala Gly Tyr Val Gly Met Leu Thr Gly
180 185 190

Phe Lys Pro Gly Leu Phe Ser Leu Thr Leu Asn Glu Arg Phe Ser Ile
195 200 205

Asn Gly Gly Tyr Leu Gly Ile Leu Glu Trp Ile Leu Gly Lys Lys Asp
210 215 220

Val Met Trp Ile Gly Phe Leu Thr Arg Thr Val Leu Glu Asn Ser Thr
225 230 235 240

Ser Tyr Glu Glu Ala Lys Asn Leu Leu Thr Lys Thr Lys Ile Leu Ala
245 250 255

Pro Ala Tyr Phe Ile Leu Gly Gly Asn Gln Ser Gly Glu Gly Cys Val
260 265 270

Ile Thr Arg Asp Arg Lys Glu Ser Leu Asp Val Tyr Glu Leu Asp Ala
275 280 285

Lys Gln Gly Arg Trp Tyr Val Val Gln Thr Asn Tyr Asp Arg Trp Lys
290 295 300

His Pro Phe Phe Leu Asp Asp Arg Arg Thr Pro Ala Lys Met Cys Leu
305 310 315 320

Asn Arg Thr Ser Gln Glu Asn Ile Ser Phe Glu Thr Met Tyr Asp Val
325 330 335

Leu Ser Thr Lys Pro Val Leu Asn Lys Leu Thr Val Tyr Thr Thr Leu
340 345 350

Ile Asp Val Thr Lys Gly Gln Phe Glu Thr Tyr Leu Arg Asp Cys Pro
355 360 365

Asp Pro Cys Ile Gly Trp
370

<210> 87
<211> 435
<212> PRT
<213> Homo sapiens

<400> 87

Gln Pro Pro Arg Arg Tyr Thr Pro Asp Trp Pro Ser Leu Asp Ser Arg
1 5 10 15

Pro Leu Pro Ala Trp Phe Asp Glu Ala Lys Phe Gly Val Phe Ile His
20 25 30

Trp Gly Val Phe Ser Val Pro Ala Trp Gly Ser Glu Trp Phe Trp Trp
35 40 45

His Trp Gln Gly Glu Gly Arg Pro Gln Tyr Gln Arg Phe Met Arg Asp
50 55 60

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

Ala Arg Phe Phe His Pro Glu Glu Trp Ala Asp Leu Phe Gln Ala Ala
85 90 95

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

Asn Trp Pro Ser Pro Val Ser Trp Asn Trp Asn Ser Lys Asp Val Gly
115 120 125

Pro His Arg Asp Leu Val Gly Glu Leu Gly Thr Ala Leu Arg Lys Arg
130 135 140

Asn Ile Arg Tyr Gly Leu Tyr His Ser Leu Leu Glu Trp Phe His Pro
 145 150 155 160

Leu Tyr Leu Leu Asp Lys Lys Asn Gly Phe Lys Thr Gln His Phe Val
 165 170 175

Ser Ala Lys Thr Met Pro Glu Leu Tyr Asp Leu Val Asn Ser Tyr Lys
 180 185 190

Pro Asp Leu Ile Trp Ser Asp Gly Glu Trp Glu Cys Pro Asp Thr Tyr
 195 200 205

Trp Asn Ser Thr Asn Phe Leu Ser Trp Leu Tyr Asn Asp Ser Pro Val
 210 215 220

Lys Asp Glu Val Val Val Asn Asp Arg Trp Gly Gln Asn Cys Ser Cys
 225 230 235 240

His His Gly Gly Tyr Tyr Asn Cys Glu Asp Lys Phe Lys Pro Gln Ser
 245 250 255

Leu Pro Asp His Lys Trp Glu Met Cys Thr Ser Ile Asp Lys Phe Ser
 260 265 270

Trp Gly Tyr Arg Arg Asp Met Ala Leu Ser Asp Val Thr Glu Glu Ser
 275 280 285

Glu Ile Ile Ser Glu Leu Val Gln Thr Val Ser Leu Gly Gly Asn Tyr
 290 295 300

Leu Leu Asn Ile Gly Pro Thr Lys Asp Gly Leu Ile Val Pro Ile Phe
 305 310 315 320

Gln Glu Arg Leu Leu Ala Val Gly Lys Trp Leu Ser Ile Asn Gly Glu
 325 330 335

Ala Ile Tyr Ala Ser Lys Pro Trp Arg Val Gln Trp Glu Lys Asn Thr
340 345 350

Thr Ser Val Trp Tyr Thr Ser Lys Gly Ser Ala Val Tyr Ala Ile Phe
355 360 365

Leu His Trp Pro Glu Asn Gly Val Leu Asn Leu Glu Ser Pro Ile Thr
370 375 380

Thr Ser Thr Thr Lys Ile Thr Met Leu Gly Ile Gln Gly Asp Leu Lys
385 390 395 400

Trp Ser Thr Asp Pro Asp Lys Gly Leu Phe Ile Ser Leu Pro Gln Leu
405 410 415

Pro Pro Ser Ala Val Pro Ala Glu Phe Ala Trp Thr Ile Lys Leu Thr
420 425 430

Gly Val Lys
435

<210> 88
<211> 962
<212> PRT
<213> Homo sapiens

<400> 88

Gly Gly Tyr Glu Thr Cys Pro Thr Val Gln Pro Asn Met Leu Asn Val
1 5 10 15

His Leu Leu Pro His Thr His Asp Asp Val Gly Trp Leu Lys Thr Val
20 25 30

Asp Gln Tyr Phe Tyr Gly Ile Lys Asn Asp Ile Gln His Ala Gly Val
35 40 45

Gln Tyr Ile Leu Asp Ser Val Ile Ser Ala Leu Leu Ala Asp Pro Thr

50

55

60

Arg Arg Phe Ile Tyr Val Glu Ile Ala Phe Phe Ser Arg Trp Trp His
65 70 75 80

Gln Gln Thr Asn Ala Thr Gln Glu Val Val Arg Asp Leu Val Arg Gln
85 90 95

Gly Arg Leu Glu Phe Ala Asn Gly Gly Trp Val Met Asn Asp Glu Ala
100 105 110

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

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

His Ile Asp Pro Phe Gly His Ser Arg Glu Gln Ala Ser Leu Phe Ala
145 150 155 160

Gln Met Gly Phe Asp Gly Phe Phe Phe Gly Arg Leu Asp Tyr Gln Asp
165 170 175

Lys Trp Val Arg Met Gln Lys Leu Glu Met Glu Gln Val Trp Arg Ala
180 185 190

Ser Thr Ser Leu Lys Pro Pro Thr Ala Asp Leu Phe Thr Gly Val Leu
195 200 205

Pro Asn Gly Tyr Asn Pro Pro Arg Asn Leu Cys Trp Asp Val Leu Cys
210 215 220

Val Asp Gln Pro Leu Val Glu Asp Pro Arg Ser Pro Glu Tyr Asn Ala
225 230 235 240

Lys Glu Leu Val Asp Tyr Phe Leu Asn Val Ala Thr Ala Gln Gly Arg
245 250 255

Tyr Tyr Arg Thr Asn His Thr Val Met Thr Met Gly Ser Asp Phe Gln
260 265 270

Tyr Glu Asn Ala Asn Met Trp Phe Lys Asn Leu Asp Lys Leu Ile Arg
275 280 285

Leu Val Asn Ala Gln Gln Ala Lys Gly Ser Ser Val His Val Leu Tyr
290 295 300

Ser Thr Pro Ala Cys Tyr Leu Trp Glu Leu Asn Lys Ala Asn Leu Thr
305 310 315 320

Trp Ser Val Lys His Asp Asp Phe Phe Pro Tyr Ala Asp Gly Pro His
325 330 335

Gln Phe Trp Thr Gly Tyr Phe Ser Ser Arg Pro Ala Leu Lys Arg Tyr
340 345 350

Glu Arg Leu Ser Tyr Asn Phe Leu Gln Val Cys Asn Gln Leu Glu Ala
355 360 365

Leu Val Gly Leu Ala Ala Asn Val Gly Pro Tyr Gly Ser Gly Asp Ser
370 375 380

Ala Pro Leu Asn Glu Ala Met Ala Val Leu Gln His His Asp Ala Val
385 390 395 400

Ser Gly Thr Ser Arg Gln His Val Ala Asn Asp Tyr Ala Arg Gln Leu
405 410 415

Ala Ala Gly Trp Gly Pro Cys Glu Val Leu Leu Ser Asn Ala Leu Ala
420 425 430

Arg Leu Arg Gly Phe Lys Asp His Phe Thr Phe Cys Gln Gln Leu Asn
435 440 445

Ile Ser Ile Cys Pro Leu Ser Gln Thr Ala Ala Arg Phe Gln Val Ile
450 455 460

Val Tyr Asn Pro Leu Gly Arg Lys Val Asn Trp Met Val Arg Leu Pro
465 470 475 480

Val Ser Glu Gly Val Phe Val Val Lys Asp Pro Asn Gly Arg Thr Val
485 490 495

Pro Ser Asp Val Val Ile Phe Pro Ser Ser Asp Ser Gln Ala His Pro
500 505 510

Pro Glu Leu Leu Phe Ser Ala Ser Leu Pro Ala Leu Gly Phe Ser Thr
515 520 525

Tyr Ser Val Ala Gln Val Pro Arg Trp Lys Pro Gln Ala Arg Ala Pro
530 535 540

Gln Pro Ile Pro Arg Arg Ser Trp Ser Pro Ala Leu Thr Ile Glu Asn
545 550 555 560

Glu His Ile Arg Ala Thr Phe Asp Pro Asp Thr Gly Leu Leu Met Glu
565 570 575

Ile Met Asn Met Asn Gln Gln Leu Leu Leu Pro Val Arg Gln Thr Phe
580 585 590

Phe Trp Tyr Asn Ala Ser Ile Gly Asp Asn Glu Ser Asp Gln Ala Ser
595 600 605

Gly Ala Tyr Ile Phe Arg Pro Asn Gln Gln Lys Pro Leu Pro Val Ser
610 615 620

Arg Trp Ala Gln Ile His Leu Val Lys Thr Pro Leu Val Gln Glu Val
625 630 635 640

His Gln Asn Phe Ser Ala Trp Cys Ser Gln Val Val Arg Leu Tyr Pro
645 650 655

Gly Gln Arg His Leu Glu Leu Glu Trp Ser Val Gly Pro Ile Pro Val
660 665 670

Gly Asp Thr Trp Gly Lys Glu Val Ile Ser Arg Phe Asp Thr Pro Leu
675 680 685

Glu Thr Lys Gly Arg Phe Tyr Thr Asp Ser Asn Gly Arg Glu Ile Leu
690 695 700

Glu Arg Arg Arg Asp Tyr Arg Pro Thr Trp Lys Leu Asn Gln Thr Glu
705 710 715 720

Pro Val Ala Gly Asn Tyr Tyr Pro Val Asn Thr Arg Ile Tyr Ile Thr
725 730 735

Asp Gly Asn Met Gln Leu Thr Val Leu Thr Asp Arg Ser Gln Gly Gly
740 745 750

Ser Ser Leu Arg Asp Gly Ser Leu Glu Leu Met Val His Arg Arg Leu
755 760 765

Leu Lys Asp Asp Gly Arg Gly Val Ser Glu Pro Leu Met Glu Asn Gly
770 775 780

Ser Gly Ala Trp Val Arg Gly Arg His Leu Val Leu Leu Asp Thr Ala
785 790 795 800

Gln Ala Ala Ala Ala Gly His Arg Leu Leu Ala Glu Gln Glu Val Leu
805 810 815

Ala Pro Gln Val Val Leu Ala Pro Gly Gly Gly Ala Ala Tyr Asn Leu
820 825 830

Gly Ala Pro Pro Arg Thr Gln Phe Ser Gly Leu Arg Arg Asp Leu Pro

835

840

845

Pro Ser Val His Leu Leu Thr Leu Ala Ser Trp Gly Pro Glu Met Val
 850 855 860

Leu Leu Arg Leu Glu His Gln Phe Ala Val Gly Glu Asp Ser Gly Arg
 865 870 875 880

Asn Leu Ser Ala Pro Val Thr Leu Asn Leu Arg Asp Leu Phe Ser Thr
 885 890 895

Phe Thr Ile Thr Arg Leu Gln Glu Thr Thr Leu Val Ala Asn Gln Leu
 900 905 910

Arg Glu Ala Ala Ser Arg Leu Lys Trp Thr Thr Asn Thr Gly Pro Thr
 915 920 925

Pro His Gln Thr Pro Tyr Gln Leu Asp Pro Ala Asn Ile Thr Leu Glu
 930 935 940

Pro Met Glu Ile Arg Thr Phe Leu Ala Ser Val Gln Trp Lys Glu Val
 945 950 955 960

Asp Gly

<210> 89

<211> 1124

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
 humanized anti-hTfR antibody No. 3N and hGAA

<400> 89

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Ala His Pro Gly Arg Pro Arg Ala Val Pro Thr Gln Cys Asp Val
245 250 255

Pro Pro Asn Ser Arg Phe Asp Cys Ala Pro Asp Lys Ala Ile Thr Gln
260 265 270

Glu Gln Cys Glu Ala Arg Gly Cys Cys Tyr Ile Pro Ala Lys Gln Gly
275 280 285

Leu Gln Gly Ala Gln Met Gly Gln Pro Trp Cys Phe Phe Pro Pro Ser
290 295 300

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

Thr Ala Thr Leu Thr Arg Thr Thr Pro Thr Phe Phe Pro Lys Asp Ile
325 330 335

Leu Thr Leu Arg Leu Asp Val Met Met Glu Thr Glu Asn Arg Leu His
340 345 350

Phe Thr Ile Lys Asp Pro Ala Asn Arg Arg Tyr Glu Val Pro Leu Glu
355 360 365

Thr Pro Arg Val His Ser Arg Ala Pro Ser Pro Leu Tyr Ser Val Glu
370 375 380

Phe Ser Glu Glu Pro Phe Gly Val Ile Val His Arg Gln Leu Asp Gly
385 390 395 400

Arg Val Leu Leu Asn Thr Thr Val Ala Pro Leu Phe Phe Ala Asp Gln

405

410

415

Phe Leu Gln Leu Ser Thr Ser Leu Pro Ser Gln Tyr Ile Thr Gly Leu
 420 425 430

Ala Glu His Leu Ser Pro Leu Met Leu Ser Thr Ser Trp Thr Arg Ile
 435 440 445

Thr Leu Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly Ala Asn Leu Tyr
 450 455 460

Gly Ser His Pro Phe Tyr Leu Ala Leu Glu Asp Gly Gly Ser Ala His
 465 470 475 480

Gly Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val Val Leu Gln Pro
 485 490 495

Ser Pro Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile Leu Asp Val Tyr
 500 505 510

Ile Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln Gln Tyr Leu Asp
 515 520 525

Val Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly Leu Gly Phe His
 530 535 540

Leu Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr Arg Gln Val Val
 545 550 555 560

Glu Asn Met Thr Arg Ala His Phe Pro Leu Asp Val Gln Trp Asn Asp
 565 570 575

Leu Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe Asn Lys Asp Gly
 580 585 590

Phe Arg Asp Phe Pro Ala Met Val Gln Glu Leu His Gln Gly Gly Arg
 595 600 605

Arg Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser Ser Gly Pro Ala
610 615 620

Gly Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg Gly Val Phe Ile
625 630 635 640

Thr Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val Trp Pro Gly Ser
645 650 655

Thr Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu Ala Trp Trp Glu
660 665 670

Asp Met Val Ala Glu Phe His Asp Gln Val Pro Phe Asp Gly Met Trp
675 680 685

Ile Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly Ser Glu Asp Gly
690 695 700

Cys Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val Pro Gly Val Val
705 710 715 720

Gly Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser Ser His Gln Phe
725 730 735

Leu Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly Leu Thr Glu Ala
740 745 750

Ile Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly Thr Arg Pro Phe
755 760 765

Val Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg Tyr Ala Gly His
770 775 780

Trp Thr Gly Asp Val Trp Ser Ser Trp Glu Gln Leu Ala Ser Ser Val
785 790 795 800

Pro Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro Leu Val Gly Ala
805 810 815

Asp Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu Leu Cys Val Arg
820 825 830

Trp Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg Asn His Asn Ser
835 840 845

Leu Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe Ser Glu Pro Ala Gln
850 855 860

Gln Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala Leu Leu Pro His
865 870 875 880

Leu Tyr Thr Leu Phe His Gln Ala His Val Ala Gly Glu Thr Val Ala
885 890 895

Arg Pro Leu Phe Leu Glu Phe Pro Lys Asp Ser Ser Thr Trp Thr Val
900 905 910

Asp His Gln Leu Leu Trp Gly Glu Ala Leu Leu Ile Thr Pro Val Leu
915 920 925

Gln Ala Gly Lys Ala Glu Val Thr Gly Tyr Phe Pro Leu Gly Thr Trp
930 935 940

Tyr Asp Leu Gln Thr Val Pro Ile Glu Ala Leu Gly Ser Leu Pro Pro
945 950 955 960

Pro Pro Ala Ala Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln Trp
965 970 975

Val Thr Leu Pro Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg Ala
980 985 990

Gly Tyr Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu Ser
995 1000 1005

Arg Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly
1010 1015 1020

Glu Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu
1025 1030 1035

Val Leu Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala Arg
1040 1045 1050

Asn Asn Thr Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly
1055 1060 1065

Ala Gly Leu Gln Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr
1070 1075 1080

Ala Pro Gln Gln Val Leu Ser Asn Gly Val Pro Val Ser Asn Phe
1085 1090 1095

Thr Tyr Ser Pro Asp Thr Lys Val Leu Asp Ile Cys Val Ser Leu
1100 1105 1110

Leu Met Gly Glu Gln Phe Leu Val Ser Trp Cys
1115 1120

<210> 90

<211> 1075

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hIDUA, IgG4
HC-IDUA

<400> 90

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu

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

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Ala
435 440 445

Glu Ala Pro His Leu Val His Val Asp Ala Ala Arg Ala Leu Trp Pro
450 455 460

Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu Pro His
465 470 475 480

Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu
485 490 495

Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr
500 505 510

His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly
515 520 525

Leu Ser Tyr Asn Phe Thr His Leu Asp Gly Tyr Leu Asp Leu Leu Arg
530 535 540

Glu Asn Gln Leu Leu Pro Gly Phe Glu Leu Met Gly Ser Ala Ser Gly
545 550 555 560

His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val Phe Glu Trp Lys Asp
565 570 575

Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala
580 585 590

His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His
595 600 605

Asp Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr
610 615 620

Asp Ala Cys Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu
625 630 635 640

Gly Gly Pro Gly Asp Ser Phe His Thr Pro Pro Arg Ser Pro Leu Ser
645 650 655

Trp Gly Leu Leu Arg His Cys His Asp Gly Thr Asn Phe Phe Thr Gly
660 665 670

Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His Arg Lys Gly Ala
675 680 685

Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln Gln
690 695 700

Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp
705 710 715 720

Glu Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala
725 730 735

Asp Val Thr Tyr Ala Ala Met Val Val Lys Val Ile Ala Gln His Gln
740 745 750

Asn Leu Leu Leu Ala Asn Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu
755 760 765

Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro His Pro Phe Ala Gln
770 775 780

Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg Pro Pro His

785		790		795		800									
Val	Gln	Leu	Leu	Arg	Lys	Pro	Val	Leu	Thr	Ala	Met	Gly	Leu	Leu	Ala
				805					810					815	
Leu	Leu	Asp	Glu	Glu	Gln	Leu	Trp	Ala	Glu	Val	Ser	Gln	Ala	Gly	Thr
			820					825					830		
Val	Leu	Asp	Ser	Asn	His	Thr	Val	Gly	Val	Leu	Ala	Ser	Ala	His	Arg
		835					840					845			
Pro	Gln	Gly	Pro	Ala	Asp	Ala	Trp	Arg	Ala	Ala	Val	Leu	Ile	Tyr	Ala
	850					855					860				
Ser	Asp	Asp	Thr	Arg	Ala	His	Pro	Asn	Arg	Ser	Val	Ala	Val	Thr	Leu
865					870					875					880
Arg	Leu	Arg	Gly	Val	Pro	Pro	Gly	Pro	Gly	Leu	Val	Tyr	Val	Thr	Arg
			885						890					895	
Tyr	Leu	Asp	Asn	Gly	Leu	Cys	Ser	Pro	Asp	Gly	Glu	Trp	Arg	Arg	Leu
			900					905					910		
Gly	Arg	Pro	Val	Phe	Pro	Thr	Ala	Glu	Gln	Phe	Arg	Arg	Met	Arg	Ala
		915					920					925			
Ala	Glu	Asp	Pro	Val	Ala	Ala	Ala	Pro	Arg	Pro	Leu	Pro	Ala	Gly	Gly
	930					935					940				
Arg	Leu	Thr	Leu	Arg	Pro	Ala	Leu	Arg	Leu	Pro	Ser	Leu	Leu	Leu	Val
945					950					955					960
His	Val	Cys	Ala	Arg	Pro	Glu	Lys	Pro	Pro	Gly	Gln	Val	Thr	Arg	Leu
				965					970					975	
Arg	Ala	Leu	Pro	Leu	Thr	Gln	Gly	Gln	Leu	Val	Leu	Val	Trp	Ser	Asp
			980					985					990		

Glu His Val Gly Ser Lys Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser
 995 1000 1005

Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro Ser Thr
 1010 1015 1020

Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly
 1025 1030 1035

Ser Tyr Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro
 1040 1045 1050

Phe Ser Asp Pro Val Pro Tyr Leu Glu Val Pro Val Pro Arg Gly
 1055 1060 1065

Pro Pro Ser Pro Gly Asn Pro
 1070 1075

<210> 91
 <211> 1113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hIDUA, IgG4
 HC-GS8-IDUA

<400> 91

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Gly

435

440

445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 465 470 475 480

Gly Ser Gly Gly Gly Gly Ser Ala Pro His Leu Val His Val Asp Ala
 485 490 495

Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe
 500 505 510

Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp
 515 520 525

Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly
 530 535 540

Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu Val Thr Thr Arg
 545 550 555 560

Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His Leu Asp Gly
 565 570 575

Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu Leu
 580 585 590

Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln
 595 600 605

Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile
 610 615 620

Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp
 625 630 635 640

Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser Met Thr Met Gln
645 650 655

Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly Leu Arg Ala Ala
660 665 670

Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser Phe His Thr Pro
675 680 685

Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp Gly
690 695 700

Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser
705 710 715 720

Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu
725 730 735

Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp
740 745 750

Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly Trp Ser Leu
755 760 765

Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met Val Val Lys
770 775 780

Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr Ser Ala
785 790 795 800

Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His
805 810 815

Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn
820 825 830

Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr
835 840 845

Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu
850 855 860

Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr Val Gly Val
865 870 875 880

Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala Trp Arg Ala
885 890 895

Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn Arg
900 905 910

Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly
915 920 925

Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp
930 935 940

Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln
945 950 955 960

Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg
965 970 975

Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala Leu Arg Leu
980 985 990

Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys Pro Pro
995 1000 1005

Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln
1010 1015 1020

Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu
1025 1030 1035

Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr
1040 1045 1050

Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
1055 1060 1065

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu
1070 1075 1080

Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr
1085 1090 1095

Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
1100 1105 1110

<210> 92

<211> 1173

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hIDUA, IgG4
HC-GS20-IDUA

<400> 92

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe

50

55

60

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Ala Glu Ala Pro His Leu Val His Val Asp Ala Ala Arg Ala Leu
545 550 555 560

Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu
565 570 575

Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu
580 585 590

Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val
595 600 605

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

Arg Gly Leu Ser Tyr Asn Phe Thr His Leu Asp Gly Tyr Leu Asp Leu
625 630 635 640

Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu Leu Met Gly Ser Ala
645 650 655

Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val Phe Glu Trp
660 665 670

Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly
675 680 685

Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp
690 695 700

His His Asp Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn
705 710 715 720

Tyr Tyr Asp Ala Cys Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu
725 730 735

Arg Leu Gly Gly Pro Gly Asp Ser Phe His Thr Pro Pro Arg Ser Pro
740 745 750

Leu Ser Trp Gly Leu Leu Arg His Cys His Asp Gly Thr Asn Phe Phe
755 760 765

Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His Arg Lys
770 775 780

Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala
785 790 795 800

Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr
805 810 815

Asn Asp Glu Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp
820 825 830

Arg Ala Asp Val Thr Tyr Ala Ala Met Val Val Lys Val Ile Ala Gln

835

840

845

His Gln Asn Leu Leu Leu Ala Asn Thr Thr Ser Ala Phe Pro Tyr Ala
 850 855 860

Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro His Pro Phe
 865 870 875 880

Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg Pro
 885 890 895

Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu
 900 905 910

Leu Ala Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala
 915 920 925

Gly Thr Val Leu Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala
 930 935 940

His Arg Pro Gln Gly Pro Ala Asp Ala Trp Arg Ala Ala Val Leu Ile
 945 950 955 960

Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn Arg Ser Val Ala Val
 965 970 975

Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val Tyr Val
 980 985 990

Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg
 995 1000 1005

Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg
 1010 1015 1020

Met Arg Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu
 1025 1030 1035

Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala Leu Arg Leu Pro
1040 1045 1050

Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys Pro Pro
1055 1060 1065

Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln
1070 1075 1080

Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu
1085 1090 1095

Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr
1100 1105 1110

Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
1115 1120 1125

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu
1130 1135 1140

Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr
1145 1150 1155

Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
1160 1165 1170

<210> 93

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hIDUA, Fab HC-GS3-IDUA

<400> 93

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195

200

205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 225 230 235 240

Ser Ala Glu Ala Pro His Leu Val His Val Asp Ala Ala Arg Ala Leu
 245 250 255

Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu
 260 265 270

Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu
 275 280 285

Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val
 290 295 300

Arg Thr His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly
 305 310 315 320

Arg Gly Leu Ser Tyr Asn Phe Thr His Leu Asp Gly Tyr Leu Asp Leu
 325 330 335

Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu Leu Met Gly Ser Ala
 340 345 350

Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val Phe Glu Trp
 355 360 365

Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly
 370 375 380

Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp
 385 390 395 400

His His Asp Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn
405 410 415

Tyr Tyr Asp Ala Cys Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu
420 425 430

Arg Leu Gly Gly Pro Gly Asp Ser Phe His Thr Pro Pro Arg Ser Pro
435 440 445

Leu Ser Trp Gly Leu Leu Arg His Cys His Asp Gly Thr Asn Phe Phe
450 455 460

Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His Arg Lys
465 470 475 480

Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala
485 490 495

Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr
500 505 510

Asn Asp Glu Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp
515 520 525

Arg Ala Asp Val Thr Tyr Ala Ala Met Val Val Lys Val Ile Ala Gln
530 535 540

His Gln Asn Leu Leu Leu Ala Asn Thr Thr Ser Ala Phe Pro Tyr Ala
545 550 555 560

Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro His Pro Phe
565 570 575

Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg Pro
580 585 590

Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu
595 600 605

Leu Ala Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala
610 615 620

Gly Thr Val Leu Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala
625 630 635 640

His Arg Pro Gln Gly Pro Ala Asp Ala Trp Arg Ala Ala Val Leu Ile
645 650 655

Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn Arg Ser Val Ala Val
660 665 670

Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val Tyr Val
675 680 685

Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg
690 695 700

Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met
705 710 715 720

Arg Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala
725 730 735

Gly Gly Arg Leu Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu
740 745 750

Leu Val His Val Cys Ala Arg Pro Glu Lys Pro Pro Gly Gln Val Thr
755 760 765

Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln Leu Val Leu Val Trp
770 775 780

Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr Tyr Glu Ile Gln
785 790 795 800

Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro Ser
805 810 815

Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly
820 825 830

Ser Tyr Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe
835 840 845

Ser Asp Pro Val Pro Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro
850 855 860

Ser Pro Gly Asn Pro
865

<210> 94
<211> 879
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hIDUA, Fab HC-GS5-IDUA

<400> 94

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Ala Pro His
245 250 255

Leu Val His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe
260 265 270

Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp
275 280 285

Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly
290 295 300

Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu
305 310 315 320

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

Phe Thr His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu
340 345 350

Leu Pro Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp
355 360 365

Phe Glu Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser
370 375 380

Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys
385 390 395 400

Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn
405 410 415

Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser
420 425 430

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

Asp Ser Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu
450 455 460

Arg His Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val
465 470 475 480

Arg Leu Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile
485 490 495

Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu
500 505 510

Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro
515 520 525

Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr
530 535 540

Ala Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu
545 550 555 560

Ala Asn Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn
565 570 575

Ala Phe Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr
580 585 590

Ala Arg Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu
595 600 605

Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu
610 615 620

Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser
625 630 635 640

Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro

645

650

655

Ala Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr
 660 665 670

Arg Ala His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly
 675 680 685

Val Pro Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn
 690 695 700

Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val
 705 710 715 720

Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro
 725 730 735

Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu
 740 745 750

Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala
 755 760 765

Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro
 770 775 780

Leu Thr Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly
 785 790 795 800

Ser Lys Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys
 805 810 815

Ala Tyr Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val
 820 825 830

Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala
 835 840 845

Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr
850 855 860

Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
865 870 875

<210> 95
<211> 904
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hIDUA, Fab HC-GS10-IDUA

<400> 95

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Ala Glu Ala Pro His Leu Val His Val Asp Ala Ala
275 280 285

Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys
290 295 300

Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp

305		310		315		320
Gln Gln Leu Asn	Leu Ala Tyr Val	Gly Ala Val Pro His Arg	Gly Ile			
	325		330			335
Lys Gln Val Arg	Thr His Trp Leu	Leu Glu Leu Val Thr	Thr Arg Gly			
	340		345			350
Ser Thr Gly Arg	Gly Leu Ser Tyr	Asn Phe Thr His	Leu Asp Gly Tyr			
	355		360			365
Leu Asp Leu Leu	Arg Glu Asn Gln	Leu Leu Pro Gly	Phe Glu Leu Met			
	370		375			380
Gly Ser Ala Ser	Gly His Phe Thr	Asp Phe Glu Asp	Lys Gln Gln Val			
385		390		395		400
Phe Glu Trp Lys	Asp Leu Val Ser	Ser Leu Ala Arg	Arg Tyr Ile Gly			
	405		410			415
Arg Tyr Gly Leu	Ala His Val Ser	Lys Trp Asn Phe	Glu Thr Trp Asn			
	420		425			430
Glu Pro Asp His	His Asp Phe Asp	Asn Val Ser Met	Thr Met Gln Gly			
	435		440			445
Phe Leu Asn Tyr	Tyr Asp Ala Cys	Ser Glu Gly Leu	Arg Ala Ala Ser			
	450		455			460
Pro Ala Leu Arg	Leu Gly Gly Pro	Gly Asp Ser Phe	His Thr Pro Pro			
465		470		475		480
Arg Ser Pro Leu	Ser Trp Gly Leu	Leu Arg His Cys	His Asp Gly Thr			
	485		490			495
Asn Phe Phe Thr	Gly Glu Ala Gly	Val Arg Leu Asp	Tyr Ile Ser Leu			
	500		505			510

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

Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr
530 535 540

Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly Trp Ser Leu Pro
545 550 555 560

Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met Val Val Lys Val
565 570 575

Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr Ser Ala Phe
580 585 590

Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro
595 600 605

His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn
610 615 620

Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala
625 630 635 640

Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val
645 650 655

Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr Val Gly Val Leu
660 665 670

Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala Trp Arg Ala Ala
675 680 685

Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn Arg Ser
690 695 700

Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu
705 710 715 720

Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly
725 730 735

Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe
740 745 750

Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro
755 760 765

Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala Leu Arg Leu Pro
770 775 780

Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys Pro Pro Gly
785 790 795 800

Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln Leu Val
805 810 815

Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr Tyr
820 825 830

Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg
835 840 845

Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala
850 855 860

Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro
865 870 875 880

Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val Pro Val Pro Arg
885 890 895

Gly Pro Pro Ser Pro Gly Asn Pro
900

<210> 96

<211> 954

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hIDUA, Fab HC-GS20-IDUA

<400> 96

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
290 295 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305 310 315 320

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

Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly
340 345 350

Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser
355 360 365

Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg
370 375 380

Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu Val Thr Thr
385 390 395 400

Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His Leu Asp
405 410 415

Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu
420 425 430

Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln
435 440 445

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

Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr
465 470 475 480

Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser Met Thr Met
485 490 495

Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly Leu Arg Ala
500 505 510

Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser Phe His Thr
515 520 525

Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp
530 535 540

Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile
545 550 555 560

Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln
565 570 575

Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala
580 585 590

Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly Trp Ser
595 600 605

Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met Val Val
610 615 620

Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr Ser
625 630 635 640

Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr
645 650 655

His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val
660 665 670

Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu
675 680 685

Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu Trp Ala
690 695 700

Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr Val Gly
705 710 715 720

Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala Trp Arg

725

730

735

Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn
740 745 750

Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro
755 760 765

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

Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu
785 790 795 800

Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala Ala Ala Pro
805 810 815

Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala Leu Arg
820 825 830

Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys Pro
835 840 845

Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln
850 855 860

Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp
865 870 875 880

Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val
885 890 895

Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr
900 905 910

Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp Tyr Trp Ala
915 920 925

Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val Pro Val
 930 935 940

Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
 945 950

<210> 97
 <211> 1140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of fusion protein of the Fab heavy chain of
 humanized anti-hTfR antibody No. 3N and hIDUA, Tandem Fab HC-IDUA

<400> 97

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
260 265 270

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
275 280 285

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
290 295 300

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe

305		310		315		320
Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr						
		325		330		335
Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys						
		340		345		350
Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr						
		355		360		365
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro						
		370		375		380
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly						
385		390		395		400
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn						
		405		410		415
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln						
		420		425		430
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser						
		435		440		445
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser						
450		455		460		
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr						
465		470		475		480
His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly						
		485		490		495
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser						
		500		505		510

Ala Glu Ala Pro His Leu Val His Val Asp Ala Ala Arg Ala Leu Trp
515 520 525

Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu Pro
530 535 540

His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn
545 550 555 560

Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg
565 570 575

Thr His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg
580 585 590

Gly Leu Ser Tyr Asn Phe Thr His Leu Asp Gly Tyr Leu Asp Leu Leu
595 600 605

Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu Leu Met Gly Ser Ala Ser
610 615 620

Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val Phe Glu Trp Lys
625 630 635 640

Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly Leu
645 650 655

Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His
660 665 670

His Asp Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr
675 680 685

Tyr Asp Ala Cys Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg
690 695 700

Leu Gly Gly Pro Gly Asp Ser Phe His Thr Pro Pro Arg Ser Pro Leu
705 710 715 720

Ser Trp Gly Leu Leu Arg His Cys His Asp Gly Thr Asn Phe Phe Thr
725 730 735

Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His Arg Lys Gly
740 745 750

Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln
755 760 765

Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn
770 775 780

Asp Glu Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg
785 790 795 800

Ala Asp Val Thr Tyr Ala Ala Met Val Val Lys Val Ile Ala Gln His
805 810 815

Gln Asn Leu Leu Leu Ala Asn Thr Thr Ser Ala Phe Pro Tyr Ala Leu
820 825 830

Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro His Pro Phe Ala
835 840 845

Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg Pro Pro
850 855 860

His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu
865 870 875 880

Ala Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly
885 890 895

Thr Val Leu Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His
900 905 910

Arg Pro Gln Gly Pro Ala Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr
915 920 925

Ala Ser Asp Asp Thr Arg Ala His Pro Asn Arg Ser Val Ala Val Thr
930 935 940

Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val Tyr Val Thr
945 950 955 960

Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg Arg
965 970 975

Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg
980 985 990

Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly
995 1000 1005

Gly Arg Leu Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu
1010 1015 1020

Leu Val His Val Cys Ala Arg Pro Glu Lys Pro Pro Gly Gln Val
1025 1030 1035

Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln Leu Val Leu
1040 1045 1050

Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr Tyr
1055 1060 1065

Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser
1070 1075 1080

Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr

1085

1090

1095

Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp Tyr Trp
 1100 1105 1110

Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val
 1115 1120 1125

Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
 1130 1135 1140

<210> 98

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of single-chain humanized anti-hTfR antibody
 No. 3N (2)

<400> 98

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr
260 265 270

Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val
275 280 285

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
290 295 300

Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
305 310 315 320

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
325 330 335

Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser
340 345 350

Gln Ser Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
355 360 365

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
370 375 380

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
385 390 395 400

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
405 410 415

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
420 425 430

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
435 440 445

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
450 455 460

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
465 470 475

<210> 99

<211> 1112
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of single-chain humanized anti-hTfR antibody No. 3N and hIDUA

<400> 99

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr
260 265 270

Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val
275 280 285

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
290 295 300

Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
305 310 315 320

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
325 330 335

Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser
340 345 350

Gln Ser Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
355 360 365

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
370 375 380

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
385 390 395 400

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
405 410 415

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
420 425 430

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
435 440 445

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
450 455 460

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly
465 470 475 480

Gly Ser Gly Ser Ala Glu Ala Pro His Leu Val His Val Asp Ala Ala
485 490 495

Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys
500 505 510

Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp
515 520 525

Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile
530 535 540

Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly

545		550		555		560
Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His Leu Asp Gly Tyr						
		565		570		575
Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu Leu Met						
		580		585		590
Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val						
		595		600		605
Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly						
		610		615		620
Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn						
		625		630		635
						640
Glu Pro Asp His His Asp Phe Asp Asn Val Ser Met Thr Met Gln Gly						
		645		650		655
Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly Leu Arg Ala Ala Ser						
		660		665		670
Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser Phe His Thr Pro Pro						
		675		680		685
Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp Gly Thr						
		690		695		700
Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu						
		705		710		715
						720
His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys						
		725		730		735
Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr						
		740		745		750

Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly Trp Ser Leu Pro
755 760 765

Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met Val Val Lys Val
770 775 780

Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr Ser Ala Phe
785 790 795 800

Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro
805 810 815

His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn
820 825 830

Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala
835 840 845

Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val
850 855 860

Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr Val Gly Val Leu
865 870 875 880

Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala Trp Arg Ala Ala
885 890 895

Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn Arg Ser
900 905 910

Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu
915 920 925

Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly
930 935 940

Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe
 945 950 955 960

Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro
 965 970 975

Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala Leu Arg Leu Pro
 980 985 990

Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys Pro Pro Gly
 995 1000 1005

Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln Leu
 1010 1015 1020

Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp
 1025 1030 1035

Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro
 1040 1045 1050

Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro
 1055 1060 1065

Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
 1070 1075 1080

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu
 1085 1090 1095

Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
 1100 1105 1110

<210> 100
 <211> 726
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hPPT-1, IgG4 HC-PPT1

<400> 100

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165

170

175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Asp
435 440 445

Pro Pro Ala Pro Leu Pro Leu Val Ile Trp His Gly Met Gly Asp Ser
450 455 460

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

Lys Ile Pro Gly Ile Tyr Val Leu Ser Leu Glu Ile Gly Lys Thr Leu
485 490 495

Met Glu Asp Val Glu Asn Ser Phe Phe Leu Asn Val Asn Ser Gln Val
500 505 510

Thr Thr Val Cys Gln Ala Leu Ala Lys Asp Pro Lys Leu Gln Gln Gly
515 520 525

Tyr Asn Ala Met Gly Phe Ser Gln Gly Gly Gln Phe Leu Arg Ala Val
530 535 540

Ala Gln Arg Cys Pro Ser Pro Pro Met Ile Asn Leu Ile Ser Val Gly
545 550 555 560

Gly Gln His Gln Gly Val Phe Gly Leu Pro Arg Cys Pro Gly Glu Ser
565 570 575

Ser His Ile Cys Asp Phe Ile Arg Lys Thr Leu Asn Ala Gly Ala Tyr
580 585 590

Ser Lys Val Val Gln Glu Arg Leu Val Gln Ala Glu Tyr Trp His Asp
595 600 605

Pro Ile Lys Glu Asp Val Tyr Arg Asn His Ser Ile Phe Leu Ala Asp
610 615 620

Ile Asn Gln Glu Arg Gly Ile Asn Glu Ser Tyr Lys Lys Asn Leu Met
625 630 635 640

Ala Leu Lys Lys Phe Val Met Val Lys Phe Leu Asn Asp Ser Ile Val
645 650 655

Asp Pro Val Asp Ser Glu Trp Phe Gly Phe Tyr Arg Ser Gly Gln Ala
660 665 670

Lys Glu Thr Ile Pro Leu Gln Glu Thr Ser Leu Tyr Thr Gln Asp Arg
675 680 685

Leu Gly Leu Lys Glu Met Asp Asn Ala Gly Gln Leu Val Phe Leu Ala
690 695 700

Thr Glu Gly Asp His Leu Gln Leu Ser Glu Glu Trp Phe Tyr Ala His
705 710 715 720

Ile Ile Pro Phe Leu Gly
725

<210> 101
<211> 749
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hPPT-1, IgG4 HC-GS5-PPT1

<400> 101

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165

170

175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Asp Pro Pro Ala Pro Leu Pro Leu Val Ile
 465 470 475 480

Trp His Gly Met Gly Asp Ser Cys Cys Asn Pro Leu Ser Met Gly Ala
 485 490 495

Ile Lys Lys Met Val Glu Lys Lys Ile Pro Gly Ile Tyr Val Leu Ser
 500 505 510

Leu Glu Ile Gly Lys Thr Leu Met Glu Asp Val Glu Asn Ser Phe Phe
 515 520 525

Leu Asn Val Asn Ser Gln Val Thr Thr Val Cys Gln Ala Leu Ala Lys
 530 535 540

Asp Pro Lys Leu Gln Gln Gly Tyr Asn Ala Met Gly Phe Ser Gln Gly
 545 550 555 560

Gly Gln Phe Leu Arg Ala Val Ala Gln Arg Cys Pro Ser Pro Pro Met
565 570 575

Ile Asn Leu Ile Ser Val Gly Gly Gln His Gln Gly Val Phe Gly Leu
580 585 590

Pro Arg Cys Pro Gly Glu Ser Ser His Ile Cys Asp Phe Ile Arg Lys
595 600 605

Thr Leu Asn Ala Gly Ala Tyr Ser Lys Val Val Gln Glu Arg Leu Val
610 615 620

Gln Ala Glu Tyr Trp His Asp Pro Ile Lys Glu Asp Val Tyr Arg Asn
625 630 635 640

His Ser Ile Phe Leu Ala Asp Ile Asn Gln Glu Arg Gly Ile Asn Glu
645 650 655

Ser Tyr Lys Lys Asn Leu Met Ala Leu Lys Lys Phe Val Met Val Lys
660 665 670

Phe Leu Asn Asp Ser Ile Val Asp Pro Val Asp Ser Glu Trp Phe Gly
675 680 685

Phe Tyr Arg Ser Gly Gln Ala Lys Glu Thr Ile Pro Leu Gln Glu Thr
690 695 700

Ser Leu Tyr Thr Gln Asp Arg Leu Gly Leu Lys Glu Met Asp Asn Ala
705 710 715 720

Gly Gln Leu Val Phe Leu Ala Thr Glu Gly Asp His Leu Gln Leu Ser
725 730 735

Glu Glu Trp Phe Tyr Ala His Ile Ile Pro Phe Leu Gly
740 745

<210> 102
<211> 774
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hPPT-1, IgG4 HC-GS10-PPT1

<400> 102

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
485 490 495

Pro Pro Ala Pro Leu Pro Leu Val Ile Trp His Gly Met Gly Asp Ser
500 505 510

Cys Cys Asn Pro Leu Ser Met Gly Ala Ile Lys Lys Met Val Glu Lys
515 520 525

Lys Ile Pro Gly Ile Tyr Val Leu Ser Leu Glu Ile Gly Lys Thr Leu
530 535 540

Met Glu Asp Val Glu Asn Ser Phe Phe Leu Asn Val Asn Ser Gln Val
545 550 555 560

Thr Thr Val Cys Gln Ala Leu Ala Lys Asp Pro Lys Leu Gln Gln Gly
565 570 575

Tyr Asn Ala Met Gly Phe Ser Gln Gly Gly Gln Phe Leu Arg Ala Val
580 585 590

Ala Gln Arg Cys Pro Ser Pro Pro Met Ile Asn Leu Ile Ser Val Gly
595 600 605

Gly Gln His Gln Gly Val Phe Gly Leu Pro Arg Cys Pro Gly Glu Ser
610 615 620

Ser His Ile Cys Asp Phe Ile Arg Lys Thr Leu Asn Ala Gly Ala Tyr
625 630 635 640

Ser Lys Val Val Gln Glu Arg Leu Val Gln Ala Glu Tyr Trp His Asp
645 650 655

Pro Ile Lys Glu Asp Val Tyr Arg Asn His Ser Ile Phe Leu Ala Asp
660 665 670

Ile Asn Gln Glu Arg Gly Ile Asn Glu Ser Tyr Lys Lys Asn Leu Met
675 680 685

Ala Leu Lys Lys Phe Val Met Val Lys Phe Leu Asn Asp Ser Ile Val
690 695 700

Asp Pro Val Asp Ser Glu Trp Phe Gly Phe Tyr Arg Ser Gly Gln Ala
705 710 715 720

Lys Glu Thr Ile Pro Leu Gln Glu Thr Ser Leu Tyr Thr Gln Asp Arg
725 730 735

Leu Gly Leu Lys Glu Met Asp Asn Ala Gly Gln Leu Val Phe Leu Ala
740 745 750

Thr Glu Gly Asp His Leu Gln Leu Ser Glu Glu Trp Phe Tyr Ala His
755 760 765

Ile Ile Pro Phe Leu Gly
770

<210> 103

<211> 824

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hPPT-1, IgG4
HC-GS20-PPT1

<400> 103

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr

100	105	110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro		
115	120	125
Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly		
130	135	140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn		
145	150	155
160		
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		
165	170	175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser		
180	185	190
Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser		
195	200	205
Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys		
210	215	220
Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu		
225	230	235
240		
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu		
245	250	255
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln		
260	265	270
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys		
275	280	285
Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu		
290	295	300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Asp Pro Pro Ala Pro Leu Pro Leu Val Ile Trp His Gly Met Gly
545 550 555 560

Asp Ser Cys Cys Asn Pro Leu Ser Met Gly Ala Ile Lys Lys Met Val
565 570 575

Glu Lys Lys Ile Pro Gly Ile Tyr Val Leu Ser Leu Glu Ile Gly Lys
580 585 590

Thr Leu Met Glu Asp Val Glu Asn Ser Phe Phe Leu Asn Val Asn Ser
595 600 605

Gln Val Thr Thr Val Cys Gln Ala Leu Ala Lys Asp Pro Lys Leu Gln
610 615 620

Gln Gly Tyr Asn Ala Met Gly Phe Ser Gln Gly Gly Gln Phe Leu Arg
625 630 635 640

Ala Val Ala Gln Arg Cys Pro Ser Pro Pro Met Ile Asn Leu Ile Ser
645 650 655

Val Gly Gly Gln His Gln Gly Val Phe Gly Leu Pro Arg Cys Pro Gly
660 665 670

Glu Ser Ser His Ile Cys Asp Phe Ile Arg Lys Thr Leu Asn Ala Gly
675 680 685

Ala Tyr Ser Lys Val Val Gln Glu Arg Leu Val Gln Ala Glu Tyr Trp
690 695 700

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

Ala Asp Ile Asn Gln Glu Arg Gly Ile Asn Glu Ser Tyr Lys Lys Asn
725 730 735

Leu Met Ala Leu Lys Lys Phe Val Met Val Lys Phe Leu Asn Asp Ser
740 745 750

Ile Val Asp Pro Val Asp Ser Glu Trp Phe Gly Phe Tyr Arg Ser Gly
755 760 765

Gln Ala Lys Glu Thr Ile Pro Leu Gln Glu Thr Ser Leu Tyr Thr Gln
770 775 780

Asp Arg Leu Gly Leu Lys Glu Met Asp Asn Ala Gly Gln Leu Val Phe
785 790 795 800

Leu Ala Thr Glu Gly Asp His Leu Gln Leu Ser Glu Glu Trp Phe Tyr
805 810 815

Ala His Ile Ile Pro Phe Leu Gly
820

<210> 104

<211> 520

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hPPT-1, Fab HC-GS3-PPT1

<400> 104

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Asp Pro Pro Ala Pro Leu Pro Leu Val Ile Trp His Gly Met Gly
245 250 255

Asp Ser Cys Cys Asn Pro Leu Ser Met Gly Ala Ile Lys Lys Met Val
260 265 270

Glu Lys Lys Ile Pro Gly Ile Tyr Val Leu Ser Leu Glu Ile Gly Lys
275 280 285

Thr Leu Met Glu Asp Val Glu Asn Ser Phe Phe Leu Asn Val Asn Ser
290 295 300

Gln Val Thr Thr Val Cys Gln Ala Leu Ala Lys Asp Pro Lys Leu Gln
305 310 315 320

Gln Gly Tyr Asn Ala Met Gly Phe Ser Gln Gly Gly Gln Phe Leu Arg
325 330 335

Ala Val Ala Gln Arg Cys Pro Ser Pro Pro Met Ile Asn Leu Ile Ser
340 345 350

Val Gly Gly Gln His Gln Gly Val Phe Gly Leu Pro Arg Cys Pro Gly
355 360 365

Glu Ser Ser His Ile Cys Asp Phe Ile Arg Lys Thr Leu Asn Ala Gly
370 375 380

Ala Tyr Ser Lys Val Val Gln Glu Arg Leu Val Gln Ala Glu Tyr Trp
385 390 395 400

His Asp Pro Ile Lys Glu Asp Val Tyr Arg Asn His Ser Ile Phe Leu
405 410 415

Ala Asp Ile Asn Gln Glu Arg Gly Ile Asn Glu Ser Tyr Lys Lys Asn
420 425 430

Leu Met Ala Leu Lys Lys Phe Val Met Val Lys Phe Leu Asn Asp Ser
435 440 445

Ile Val Asp Pro Val Asp Ser Glu Trp Phe Gly Phe Tyr Arg Ser Gly
450 455 460

Gln Ala Lys Glu Thr Ile Pro Leu Gln Glu Thr Ser Leu Tyr Thr Gln
465 470 475 480

Asp Arg Leu Gly Leu Lys Glu Met Asp Asn Ala Gly Gln Leu Val Phe
485 490 495

Leu Ala Thr Glu Gly Asp His Leu Gln Leu Ser Glu Glu Trp Phe Tyr
500 505 510

Ala His Ile Ile Pro Phe Leu Gly
515 520

<210> 105

<211> 791

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hPPT-1, Tandem Fab
HC-PPT1

<400> 105

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr

20

25

30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
260 265 270

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
275 280 285

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
290 295 300

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

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
325 330 335

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
340 345 350

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
370 375 380

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
385 390 395 400

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
405 410 415

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
420 425 430

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
435 440 445

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
450 455 460

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
465 470 475 480

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
485 490 495

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
500 505 510

Asp Pro Pro Ala Pro Leu Pro Leu Val Ile Trp His Gly Met Gly Asp
515 520 525

Ser Cys Cys Asn Pro Leu Ser Met Gly Ala Ile Lys Lys Met Val Glu
530 535 540

Lys Lys Ile Pro Gly Ile Tyr Val Leu Ser Leu Glu Ile Gly Lys Thr
545 550 555 560

Leu Met Glu Asp Val Glu Asn Ser Phe Phe Leu Asn Val Asn Ser Gln
565 570 575

Val Thr Thr Val Cys Gln Ala Leu Ala Lys Asp Pro Lys Leu Gln Gln
580 585 590

Gly Tyr Asn Ala Met Gly Phe Ser Gln Gly Gly Gln Phe Leu Arg Ala
595 600 605

Val Ala Gln Arg Cys Pro Ser Pro Pro Met Ile Asn Leu Ile Ser Val
610 615 620

Gly Gly Gln His Gln Gly Val Phe Gly Leu Pro Arg Cys Pro Gly Glu
625 630 635 640

Ser Ser His Ile Cys Asp Phe Ile Arg Lys Thr Leu Asn Ala Gly Ala
645 650 655

Tyr Ser Lys Val Val Gln Glu Arg Leu Val Gln Ala Glu Tyr Trp His
660 665 670

Asp Pro Ile Lys Glu Asp Val Tyr Arg Asn His Ser Ile Phe Leu Ala
675 680 685

Asp Ile Asn Gln Glu Arg Gly Ile Asn Glu Ser Tyr Lys Lys Asn Leu
690 695 700

Met Ala Leu Lys Lys Phe Val Met Val Lys Phe Leu Asn Asp Ser Ile
705 710 715 720

Val Asp Pro Val Asp Ser Glu Trp Phe Gly Phe Tyr Arg Ser Gly Gln
725 730 735

Ala Lys Glu Thr Ile Pro Leu Gln Glu Thr Ser Leu Tyr Thr Gln Asp
740 745 750

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

Ala Thr Glu Gly Asp His Leu Gln Leu Ser Glu Glu Trp Phe Tyr Ala
770 775 780

His Ile Ile Pro Phe Leu Gly
785 790

<210> 106

<211> 1030
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hASM, IgG4 HC-ASM

<400> 106

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Ser Asp Ser Arg Val Leu Trp Ala Pro Ala Glu Ala His Pro Leu Ser
450 455 460

Pro Gln Gly His Pro Ala Arg Leu His Arg Ile Val Pro Arg Leu Arg
465 470 475 480

Asp Val Phe Gly Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys Gly Leu
485 490 495

Phe Thr Ala Ile Asn Leu Gly Leu Lys Lys Glu Pro Asn Val Ala Arg
500 505 510

Val Gly Ser Val Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile Ala Pro
515 520 525

Pro Ala Val Cys Gln Ser Ile Val His Leu Phe Glu Asp Asp Met Val
530 535 540

Glu Val Trp Arg Arg Ser Val Leu Ser Pro Ser Glu Ala Cys Gly Leu

545		550		555		560									
Leu	Leu	Gly	Ser	Thr	Cys	Gly	His	Trp	Asp	Ile	Phe	Ser	Ser	Trp	Asn
				565					570					575	
Ile	Ser	Leu	Pro	Thr	Val	Pro	Lys	Pro	Pro	Pro	Lys	Pro	Pro	Ser	Pro
			580					585					590		
Pro	Ala	Pro	Gly	Ala	Pro	Val	Ser	Arg	Ile	Leu	Phe	Leu	Thr	Asp	Leu
		595					600					605			
His	Trp	Asp	His	Asp	Tyr	Leu	Glu	Gly	Thr	Asp	Pro	Asp	Cys	Ala	Asp
	610					615					620				
Pro	Leu	Cys	Cys	Arg	Arg	Gly	Ser	Gly	Leu	Pro	Pro	Ala	Ser	Arg	Pro
625					630					635					640
Gly	Ala	Gly	Tyr	Trp	Gly	Glu	Tyr	Ser	Lys	Cys	Asp	Leu	Pro	Leu	Arg
				645					650					655	
Thr	Leu	Glu	Ser	Leu	Leu	Ser	Gly	Leu	Gly	Pro	Ala	Gly	Pro	Phe	Asp
			660					665					670		
Met	Val	Tyr	Trp	Thr	Gly	Asp	Ile	Pro	Ala	His	Asp	Val	Trp	His	Gln
		675					680					685			
Thr	Arg	Gln	Asp	Gln	Leu	Arg	Ala	Leu	Thr	Thr	Val	Thr	Ala	Leu	Val
	690					695					700				
Arg	Lys	Phe	Leu	Gly	Pro	Val	Pro	Val	Tyr	Pro	Ala	Val	Gly	Asn	His
705					710					715					720
Glu	Ser	Thr	Pro	Val	Asn	Ser	Phe	Pro	Pro	Pro	Phe	Ile	Glu	Gly	Asn
				725					730					735	
His	Ser	Ser	Arg	Trp	Leu	Tyr	Glu	Ala	Met	Ala	Lys	Ala	Trp	Glu	Pro
			740					745					750		

Trp Leu Pro Ala Glu Ala Leu Arg Thr Leu Arg Ile Gly Gly Phe Tyr
755 760 765

Ala Leu Ser Pro Tyr Pro Gly Leu Arg Leu Ile Ser Leu Asn Met Asn
770 775 780

Phe Cys Ser Arg Glu Asn Phe Trp Leu Leu Ile Asn Ser Thr Asp Pro
785 790 795 800

Ala Gly Gln Leu Gln Trp Leu Val Gly Glu Leu Gln Ala Ala Glu Asp
805 810 815

Arg Gly Asp Lys Val His Ile Ile Gly His Ile Pro Pro Gly His Cys
820 825 830

Leu Lys Ser Trp Ser Trp Asn Tyr Tyr Arg Ile Val Ala Arg Tyr Glu
835 840 845

Asn Thr Leu Ala Ala Gln Phe Phe Gly His Thr His Val Asp Glu Phe
850 855 860

Glu Val Phe Tyr Asp Glu Glu Thr Leu Ser Arg Pro Leu Ala Val Ala
865 870 875 880

Phe Leu Ala Pro Ser Ala Thr Thr Tyr Ile Gly Leu Asn Pro Gly Tyr
885 890 895

Arg Val Tyr Gln Ile Asp Gly Asn Tyr Ser Gly Ser Ser His Val Val
900 905 910

Leu Asp His Glu Thr Tyr Ile Leu Asn Leu Thr Gln Ala Asn Ile Pro
915 920 925

Gly Ala Ile Pro His Trp Gln Leu Leu Tyr Arg Ala Arg Glu Thr Tyr
930 935 940

Gly Leu Pro Asn Thr Leu Pro Thr Ala Trp His Asn Leu Val Tyr Arg
 945 950 955 960

Met Arg Gly Asp Met Gln Leu Phe Gln Thr Phe Trp Phe Leu Tyr His
 965 970 975

Lys Gly His Pro Pro Ser Glu Pro Cys Gly Thr Pro Cys Arg Leu Ala
 980 985 990

Thr Leu Cys Ala Gln Leu Ser Ala Arg Ala Asp Ser Pro Ala Leu Cys
 995 1000 1005

Arg His Leu Met Pro Asp Gly Ser Leu Pro Glu Ala Gln Ser Leu
 1010 1015 1020

Trp Pro Arg Pro Leu Phe Cys
 1025 1030

<210> 107

<211> 1053

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hASM, IgG4
 HC-GS5-ASM

<400> 107

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

245

250

255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Leu Ser Asp Ser Arg Val Leu Trp Ala Pro
465 470 475 480

Ala Glu Ala His Pro Leu Ser Pro Gln Gly His Pro Ala Arg Leu His
485 490 495

Arg Ile Val Pro Arg Leu Arg Asp Val Phe Gly Trp Gly Asn Leu Thr
500 505 510

Cys Pro Ile Cys Lys Gly Leu Phe Thr Ala Ile Asn Leu Gly Leu Lys
515 520 525

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

Asn Leu Leu Lys Ile Ala Pro Pro Ala Val Cys Gln Ser Ile Val His
545 550 555 560

Leu Phe Glu Asp Asp Met Val Glu Val Trp Arg Arg Ser Val Leu Ser
565 570 575

Pro Ser Glu Ala Cys Gly Leu Leu Leu Gly Ser Thr Cys Gly His Trp
580 585 590

Asp Ile Phe Ser Ser Trp Asn Ile Ser Leu Pro Thr Val Pro Lys Pro
595 600 605

Pro Pro Lys Pro Pro Ser Pro Pro Ala Pro Gly Ala Pro Val Ser Arg
610 615 620

Ile Leu Phe Leu Thr Asp Leu His Trp Asp His Asp Tyr Leu Glu Gly
625 630 635 640

Thr Asp Pro Asp Cys Ala Asp Pro Leu Cys Cys Arg Arg Gly Ser Gly
645 650 655

Leu Pro Pro Ala Ser Arg Pro Gly Ala Gly Tyr Trp Gly Glu Tyr Ser
660 665 670

Lys Cys Asp Leu Pro Leu Arg Thr Leu Glu Ser Leu Leu Ser Gly Leu
675 680 685

Gly Pro Ala Gly Pro Phe Asp Met Val Tyr Trp Thr Gly Asp Ile Pro
690 695 700

Ala His Asp Val Trp His Gln Thr Arg Gln Asp Gln Leu Arg Ala Leu
705 710 715 720

Thr Thr Val Thr Ala Leu Val Arg Lys Phe Leu Gly Pro Val Pro Val
725 730 735

Tyr Pro Ala Val Gly Asn His Glu Ser Thr Pro Val Asn Ser Phe Pro
740 745 750

Pro Pro Phe Ile Glu Gly Asn His Ser Ser Arg Trp Leu Tyr Glu Ala
755 760 765

Met Ala Lys Ala Trp Glu Pro Trp Leu Pro Ala Glu Ala Leu Arg Thr
770 775 780

Leu Arg Ile Gly Gly Phe Tyr Ala Leu Ser Pro Tyr Pro Gly Leu Arg
785 790 795 800

Leu Ile Ser Leu Asn Met Asn Phe Cys Ser Arg Glu Asn Phe Trp Leu
805 810 815

Leu Ile Asn Ser Thr Asp Pro Ala Gly Gln Leu Gln Trp Leu Val Gly
820 825 830

Glu Leu Gln Ala Ala Glu Asp Arg Gly Asp Lys Val His Ile Ile Gly
835 840 845

His Ile Pro Pro Gly His Cys Leu Lys Ser Trp Ser Trp Asn Tyr Tyr
850 855 860

Arg Ile Val Ala Arg Tyr Glu Asn Thr Leu Ala Ala Gln Phe Phe Gly
865 870 875 880

His Thr His Val Asp Glu Phe Glu Val Phe Tyr Asp Glu Glu Thr Leu
885 890 895

Ser Arg Pro Leu Ala Val Ala Phe Leu Ala Pro Ser Ala Thr Thr Tyr
900 905 910

Ile Gly Leu Asn Pro Gly Tyr Arg Val Tyr Gln Ile Asp Gly Asn Tyr
915 920 925

Ser Gly Ser Ser His Val Val Leu Asp His Glu Thr Tyr Ile Leu Asn
930 935 940

Leu Thr Gln Ala Asn Ile Pro Gly Ala Ile Pro His Trp Gln Leu Leu
945 950 955 960

Tyr Arg Ala Arg Glu Thr Tyr Gly Leu Pro Asn Thr Leu Pro Thr Ala
965 970 975

Trp His Asn Leu Val Tyr Arg Met Arg Gly Asp Met Gln Leu Phe Gln
980 985 990

Thr Phe Trp Phe Leu Tyr His Lys Gly His Pro Pro Ser Glu Pro Cys
995 1000 1005

Gly Thr Pro Cys Arg Leu Ala Thr Leu Cys Ala Gln Leu Ser Ala
1010 1015 1020

Arg Ala Asp Ser Pro Ala Leu Cys Arg His Leu Met Pro Asp Gly

1025

1030

1035

Ser Leu Pro Glu Ala Gln Ser Leu Trp Pro Arg Pro Leu Phe Cys
 1040 1045 1050

<210> 108

<211> 1078

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hASM, IgG4
 HC-GS10-ASM

<400> 108

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu
485 490 495

Ser Asp Ser Arg Val Leu Trp Ala Pro Ala Glu Ala His Pro Leu Ser
500 505 510

Pro Gln Gly His Pro Ala Arg Leu His Arg Ile Val Pro Arg Leu Arg
515 520 525

Asp Val Phe Gly Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys Gly Leu
530 535 540

Phe Thr Ala Ile Asn Leu Gly Leu Lys Lys Glu Pro Asn Val Ala Arg
545 550 555 560

Val Gly Ser Val Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile Ala Pro
565 570 575

Pro Ala Val Cys Gln Ser Ile Val His Leu Phe Glu Asp Asp Met Val
580 585 590

Glu Val Trp Arg Arg Ser Val Leu Ser Pro Ser Glu Ala Cys Gly Leu
595 600 605

Leu Leu Gly Ser Thr Cys Gly His Trp Asp Ile Phe Ser Ser Trp Asn
610 615 620

Ile Ser Leu Pro Thr Val Pro Lys Pro Pro Pro Lys Pro Pro Ser Pro
625 630 635 640

Pro Ala Pro Gly Ala Pro Val Ser Arg Ile Leu Phe Leu Thr Asp Leu
645 650 655

His Trp Asp His Asp Tyr Leu Glu Gly Thr Asp Pro Asp Cys Ala Asp
660 665 670

Pro Leu Cys Cys Arg Arg Gly Ser Gly Leu Pro Pro Ala Ser Arg Pro
675 680 685

Gly Ala Gly Tyr Trp Gly Glu Tyr Ser Lys Cys Asp Leu Pro Leu Arg
690 695 700

Thr Leu Glu Ser Leu Leu Ser Gly Leu Gly Pro Ala Gly Pro Phe Asp

705		710		715		720
Met Val Tyr Trp Thr Gly Asp Ile Pro Ala His Asp Val Trp His Gln						
		725		730		735
Thr Arg Gln Asp Gln Leu Arg Ala Leu Thr Thr Val Thr Ala Leu Val						
		740		745		750
Arg Lys Phe Leu Gly Pro Val Pro Val Tyr Pro Ala Val Gly Asn His						
		755		760		765
Glu Ser Thr Pro Val Asn Ser Phe Pro Pro Pro Phe Ile Glu Gly Asn						
		770		775		780
His Ser Ser Arg Trp Leu Tyr Glu Ala Met Ala Lys Ala Trp Glu Pro						
		785		790		795
						800
Trp Leu Pro Ala Glu Ala Leu Arg Thr Leu Arg Ile Gly Gly Phe Tyr						
		805		810		815
Ala Leu Ser Pro Tyr Pro Gly Leu Arg Leu Ile Ser Leu Asn Met Asn						
		820		825		830
Phe Cys Ser Arg Glu Asn Phe Trp Leu Leu Ile Asn Ser Thr Asp Pro						
		835		840		845
Ala Gly Gln Leu Gln Trp Leu Val Gly Glu Leu Gln Ala Ala Glu Asp						
		850		855		860
Arg Gly Asp Lys Val His Ile Ile Gly His Ile Pro Pro Gly His Cys						
		865		870		875
						880
Leu Lys Ser Trp Ser Trp Asn Tyr Tyr Arg Ile Val Ala Arg Tyr Glu						
		885		890		895
Asn Thr Leu Ala Ala Gln Phe Phe Gly His Thr His Val Asp Glu Phe						
		900		905		910

Glu Val Phe Tyr Asp Glu Glu Thr Leu Ser Arg Pro Leu Ala Val Ala
915 920 925

Phe Leu Ala Pro Ser Ala Thr Thr Tyr Ile Gly Leu Asn Pro Gly Tyr
930 935 940

Arg Val Tyr Gln Ile Asp Gly Asn Tyr Ser Gly Ser Ser His Val Val
945 950 955 960

Leu Asp His Glu Thr Tyr Ile Leu Asn Leu Thr Gln Ala Asn Ile Pro
965 970 975

Gly Ala Ile Pro His Trp Gln Leu Leu Tyr Arg Ala Arg Glu Thr Tyr
980 985 990

Gly Leu Pro Asn Thr Leu Pro Thr Ala Trp His Asn Leu Val Tyr Arg
995 1000 1005

Met Arg Gly Asp Met Gln Leu Phe Gln Thr Phe Trp Phe Leu Tyr
1010 1015 1020

His Lys Gly His Pro Pro Ser Glu Pro Cys Gly Thr Pro Cys Arg
1025 1030 1035

Leu Ala Thr Leu Cys Ala Gln Leu Ser Ala Arg Ala Asp Ser Pro
1040 1045 1050

Ala Leu Cys Arg His Leu Met Pro Asp Gly Ser Leu Pro Glu Ala
1055 1060 1065

Gln Ser Leu Trp Pro Arg Pro Leu Phe Cys
1070 1075

<210> 109
<211> 1128
<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hASM, IgG4 HC-GS20-ASM

<400> 109

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

355

360

365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 530 535 540

Ser Leu Ser Asp Ser Arg Val Leu Trp Ala Pro Ala Glu Ala His Pro
 545 550 555 560

Leu Ser Pro Gln Gly His Pro Ala Arg Leu His Arg Ile Val Pro Arg
565 570 575

Leu Arg Asp Val Phe Gly Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys
580 585 590

Gly Leu Phe Thr Ala Ile Asn Leu Gly Leu Lys Lys Glu Pro Asn Val
595 600 605

Ala Arg Val Gly Ser Val Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile
610 615 620

Ala Pro Pro Ala Val Cys Gln Ser Ile Val His Leu Phe Glu Asp Asp
625 630 635 640

Met Val Glu Val Trp Arg Arg Ser Val Leu Ser Pro Ser Glu Ala Cys
645 650 655

Gly Leu Leu Leu Gly Ser Thr Cys Gly His Trp Asp Ile Phe Ser Ser
660 665 670

Trp Asn Ile Ser Leu Pro Thr Val Pro Lys Pro Pro Pro Lys Pro Pro
675 680 685

Ser Pro Pro Ala Pro Gly Ala Pro Val Ser Arg Ile Leu Phe Leu Thr
690 695 700

Asp Leu His Trp Asp His Asp Tyr Leu Glu Gly Thr Asp Pro Asp Cys
705 710 715 720

Ala Asp Pro Leu Cys Cys Arg Arg Gly Ser Gly Leu Pro Pro Ala Ser
725 730 735

Arg Pro Gly Ala Gly Tyr Trp Gly Glu Tyr Ser Lys Cys Asp Leu Pro
740 745 750

Leu Arg Thr Leu Glu Ser Leu Leu Ser Gly Leu Gly Pro Ala Gly Pro
755 760 765

Phe Asp Met Val Tyr Trp Thr Gly Asp Ile Pro Ala His Asp Val Trp
770 775 780

His Gln Thr Arg Gln Asp Gln Leu Arg Ala Leu Thr Thr Val Thr Ala
785 790 795 800

Leu Val Arg Lys Phe Leu Gly Pro Val Pro Val Tyr Pro Ala Val Gly
805 810 815

Asn His Glu Ser Thr Pro Val Asn Ser Phe Pro Pro Pro Phe Ile Glu
820 825 830

Gly Asn His Ser Ser Arg Trp Leu Tyr Glu Ala Met Ala Lys Ala Trp
835 840 845

Glu Pro Trp Leu Pro Ala Glu Ala Leu Arg Thr Leu Arg Ile Gly Gly
850 855 860

Phe Tyr Ala Leu Ser Pro Tyr Pro Gly Leu Arg Leu Ile Ser Leu Asn
865 870 875 880

Met Asn Phe Cys Ser Arg Glu Asn Phe Trp Leu Leu Ile Asn Ser Thr
885 890 895

Asp Pro Ala Gly Gln Leu Gln Trp Leu Val Gly Glu Leu Gln Ala Ala
900 905 910

Glu Asp Arg Gly Asp Lys Val His Ile Ile Gly His Ile Pro Pro Gly
915 920 925

His Cys Leu Lys Ser Trp Ser Trp Asn Tyr Tyr Arg Ile Val Ala Arg
930 935 940

Tyr Glu Asn Thr Leu Ala Ala Gln Phe Phe Gly His Thr His Val Asp
945 950 955 960

Glu Phe Glu Val Phe Tyr Asp Glu Glu Thr Leu Ser Arg Pro Leu Ala
965 970 975

Val Ala Phe Leu Ala Pro Ser Ala Thr Thr Tyr Ile Gly Leu Asn Pro
980 985 990

Gly Tyr Arg Val Tyr Gln Ile Asp Gly Asn Tyr Ser Gly Ser Ser His
995 1000 1005

Val Val Leu Asp His Glu Thr Tyr Ile Leu Asn Leu Thr Gln Ala
1010 1015 1020

Asn Ile Pro Gly Ala Ile Pro His Trp Gln Leu Leu Tyr Arg Ala
1025 1030 1035

Arg Glu Thr Tyr Gly Leu Pro Asn Thr Leu Pro Thr Ala Trp His
1040 1045 1050

Asn Leu Val Tyr Arg Met Arg Gly Asp Met Gln Leu Phe Gln Thr
1055 1060 1065

Phe Trp Phe Leu Tyr His Lys Gly His Pro Pro Ser Glu Pro Cys
1070 1075 1080

Gly Thr Pro Cys Arg Leu Ala Thr Leu Cys Ala Gln Leu Ser Ala
1085 1090 1095

Arg Ala Asp Ser Pro Ala Leu Cys Arg His Leu Met Pro Asp Gly
1100 1105 1110

Ser Leu Pro Glu Ala Gln Ser Leu Trp Pro Arg Pro Leu Phe Cys
1115 1120 1125

<210> 110

<211> 824
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of humanized anti-hTfR antibody No. 3N and hASM, Fab HC-GS3-ASM

<400> 110

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Leu Ser Asp Ser Arg Val Leu Trp Ala Pro Ala Glu Ala His Pro
245 250 255

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

Leu Arg Asp Val Phe Gly Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys
275 280 285

Gly Leu Phe Thr Ala Ile Asn Leu Gly Leu Lys Lys Glu Pro Asn Val
290 295 300

Ala Arg Val Gly Ser Val Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile
305 310 315 320

Ala Pro Pro Ala Val Cys Gln Ser Ile Val His Leu Phe Glu Asp Asp
325 330 335

Met Val Glu Val Trp Arg Arg Ser Val Leu Ser Pro Ser Glu Ala Cys
340 345 350

Gly Leu Leu Leu Gly Ser Thr Cys Gly His Trp Asp Ile Phe Ser Ser
355 360 365

Trp Asn Ile Ser Leu Pro Thr Val Pro Lys Pro Pro Pro Lys Pro Pro
370 375 380

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

Asp Leu His Trp Asp His Asp Tyr Leu Glu Gly Thr Asp Pro Asp Cys
405 410 415

Ala Asp Pro Leu Cys Cys Arg Arg Gly Ser Gly Leu Pro Pro Ala Ser
420 425 430

Arg Pro Gly Ala Gly Tyr Trp Gly Glu Tyr Ser Lys Cys Asp Leu Pro
435 440 445

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

Phe Asp Met Val Tyr Trp Thr Gly Asp Ile Pro Ala His Asp Val Trp
465 470 475 480

His Gln Thr Arg Gln Asp Gln Leu Arg Ala Leu Thr Thr Val Thr Ala
485 490 495

Leu Val Arg Lys Phe Leu Gly Pro Val Pro Val Tyr Pro Ala Val Gly
500 505 510

Asn His Glu Ser Thr Pro Val Asn Ser Phe Pro Pro Pro Phe Ile Glu
515 520 525

Gly Asn His Ser Ser Arg Trp Leu Tyr Glu Ala Met Ala Lys Ala Trp
530 535 540

Glu Pro Trp Leu Pro Ala Glu Ala Leu Arg Thr Leu Arg Ile Gly Gly

545		550		555		560
Phe Tyr Ala Leu Ser Pro Tyr Pro Gly Leu Arg Leu Ile Ser Leu Asn						
		565		570		575
Met Asn Phe Cys Ser Arg Glu Asn Phe Trp Leu Leu Ile Asn Ser Thr						
		580		585		590
Asp Pro Ala Gly Gln Leu Gln Trp Leu Val Gly Glu Leu Gln Ala Ala						
		595		600		605
Glu Asp Arg Gly Asp Lys Val His Ile Ile Gly His Ile Pro Pro Gly						
		610		615		620
His Cys Leu Lys Ser Trp Ser Trp Asn Tyr Tyr Arg Ile Val Ala Arg						
		625		630		635
						640
Tyr Glu Asn Thr Leu Ala Ala Gln Phe Phe Gly His Thr His Val Asp						
		645		650		655
Glu Phe Glu Val Phe Tyr Asp Glu Glu Thr Leu Ser Arg Pro Leu Ala						
		660		665		670
Val Ala Phe Leu Ala Pro Ser Ala Thr Thr Tyr Ile Gly Leu Asn Pro						
		675		680		685
Gly Tyr Arg Val Tyr Gln Ile Asp Gly Asn Tyr Ser Gly Ser Ser His						
		690		695		700
Val Val Leu Asp His Glu Thr Tyr Ile Leu Asn Leu Thr Gln Ala Asn						
		705		710		715
						720
Ile Pro Gly Ala Ile Pro His Trp Gln Leu Leu Tyr Arg Ala Arg Glu						
		725		730		735
Thr Tyr Gly Leu Pro Asn Thr Leu Pro Thr Ala Trp His Asn Leu Val						
		740		745		750

Tyr Arg Met Arg Gly Asp Met Gln Leu Phe Gln Thr Phe Trp Phe Leu
755 760 765

Tyr His Lys Gly His Pro Pro Ser Glu Pro Cys Gly Thr Pro Cys Arg
770 775 780

Leu Ala Thr Leu Cys Ala Gln Leu Ser Ala Arg Ala Asp Ser Pro Ala
785 790 795 800

Leu Cys Arg His Leu Met Pro Asp Gly Ser Leu Pro Glu Ala Gln Ser
805 810 815

Leu Trp Pro Arg Pro Leu Phe Cys
820

<210> 111

<211> 834

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hASM, Fab HC-GS5-ASM

<400> 111

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Ser Asp Ser Arg
245 250 255

Val Leu Trp Ala Pro Ala Glu Ala His Pro Leu Ser Pro Gln Gly His

260

265

270

Pro Ala Arg Leu His Arg Ile Val Pro Arg Leu Arg Asp Val Phe Gly
 275 280 285

Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys Gly Leu Phe Thr Ala Ile
 290 295 300

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

Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile Ala Pro Pro Ala Val Cys
 325 330 335

Gln Ser Ile Val His Leu Phe Glu Asp Asp Met Val Glu Val Trp Arg
 340 345 350

Arg Ser Val Leu Ser Pro Ser Glu Ala Cys Gly Leu Leu Leu Gly Ser
 355 360 365

Thr Cys Gly His Trp Asp Ile Phe Ser Ser Trp Asn Ile Ser Leu Pro
 370 375 380

Thr Val Pro Lys Pro Pro Pro Lys Pro Pro Ser Pro Pro Ala Pro Gly
 385 390 395 400

Ala Pro Val Ser Arg Ile Leu Phe Leu Thr Asp Leu His Trp Asp His
 405 410 415

Asp Tyr Leu Glu Gly Thr Asp Pro Asp Cys Ala Asp Pro Leu Cys Cys
 420 425 430

Arg Arg Gly Ser Gly Leu Pro Pro Ala Ser Arg Pro Gly Ala Gly Tyr
 435 440 445

Trp Gly Glu Tyr Ser Lys Cys Asp Leu Pro Leu Arg Thr Leu Glu Ser
 450 455 460

Leu Leu Ser Gly Leu Gly Pro Ala Gly Pro Phe Asp Met Val Tyr Trp
465 470 475 480

Thr Gly Asp Ile Pro Ala His Asp Val Trp His Gln Thr Arg Gln Asp
485 490 495

Gln Leu Arg Ala Leu Thr Thr Val Thr Ala Leu Val Arg Lys Phe Leu
500 505 510

Gly Pro Val Pro Val Tyr Pro Ala Val Gly Asn His Glu Ser Thr Pro
515 520 525

Val Asn Ser Phe Pro Pro Pro Phe Ile Glu Gly Asn His Ser Ser Arg
530 535 540

Trp Leu Tyr Glu Ala Met Ala Lys Ala Trp Glu Pro Trp Leu Pro Ala
545 550 555 560

Glu Ala Leu Arg Thr Leu Arg Ile Gly Gly Phe Tyr Ala Leu Ser Pro
565 570 575

Tyr Pro Gly Leu Arg Leu Ile Ser Leu Asn Met Asn Phe Cys Ser Arg
580 585 590

Glu Asn Phe Trp Leu Leu Ile Asn Ser Thr Asp Pro Ala Gly Gln Leu
595 600 605

Gln Trp Leu Val Gly Glu Leu Gln Ala Ala Glu Asp Arg Gly Asp Lys
610 615 620

Val His Ile Ile Gly His Ile Pro Pro Gly His Cys Leu Lys Ser Trp
625 630 635 640

Ser Trp Asn Tyr Tyr Arg Ile Val Ala Arg Tyr Glu Asn Thr Leu Ala
645 650 655

Ala Gln Phe Phe Gly His Thr His Val Asp Glu Phe Glu Val Phe Tyr
660 665 670

Asp Glu Glu Thr Leu Ser Arg Pro Leu Ala Val Ala Phe Leu Ala Pro
675 680 685

Ser Ala Thr Thr Tyr Ile Gly Leu Asn Pro Gly Tyr Arg Val Tyr Gln
690 695 700

Ile Asp Gly Asn Tyr Ser Gly Ser Ser His Val Val Leu Asp His Glu
705 710 715 720

Thr Tyr Ile Leu Asn Leu Thr Gln Ala Asn Ile Pro Gly Ala Ile Pro
725 730 735

His Trp Gln Leu Leu Tyr Arg Ala Arg Glu Thr Tyr Gly Leu Pro Asn
740 745 750

Thr Leu Pro Thr Ala Trp His Asn Leu Val Tyr Arg Met Arg Gly Asp
755 760 765

Met Gln Leu Phe Gln Thr Phe Trp Phe Leu Tyr His Lys Gly His Pro
770 775 780

Pro Ser Glu Pro Cys Gly Thr Pro Cys Arg Leu Ala Thr Leu Cys Ala
785 790 795 800

Gln Leu Ser Ala Arg Ala Asp Ser Pro Ala Leu Cys Arg His Leu Met
805 810 815

Pro Asp Gly Ser Leu Pro Glu Ala Gln Ser Leu Trp Pro Arg Pro Leu
820 825 830

Phe Cys

<210> 112
<211> 859
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hASM, Fab HC-GS10-ASM

<400> 112

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Leu Ser Asp Ser Arg Val Leu Trp Ala Pro Ala Glu
275 280 285

Ala His Pro Leu Ser Pro Gln Gly His Pro Ala Arg Leu His Arg Ile
290 295 300

Val Pro Arg Leu Arg Asp Val Phe Gly Trp Gly Asn Leu Thr Cys Pro
305 310 315 320

Ile Cys Lys Gly Leu Phe Thr Ala Ile Asn Leu Gly Leu Lys Lys Glu
325 330 335

Pro Asn Val Ala Arg Val Gly Ser Val Ala Ile Lys Leu Cys Asn Leu
340 345 350

Leu Lys Ile Ala Pro Pro Ala Val Cys Gln Ser Ile Val His Leu Phe
355 360 365

Glu Asp Asp Met Val Glu Val Trp Arg Arg Ser Val Leu Ser Pro Ser
370 375 380

Glu Ala Cys Gly Leu Leu Leu Gly Ser Thr Cys Gly His Trp Asp Ile
385 390 395 400

Phe Ser Ser Trp Asn Ile Ser Leu Pro Thr Val Pro Lys Pro Pro Pro
405 410 415

Lys Pro Pro Ser Pro Pro Ala Pro Gly Ala Pro Val Ser Arg Ile Leu
420 425 430

Phe Leu Thr Asp Leu His Trp Asp His Asp Tyr Leu Glu Gly Thr Asp
435 440 445

Pro Asp Cys Ala Asp Pro Leu Cys Cys Arg Arg Gly Ser Gly Leu Pro
450 455 460

Pro Ala Ser Arg Pro Gly Ala Gly Tyr Trp Gly Glu Tyr Ser Lys Cys
465 470 475 480

Asp Leu Pro Leu Arg Thr Leu Glu Ser Leu Leu Ser Gly Leu Gly Pro
485 490 495

Ala Gly Pro Phe Asp Met Val Tyr Trp Thr Gly Asp Ile Pro Ala His
500 505 510

Asp Val Trp His Gln Thr Arg Gln Asp Gln Leu Arg Ala Leu Thr Thr
515 520 525

Val Thr Ala Leu Val Arg Lys Phe Leu Gly Pro Val Pro Val Tyr Pro
530 535 540

Ala Val Gly Asn His Glu Ser Thr Pro Val Asn Ser Phe Pro Pro Pro
545 550 555 560

Phe Ile Glu Gly Asn His Ser Ser Arg Trp Leu Tyr Glu Ala Met Ala
565 570 575

Lys Ala Trp Glu Pro Trp Leu Pro Ala Glu Ala Leu Arg Thr Leu Arg
580 585 590

Ile Gly Gly Phe Tyr Ala Leu Ser Pro Tyr Pro Gly Leu Arg Leu Ile
595 600 605

Ser Leu Asn Met Asn Phe Cys Ser Arg Glu Asn Phe Trp Leu Leu Ile
610 615 620

Asn Ser Thr Asp Pro Ala Gly Gln Leu Gln Trp Leu Val Gly Glu Leu
625 630 635 640

Gln Ala Ala Glu Asp Arg Gly Asp Lys Val His Ile Ile Gly His Ile
645 650 655

Pro Pro Gly His Cys Leu Lys Ser Trp Ser Trp Asn Tyr Tyr Arg Ile
660 665 670

Val Ala Arg Tyr Glu Asn Thr Leu Ala Ala Gln Phe Phe Gly His Thr
675 680 685

His Val Asp Glu Phe Glu Val Phe Tyr Asp Glu Glu Thr Leu Ser Arg
690 695 700

Pro Leu Ala Val Ala Phe Leu Ala Pro Ser Ala Thr Thr Tyr Ile Gly
705 710 715 720

Leu Asn Pro Gly Tyr Arg Val Tyr Gln Ile Asp Gly Asn Tyr Ser Gly
725 730 735

Ser Ser His Val Val Leu Asp His Glu Thr Tyr Ile Leu Asn Leu Thr

740

745

750

Gln Ala Asn Ile Pro Gly Ala Ile Pro His Trp Gln Leu Leu Tyr Arg
 755 760 765

Ala Arg Glu Thr Tyr Gly Leu Pro Asn Thr Leu Pro Thr Ala Trp His
 770 775 780

Asn Leu Val Tyr Arg Met Arg Gly Asp Met Gln Leu Phe Gln Thr Phe
 785 790 795 800

Trp Phe Leu Tyr His Lys Gly His Pro Pro Ser Glu Pro Cys Gly Thr
 805 810 815

Pro Cys Arg Leu Ala Thr Leu Cys Ala Gln Leu Ser Ala Arg Ala Asp
 820 825 830

Ser Pro Ala Leu Cys Arg His Leu Met Pro Asp Gly Ser Leu Pro Glu
 835 840 845

Ala Gln Ser Leu Trp Pro Arg Pro Leu Phe Cys
 850 855

<210> 113

<211> 909

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
 humanized anti-hTfR antibody No. 3N and hASM, Fab HC-GS20-ASM

<400> 113

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
290 295 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305 310 315 320

Ser Gly Gly Gly Gly Ser Leu Ser Asp Ser Arg Val Leu Trp Ala Pro
325 330 335

Ala Glu Ala His Pro Leu Ser Pro Gln Gly His Pro Ala Arg Leu His
340 345 350

Arg Ile Val Pro Arg Leu Arg Asp Val Phe Gly Trp Gly Asn Leu Thr
355 360 365

Cys Pro Ile Cys Lys Gly Leu Phe Thr Ala Ile Asn Leu Gly Leu Lys
370 375 380

Lys Glu Pro Asn Val Ala Arg Val Gly Ser Val Ala Ile Lys Leu Cys
385 390 395 400

Asn Leu Leu Lys Ile Ala Pro Pro Ala Val Cys Gln Ser Ile Val His
405 410 415

Leu Phe Glu Asp Asp Met Val Glu Val Trp Arg Arg Ser Val Leu Ser

420	425	430
Pro Ser Glu Ala Cys Gly Leu Leu Leu Gly Ser Thr Cys Gly His Trp		
435	440	445
Asp Ile Phe Ser Ser Trp Asn Ile Ser Leu Pro Thr Val Pro Lys Pro		
450	455	460
Pro Pro Lys Pro Pro Ser Pro Pro Ala Pro Gly Ala Pro Val Ser Arg		
465	470	475
Ile Leu Phe Leu Thr Asp Leu His Trp Asp His Asp Tyr Leu Glu Gly		
485	490	495
Thr Asp Pro Asp Cys Ala Asp Pro Leu Cys Cys Arg Arg Gly Ser Gly		
500	505	510
Leu Pro Pro Ala Ser Arg Pro Gly Ala Gly Tyr Trp Gly Glu Tyr Ser		
515	520	525
Lys Cys Asp Leu Pro Leu Arg Thr Leu Glu Ser Leu Leu Ser Gly Leu		
530	535	540
Gly Pro Ala Gly Pro Phe Asp Met Val Tyr Trp Thr Gly Asp Ile Pro		
545	550	555
Ala His Asp Val Trp His Gln Thr Arg Gln Asp Gln Leu Arg Ala Leu		
565	570	575
Thr Thr Val Thr Ala Leu Val Arg Lys Phe Leu Gly Pro Val Pro Val		
580	585	590
Tyr Pro Ala Val Gly Asn His Glu Ser Thr Pro Val Asn Ser Phe Pro		
595	600	605
Pro Pro Phe Ile Glu Gly Asn His Ser Ser Arg Trp Leu Tyr Glu Ala		
610	615	620

Met Ala Lys Ala Trp Glu Pro Trp Leu Pro Ala Glu Ala Leu Arg Thr
625 630 635 640

Leu Arg Ile Gly Gly Phe Tyr Ala Leu Ser Pro Tyr Pro Gly Leu Arg
645 650 655

Leu Ile Ser Leu Asn Met Asn Phe Cys Ser Arg Glu Asn Phe Trp Leu
660 665 670

Leu Ile Asn Ser Thr Asp Pro Ala Gly Gln Leu Gln Trp Leu Val Gly
675 680 685

Glu Leu Gln Ala Ala Glu Asp Arg Gly Asp Lys Val His Ile Ile Gly
690 695 700

His Ile Pro Pro Gly His Cys Leu Lys Ser Trp Ser Trp Asn Tyr Tyr
705 710 715 720

Arg Ile Val Ala Arg Tyr Glu Asn Thr Leu Ala Ala Gln Phe Phe Gly
725 730 735

His Thr His Val Asp Glu Phe Glu Val Phe Tyr Asp Glu Glu Thr Leu
740 745 750

Ser Arg Pro Leu Ala Val Ala Phe Leu Ala Pro Ser Ala Thr Thr Tyr
755 760 765

Ile Gly Leu Asn Pro Gly Tyr Arg Val Tyr Gln Ile Asp Gly Asn Tyr
770 775 780

Ser Gly Ser Ser His Val Val Leu Asp His Glu Thr Tyr Ile Leu Asn
785 790 795 800

Leu Thr Gln Ala Asn Ile Pro Gly Ala Ile Pro His Trp Gln Leu Leu
805 810 815

Tyr Arg Ala Arg Glu Thr Tyr Gly Leu Pro Asn Thr Leu Pro Thr Ala
820 825 830

Trp His Asn Leu Val Tyr Arg Met Arg Gly Asp Met Gln Leu Phe Gln
835 840 845

Thr Phe Trp Phe Leu Tyr His Lys Gly His Pro Pro Ser Glu Pro Cys
850 855 860

Gly Thr Pro Cys Arg Leu Ala Thr Leu Cys Ala Gln Leu Ser Ala Arg
865 870 875 880

Ala Asp Ser Pro Ala Leu Cys Arg His Leu Met Pro Asp Gly Ser Leu
885 890 895

Pro Glu Ala Gln Ser Leu Trp Pro Arg Pro Leu Phe Cys
900 905

<210> 114

<211> 1095

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hASM, Tandem Fab HC-ASM

<400> 114

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe

50

55

60

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
260 265 270

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
275 280 285

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
290 295 300

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

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
325 330 335

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
340 345 350

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
370 375 380

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
385 390 395 400

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
405 410 415

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
420 425 430

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
435 440 445

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
450 455 460

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
465 470 475 480

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
485 490 495

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
500 505 510

Leu Ser Asp Ser Arg Val Leu Trp Ala Pro Ala Glu Ala His Pro Leu
515 520 525

Ser Pro Gln Gly His Pro Ala Arg Leu His Arg Ile Val Pro Arg Leu
530 535 540

Arg Asp Val Phe Gly Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys Gly
545 550 555 560

Leu Phe Thr Ala Ile Asn Leu Gly Leu Lys Lys Glu Pro Asn Val Ala
565 570 575

Arg Val Gly Ser Val Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile Ala
580 585 590

Pro Pro Ala Val Cys Gln Ser Ile Val His Leu Phe Glu Asp Asp Met
595 600 605

Val Glu Val Trp Arg Arg Ser Val Leu Ser Pro Ser Glu Ala Cys Gly
610 615 620

Leu Leu Leu Gly Ser Thr Cys Gly His Trp Asp Ile Phe Ser Ser Trp
625 630 635 640

Asn Ile Ser Leu Pro Thr Val Pro Lys Pro Pro Pro Lys Pro Pro Ser
645 650 655

Pro Pro Ala Pro Gly Ala Pro Val Ser Arg Ile Leu Phe Leu Thr Asp
660 665 670

Leu His Trp Asp His Asp Tyr Leu Glu Gly Thr Asp Pro Asp Cys Ala
675 680 685

Asp Pro Leu Cys Cys Arg Arg Gly Ser Gly Leu Pro Pro Ala Ser Arg
690 695 700

Pro Gly Ala Gly Tyr Trp Gly Glu Tyr Ser Lys Cys Asp Leu Pro Leu
705 710 715 720

Arg Thr Leu Glu Ser Leu Leu Ser Gly Leu Gly Pro Ala Gly Pro Phe
725 730 735

Asp Met Val Tyr Trp Thr Gly Asp Ile Pro Ala His Asp Val Trp His
740 745 750

Gln Thr Arg Gln Asp Gln Leu Arg Ala Leu Thr Thr Val Thr Ala Leu
755 760 765

Val Arg Lys Phe Leu Gly Pro Val Pro Val Tyr Pro Ala Val Gly Asn
770 775 780

His Glu Ser Thr Pro Val Asn Ser Phe Pro Pro Pro Phe Ile Glu Gly
785 790 795 800

Asn His Ser Ser Arg Trp Leu Tyr Glu Ala Met Ala Lys Ala Trp Glu
805 810 815

Pro Trp Leu Pro Ala Glu Ala Leu Arg Thr Leu Arg Ile Gly Gly Phe
820 825 830

Tyr Ala Leu Ser Pro Tyr Pro Gly Leu Arg Leu Ile Ser Leu Asn Met

835

840

845

Asn Phe Cys Ser Arg Glu Asn Phe Trp Leu Leu Ile Asn Ser Thr Asp
 850 855 860

Pro Ala Gly Gln Leu Gln Trp Leu Val Gly Glu Leu Gln Ala Ala Glu
 865 870 875 880

Asp Arg Gly Asp Lys Val His Ile Ile Gly His Ile Pro Pro Gly His
 885 890 895

Cys Leu Lys Ser Trp Ser Trp Asn Tyr Tyr Arg Ile Val Ala Arg Tyr
 900 905 910

Glu Asn Thr Leu Ala Ala Gln Phe Phe Gly His Thr His Val Asp Glu
 915 920 925

Phe Glu Val Phe Tyr Asp Glu Glu Thr Leu Ser Arg Pro Leu Ala Val
 930 935 940

Ala Phe Leu Ala Pro Ser Ala Thr Thr Tyr Ile Gly Leu Asn Pro Gly
 945 950 955 960

Tyr Arg Val Tyr Gln Ile Asp Gly Asn Tyr Ser Gly Ser Ser His Val
 965 970 975

Val Leu Asp His Glu Thr Tyr Ile Leu Asn Leu Thr Gln Ala Asn Ile
 980 985 990

Pro Gly Ala Ile Pro His Trp Gln Leu Leu Tyr Arg Ala Arg Glu Thr
 995 1000 1005

Tyr Gly Leu Pro Asn Thr Leu Pro Thr Ala Trp His Asn Leu Val
 1010 1015 1020

Tyr Arg Met Arg Gly Asp Met Gln Leu Phe Gln Thr Phe Trp Phe
 1025 1030 1035

Leu Tyr His Lys Gly His Pro Pro Ser Glu Pro Cys Gly Thr Pro
1040 1045 1050

Cys Arg Leu Ala Thr Leu Cys Ala Gln Leu Ser Ala Arg Ala Asp
1055 1060 1065

Ser Pro Ala Leu Cys Arg His Leu Met Pro Asp Gly Ser Leu Pro
1070 1075 1080

Glu Ala Gln Ser Leu Trp Pro Arg Pro Leu Phe Cys
1085 1090 1095

<210> 115

<211> 936

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hARSA, IgG4 IgG4
HC-ARSA

<400> 115

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Arg
435 440 445

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

Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr Pro Asn Leu Asp Gln

465 470 475 480

Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe Tyr Val Pro Val Ser
485 490 495

Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu Pro Val
500 505 510

Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser Arg Gly Gly
515 520 525

Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala Ala Arg Gly
530 535 540

Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu Gly Val Gly Pro Glu
545 550 555 560

Gly Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe Leu Gly Ile
565 570 575

Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn Leu Thr Cys Phe Pro
580 585 590

Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu Val Pro Ile
595 600 605

Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro Trp Leu Pro
610 615 620

Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu Met Ala Asp
625 630 635 640

Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala Ser His His
645 650 655

Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu Arg Ser Gly
660 665 670

Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala Ala Val Gly
675 680 685

Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu Glu Thr Leu
690 695 700

Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg Met Ser Arg
705 710 715 720

Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr Thr Tyr Glu
725 730 735

Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly His Ile Ala
740 745 750

Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu Leu Pro Thr
755 760 765

Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr Leu Asp Gly
770 775 780

Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser Pro Arg Gln
785 790 795 800

Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu Val Arg Gly Val Phe
805 810 815

Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr Gln Gly Ser
820 825 830

Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala Ser Ser Ser
835 840 845

Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser Lys Asp Pro
850 855 860

Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala Thr Pro Glu
 865 870 875 880

Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala Gln Leu Asp
 885 890 895

Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly Glu Asp Pro
 900 905 910

Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg Pro Ala Cys
 915 920 925

Cys His Cys Pro Asp Pro His Ala
 930 935

<210> 116
 <211> 959
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hARSA, IgG4
 HC-GS5-ARSA

<400> 116

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln

260

265

270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Arg Pro Pro Asn Ile Val Leu Ile Phe Ala
465 470 475 480

Asp Asp Leu Gly Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser
485 490 495

Thr Thr Pro Asn Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr
500 505 510

Asp Phe Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu
515 520 525

Leu Thr Gly Arg Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu
530 535 540

Val Pro Ser Ser Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala
545 550 555 560

Glu Val Leu Ala Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp
565 570 575

His Leu Gly Val Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly
580 585 590

Phe His Arg Phe Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys
595 600 605

Gln Asn Leu Thr Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys
610 615 620

Asp Gln Gly Leu Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu
625 630 635 640

Ala Gln Pro Pro Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe
645 650 655

Ala His Asp Leu Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe
660 665 670

Leu Tyr Tyr Ala Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln
675 680 685

Ser Phe Ala Glu Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met
690 695 700

Glu Leu Asp Ala Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu
705 710 715 720

Gly Leu Leu Glu Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro
725 730 735

Glu Thr Met Arg Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys
740 745 750

Gly Lys Gly Thr Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala
755 760 765

Phe Trp Pro Gly His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser
770 775 780

Ser Leu Asp Leu Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu
785 790 795 800

Pro Asn Val Thr Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly
805 810 815

Thr Gly Lys Ser Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro
820 825 830

Asp Glu Val Arg Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala
835 840 845

His Phe Phe Thr Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro
850 855 860

Ala Cys His Ala Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu
865 870 875 880

Tyr Asp Leu Ser Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly
885 890 895

Val Ala Gly Ala Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln
900 905 910

Leu Leu Lys Ala Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln
915 920 925

Val Ala Arg Gly Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly
930 935 940

Cys Thr Pro Arg Pro Ala Cys Cys His Cys Pro Asp Pro His Ala
945 950 955

<210> 117

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hARSA, IgG4
HC-GS10-ARSA

<400> 117

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met

35

40

45

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
485 490 495

Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp Leu Gly Tyr Gly Asp
500 505 510

Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr Pro Asn Leu Asp Gln
515 520 525

Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe Tyr Val Pro Val Ser
530 535 540

Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu Pro Val
545 550 555 560

Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser Arg Gly Gly
565 570 575

Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala Ala Arg Gly
580 585 590

Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu Gly Val Gly Pro Glu
595 600 605

Gly Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe Leu Gly Ile
610 615 620

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

Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu Val Pro Ile
645 650 655

Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro Trp Leu Pro
660 665 670

Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu Met Ala Asp
675 680 685

Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala Ser His His
690 695 700

Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu Arg Ser Gly
705 710 715 720

Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala Ala Val Gly
725 730 735

Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu Glu Thr Leu
740 745 750

Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg Met Ser Arg
755 760 765

Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr Thr Tyr Glu
770 775 780

Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly His Ile Ala
785 790 795 800

Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu Leu Pro Thr
805 810 815

Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr Leu Asp Gly

820

825

830

Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser Pro Arg Gln
 835 840 845

Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu Val Arg Gly Val Phe
 850 855 860

Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr Gln Gly Ser
 865 870 875 880

Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala Ser Ser Ser
 885 890 895

Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser Lys Asp Pro
 900 905 910

Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala Thr Pro Glu
 915 920 925

Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala Gln Leu Asp
 930 935 940

Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly Glu Asp Pro
 945 950 955 960

Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg Pro Ala Cys
 965 970 975

Cys His Cys Pro Asp Pro His Ala
 980

<210> 118

<211> 1034

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hARSA, IgG4 HC-GS20-ARSA

<400> 118

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp Leu Gly Tyr
545 550 555 560

Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr Pro Asn Leu

565

570

575

Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe Tyr Val Pro
 580 585 590

Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu
 595 600 605

Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser Arg
 610 615 620

Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala Ala
 625 630 635 640

Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu Gly Val Gly
 645 650 655

Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe Leu
 660 665 670

Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn Leu Thr Cys
 675 680 685

Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu Val
 690 695 700

Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro Trp
 705 710 715 720

Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu Met
 725 730 735

Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala Ser
 740 745 750

His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu Arg
 755 760 765

Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala Ala
770 775 780

Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu Glu
785 790 795 800

Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg Met
805 810 815

Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr Thr
820 825 830

Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly His
835 840 845

Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu Leu
850 855 860

Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr Leu
865 870 875 880

Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser Pro
885 890 895

Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu Val Arg Gly
900 905 910

Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr Gln
915 920 925

Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala Ser
930 935 940

Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser Lys
945 950 955 960

Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala Thr
965 970 975

Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala Gln
980 985 990

Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly Glu
995 1000 1005

Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg
1010 1015 1020

Pro Ala Cys Cys His Cys Pro Asp Pro His Ala
1025 1030

<210> 119
<211> 730
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hARSA, Fab HC-GS3-ARSA

<400> 119

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr

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

Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe Tyr Val Pro
275 280 285

Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu
290 295 300

Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser Arg
305 310 315 320

Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala Ala
325 330 335

Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu Gly Val Gly
340 345 350

Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe Leu
355 360 365

Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn Leu Thr Cys
370 375 380

Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu Val
385 390 395 400

Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro Trp
405 410 415

Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu Met
420 425 430

Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala Ser
435 440 445

His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu Arg
450 455 460

Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala Ala
465 470 475 480

Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu Glu
485 490 495

Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg Met
500 505 510

Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr Thr
515 520 525

Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly His
530 535 540

Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu Leu
545 550 555 560

Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr Leu
565 570 575

Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser Pro
580 585 590

Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu Val Arg Gly
595 600 605

Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr Gln
610 615 620

Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala Ser
625 630 635 640

Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser Lys
645 650 655

Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala Thr
660 665 670

Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala Gln
675 680 685

Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly Glu
690 695 700

Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg Pro
705 710 715 720

Ala Cys Cys His Cys Pro Asp Pro His Ala
725 730

<210> 120
<211> 740
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hARSA, Fab HC-GS5-ARSA

<400> 120

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Pro Pro Asn Ile
245 250 255

Val Leu Ile Phe Ala Asp Asp Leu Gly Tyr Gly Asp Leu Gly Cys Tyr
260 265 270

Gly His Pro Ser Ser Thr Thr Pro Asn Leu Asp Gln Leu Ala Ala Gly
275 280 285

Gly Leu Arg Phe Thr Asp Phe Tyr Val Pro Val Ser Leu Cys Thr Pro
290 295 300

Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu Pro Val Arg Met Gly Met
305 310 315 320

Tyr Pro Gly Val Leu Val Pro Ser Ser Arg Gly Gly Leu Pro Leu Glu
325 330 335

Glu Val Thr Val Ala Glu Val Leu Ala Ala Arg Gly Tyr Leu Thr Gly
340 345 350

Met Ala Gly Lys Trp His Leu Gly Val Gly Pro Glu Gly Ala Phe Leu
355 360 365

Pro Pro His Gln Gly Phe His Arg Phe Leu Gly Ile Pro Tyr Ser His
370 375 380

Asp Gln Gly Pro Cys Gln Asn Leu Thr Cys Phe Pro Pro Ala Thr Pro
385 390 395 400

Cys Asp Gly Gly Cys Asp Gln Gly Leu Val Pro Ile Pro Leu Leu Ala
405 410 415

Asn Leu Ser Val Glu Ala Gln Pro Pro Trp Leu Pro Gly Leu Glu Ala
420 425 430

Arg Tyr Met Ala Phe Ala His Asp Leu Met Ala Asp Ala Gln Arg Gln
435 440 445

Asp Arg Pro Phe Phe Leu Tyr Tyr Ala Ser His His Thr His Tyr Pro
450 455 460

Gln Phe Ser Gly Gln Ser Phe Ala Glu Arg Ser Gly Arg Gly Pro Phe
465 470 475 480

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

Ala Ile Gly Asp Leu Gly Leu Leu Glu Glu Thr Leu Val Ile Phe Thr
500 505 510

Ala Asp Asn Gly Pro Glu Thr Met Arg Met Ser Arg Gly Gly Cys Ser
515 520 525

Gly Leu Leu Arg Cys Gly Lys Gly Thr Thr Tyr Glu Gly Gly Val Arg
530 535 540

Glu Pro Ala Leu Ala Phe Trp Pro Gly His Ile Ala Pro Gly Val Thr
545 550 555 560

His Glu Leu Ala Ser Ser Leu Asp Leu Leu Pro Thr Leu Ala Ala Leu
565 570 575

Ala Gly Ala Pro Leu Pro Asn Val Thr Leu Asp Gly Phe Asp Leu Ser
580 585 590

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

Tyr Pro Ser Tyr Pro Asp Glu Val Arg Gly Val Phe Ala Val Arg Thr
610 615 620

Gly Lys Tyr Lys Ala His Phe Phe Thr Gln Gly Ser Ala His Ser Asp
625 630 635 640

Thr Thr Ala Asp Pro Ala Cys His Ala Ser Ser Ser Leu Thr Ala His
645 650 655

Glu Pro Pro Leu Leu Tyr Asp Leu Ser Lys Asp Pro Gly Glu Asn Tyr

660

665

670

Asn Leu Leu Gly Gly Val Ala Gly Ala Thr Pro Glu Val Leu Gln Ala
 675 680 685

Leu Lys Gln Leu Gln Leu Leu Lys Ala Gln Leu Asp Ala Ala Val Thr
 690 695 700

Phe Gly Pro Ser Gln Val Ala Arg Gly Glu Asp Pro Ala Leu Gln Ile
 705 710 715 720

Cys Cys His Pro Gly Cys Thr Pro Arg Pro Ala Cys Cys His Cys Pro
 725 730 735

Asp Pro His Ala
 740

<210> 121
 <211> 765
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of fusion protein of the Fab heavy chain of
 humanized anti-hTfR antibody No. 3N and hARSA, Fab HC-GS10-ARSA

<400> 121

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp
275 280 285

Leu Gly Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr
290 295 300

Pro Asn Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe
305 310 315 320

Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr
325 330 335

Gly Arg Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro
340 345 350

Ser Ser Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val
355 360 365

Leu Ala Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu
370 375 380

Gly Val Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His
385 390 395 400

Arg Phe Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn
405 410 415

Leu Thr Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln
420 425 430

Gly Leu Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln
435 440 445

Pro Pro Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His

450

455

460

Asp Leu Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr
 465 470 475 480

Tyr Ala Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe
 485 490 495

Ala Glu Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu
 500 505 510

Asp Ala Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu
 515 520 525

Leu Glu Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr
 530 535 540

Met Arg Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys
 545 550 555 560

Gly Thr Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp
 565 570 575

Pro Gly His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu
 580 585 590

Asp Leu Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn
 595 600 605

Val Thr Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly
 610 615 620

Lys Ser Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu
 625 630 635 640

Val Arg Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe
 645 650 655

Phe Thr Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys
660 665 670

His Ala Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp
675 680 685

Leu Ser Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala
690 695 700

Gly Ala Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu
705 710 715 720

Lys Ala Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala
725 730 735

Arg Gly Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr
740 745 750

Pro Arg Pro Ala Cys Cys His Cys Pro Asp Pro His Ala
755 760 765

<210> 122
<211> 815
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hARSA, Fab HC-GS20-ARSA

<400> 122

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

225		230		235		240
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser						
		245		250		255
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly						
		260		265		270
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly						
		275		280		285
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly						
		290		295		300
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly						
		305		310		315
						320
Ser Gly Gly Gly Gly Ser Arg Pro Pro Asn Ile Val Leu Ile Phe Ala						
		325		330		335
Asp Asp Leu Gly Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser						
		340		345		350
Thr Thr Pro Asn Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr						
		355		360		365
Asp Phe Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu						
		370		375		380
Leu Thr Gly Arg Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu						
		385		390		395
						400
Val Pro Ser Ser Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala						
		405		410		415
Glu Val Leu Ala Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp						
		420		425		430

His Leu Gly Val Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly
435 440 445

Phe His Arg Phe Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys
450 455 460

Gln Asn Leu Thr Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys
465 470 475 480

Asp Gln Gly Leu Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu
485 490 495

Ala Gln Pro Pro Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe
500 505 510

Ala His Asp Leu Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe
515 520 525

Leu Tyr Tyr Ala Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln
530 535 540

Ser Phe Ala Glu Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met
545 550 555 560

Glu Leu Asp Ala Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu
565 570 575

Gly Leu Leu Glu Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro
580 585 590

Glu Thr Met Arg Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys
595 600 605

Gly Lys Gly Thr Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala
610 615 620

Phe Trp Pro Gly His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser
625 630 635 640

Ser Leu Asp Leu Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu
645 650 655

Pro Asn Val Thr Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly
660 665 670

Thr Gly Lys Ser Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro
675 680 685

Asp Glu Val Arg Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala
690 695 700

His Phe Phe Thr Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro
705 710 715 720

Ala Cys His Ala Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu
725 730 735

Tyr Asp Leu Ser Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly
740 745 750

Val Ala Gly Ala Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln
755 760 765

Leu Leu Lys Ala Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln
770 775 780

Val Ala Arg Gly Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly
785 790 795 800

Cys Thr Pro Arg Pro Ala Cys Cys His Cys Pro Asp Pro His Ala
805 810 815

<210> 123
<211> 1001
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hARSA, Tandem Fab HC-ARSA

<400> 123

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
260 265 270

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
275 280 285

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
290 295 300

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

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
325 330 335

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
340 345 350

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
370 375 380

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
385 390 395 400

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
405 410 415

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
420 425 430

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
435 440 445

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
450 455 460

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
465 470 475 480

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
485 490 495

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
500 505 510

Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp Leu Gly Tyr Gly
515 520 525

Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr Pro Asn Leu Asp
530 535 540

Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe Tyr Val Pro Val
545 550 555 560

Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu Pro
565 570 575

Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser Arg Gly
580 585 590

Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala Ala Arg
595 600 605

Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu Gly Val Gly Pro
610 615 620

Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe Leu Gly
625 630 635 640

Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn Leu Thr Cys Phe
645 650 655

Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu Val Pro
660 665 670

Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro Trp Leu
675 680 685

Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu Met Ala
690 695 700

Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala Ser His
705 710 715 720

His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu Arg Ser
725 730 735

Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala Ala Val

740

745

750

Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu Glu Thr
 755 760 765

Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg Met Ser
 770 775 780

Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr Thr Tyr
 785 790 795 800

Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly His Ile
 805 810 815

Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu Leu Pro
 820 825 830

Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr Leu Asp
 835 840 845

Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser Pro Arg
 850 855 860

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

Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr Gln Gly
 885 890 895

Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala Ser Ser
 900 905 910

Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser Lys Asp
 915 920 925

Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala Thr Pro
 930 935 940

Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala Gln Leu
945 950 955 960

Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly Glu Asp
965 970 975

Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg Pro Ala
980 985 990

Cys Cys His Cys Pro Asp Pro His Ala
995 1000

<210> 124

<211> 929

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hSGSH IgG4, IgG4
HC-SGSH

<400> 124

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Arg
435 440 445

Pro Arg Asn Ala Leu Leu Leu Leu Ala Asp Asp Gly Gly Phe Glu Ser
450 455 460

Gly Ala Tyr Asn Asn Ser Ala Ile Ala Thr Pro His Leu Asp Ala Leu

465		470		475		480
Ala Arg Arg Ser	Leu Leu Phe Arg Asn	Ala Phe Thr Ser	Val Ser Ser			
	485	490	495			
Cys Ser Pro Ser	Arg Ala Ser Leu	Leu Thr Gly Leu	Pro Gln His Gln			
	500	505	510			
Asn Gly Met Tyr	Gly Leu His Gln	Asp Val His His	Phe Asn Ser Phe			
	515	520	525			
Asp Lys Val Arg	Ser Leu Pro Leu	Leu Leu Ser	Gln Ala Gly Val	Arg		
	530	535	540			
Thr Gly Ile Ile	Gly Lys Lys His	Val Gly Pro Glu	Thr Val Tyr Pro			
545	550	555	560			
Phe Asp Phe Ala	Tyr Thr Glu Glu	Asn Gly Ser Val	Leu Gln Val Gly			
	565	570	575			
Arg Asn Ile Thr	Arg Ile Lys Leu	Leu Val Arg Lys	Phe Leu Gln Thr			
	580	585	590			
Gln Asp Asp Arg	Pro Phe Phe Leu	Tyr Val Ala Phe	His Asp Pro His			
	595	600	605			
Arg Cys Gly His	Ser Gln Pro Gln	Tyr Gly Thr Phe	Cys Glu Lys Phe			
	610	615	620			
Gly Asn Gly Glu	Ser Gly Met Gly	Arg Ile Pro Asp	Trp Thr Pro Gln			
625	630	635	640			
Ala Tyr Asp Pro	Leu Asp Val Leu	Val Pro Tyr Phe	Val Pro Asn Thr			
	645	650	655			
Pro Ala Ala Arg	Ala Asp Leu Ala	Ala Gln Tyr Thr	Thr Val Gly Arg			
	660	665	670			

Met Asp Gln Gly Val Gly Leu Val Leu Gln Glu Leu Arg Asp Ala Gly
675 680 685

Val Leu Asn Asp Thr Leu Val Ile Phe Thr Ser Asp Asn Gly Ile Pro
690 695 700

Phe Pro Ser Gly Arg Thr Asn Leu Tyr Trp Pro Gly Thr Ala Glu Pro
705 710 715 720

Leu Leu Val Ser Ser Pro Glu His Pro Lys Arg Trp Gly Gln Val Ser
725 730 735

Glu Ala Tyr Val Ser Leu Leu Asp Leu Thr Pro Thr Ile Leu Asp Trp
740 745 750

Phe Ser Ile Pro Tyr Pro Ser Tyr Ala Ile Phe Gly Ser Lys Thr Ile
755 760 765

His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu Glu Ala Glu Pro Leu
770 775 780

Trp Ala Thr Val Phe Gly Ser Gln Ser His His Glu Val Thr Met Ser
785 790 795 800

Tyr Pro Met Arg Ser Val Gln His Arg His Phe Arg Leu Val His Asn
805 810 815

Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln Asp Phe Tyr Val Ser
820 825 830

Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr Ala Gly Gln Pro Thr
835 840 845

Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr Arg Ala Arg Trp Glu
850 855 860

Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr Gln Asn Leu Ala Thr
865 870 875 880

Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu Arg Asp Gln Leu Ala
885 890 895

Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val Cys Ala Pro Asp Gly
900 905 910

Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln Pro Leu His Asn Glu
915 920 925

Leu

<210> 125
<211> 952
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hSGSH IgG4, IgG4
HC-GS5-SGSH

<400> 125

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln

260

265

270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Arg Pro Arg Asn Ala Leu Leu Leu Leu Ala
 465 470 475 480

Asp Asp Gly Gly Phe Glu Ser Gly Ala Tyr Asn Asn Ser Ala Ile Ala
 485 490 495

Thr Pro His Leu Asp Ala Leu Ala Arg Arg Ser Leu Leu Phe Arg Asn
 500 505 510

Ala Phe Thr Ser Val Ser Ser Cys Ser Pro Ser Arg Ala Ser Leu Leu
 515 520 525

Thr Gly Leu Pro Gln His Gln Asn Gly Met Tyr Gly Leu His Gln Asp
 530 535 540

Val His His Phe Asn Ser Phe Asp Lys Val Arg Ser Leu Pro Leu Leu
 545 550 555 560

Leu Ser Gln Ala Gly Val Arg Thr Gly Ile Ile Gly Lys Lys His Val
 565 570 575

Gly Pro Glu Thr Val Tyr Pro Phe Asp Phe Ala Tyr Thr Glu Glu Asn
 580 585 590

Gly Ser Val Leu Gln Val Gly Arg Asn Ile Thr Arg Ile Lys Leu Leu
 595 600 605

Val Arg Lys Phe Leu Gln Thr Gln Asp Asp Arg Pro Phe Phe Leu Tyr
 610 615 620

Val Ala Phe His Asp Pro His Arg Cys Gly His Ser Gln Pro Gln Tyr
 625 630 635 640

Gly Thr Phe Cys Glu Lys Phe Gly Asn Gly Glu Ser Gly Met Gly Arg
 645 650 655

Ile Pro Asp Trp Thr Pro Gln Ala Tyr Asp Pro Leu Asp Val Leu Val
660 665 670

Pro Tyr Phe Val Pro Asn Thr Pro Ala Ala Arg Ala Asp Leu Ala Ala
675 680 685

Gln Tyr Thr Thr Val Gly Arg Met Asp Gln Gly Val Gly Leu Val Leu
690 695 700

Gln Glu Leu Arg Asp Ala Gly Val Leu Asn Asp Thr Leu Val Ile Phe
705 710 715 720

Thr Ser Asp Asn Gly Ile Pro Phe Pro Ser Gly Arg Thr Asn Leu Tyr
725 730 735

Trp Pro Gly Thr Ala Glu Pro Leu Leu Val Ser Ser Pro Glu His Pro
740 745 750

Lys Arg Trp Gly Gln Val Ser Glu Ala Tyr Val Ser Leu Leu Asp Leu
755 760 765

Thr Pro Thr Ile Leu Asp Trp Phe Ser Ile Pro Tyr Pro Ser Tyr Ala
770 775 780

Ile Phe Gly Ser Lys Thr Ile His Leu Thr Gly Arg Ser Leu Leu Pro
785 790 795 800

Ala Leu Glu Ala Glu Pro Leu Trp Ala Thr Val Phe Gly Ser Gln Ser
805 810 815

His His Glu Val Thr Met Ser Tyr Pro Met Arg Ser Val Gln His Arg
820 825 830

His Phe Arg Leu Val His Asn Leu Asn Phe Lys Met Pro Phe Pro Ile
835 840 845

Asp Gln Asp Phe Tyr Val Ser Pro Thr Phe Gln Asp Leu Leu Asn Arg
850 855 860

Thr Thr Ala Gly Gln Pro Thr Gly Trp Tyr Lys Asp Leu Arg His Tyr
865 870 875 880

Tyr Tyr Arg Ala Arg Trp Glu Leu Tyr Asp Arg Ser Arg Asp Pro His
885 890 895

Glu Thr Gln Asn Leu Ala Thr Asp Pro Arg Phe Ala Gln Leu Leu Glu
900 905 910

Met Leu Arg Asp Gln Leu Ala Lys Trp Gln Trp Glu Thr His Asp Pro
915 920 925

Trp Val Cys Ala Pro Asp Gly Val Leu Glu Glu Lys Leu Ser Pro Gln
930 935 940

Cys Gln Pro Leu His Asn Glu Leu
945 950

<210> 126

<211> 977

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hSGSH, IgG4
HC-GS10-SGSH

<400> 126

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met

35

40

45

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
485 490 495

Pro Arg Asn Ala Leu Leu Leu Leu Ala Asp Asp Gly Gly Phe Glu Ser
500 505 510

Gly Ala Tyr Asn Asn Ser Ala Ile Ala Thr Pro His Leu Asp Ala Leu
515 520 525

Ala Arg Arg Ser Leu Leu Phe Arg Asn Ala Phe Thr Ser Val Ser Ser
530 535 540

Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Leu Pro Gln His Gln
545 550 555 560

Asn Gly Met Tyr Gly Leu His Gln Asp Val His His Phe Asn Ser Phe
565 570 575

Asp Lys Val Arg Ser Leu Pro Leu Leu Leu Ser Gln Ala Gly Val Arg
580 585 590

Thr Gly Ile Ile Gly Lys Lys His Val Gly Pro Glu Thr Val Tyr Pro
595 600 605

Phe Asp Phe Ala Tyr Thr Glu Glu Asn Gly Ser Val Leu Gln Val Gly
610 615 620

Arg Asn Ile Thr Arg Ile Lys Leu Leu Val Arg Lys Phe Leu Gln Thr
625 630 635 640

Gln Asp Asp Arg Pro Phe Phe Leu Tyr Val Ala Phe His Asp Pro His
645 650 655

Arg Cys Gly His Ser Gln Pro Gln Tyr Gly Thr Phe Cys Glu Lys Phe
660 665 670

Gly Asn Gly Glu Ser Gly Met Gly Arg Ile Pro Asp Trp Thr Pro Gln
675 680 685

Ala Tyr Asp Pro Leu Asp Val Leu Val Pro Tyr Phe Val Pro Asn Thr
690 695 700

Pro Ala Ala Arg Ala Asp Leu Ala Ala Gln Tyr Thr Thr Val Gly Arg
705 710 715 720

Met Asp Gln Gly Val Gly Leu Val Leu Gln Glu Leu Arg Asp Ala Gly
725 730 735

Val Leu Asn Asp Thr Leu Val Ile Phe Thr Ser Asp Asn Gly Ile Pro
740 745 750

Phe Pro Ser Gly Arg Thr Asn Leu Tyr Trp Pro Gly Thr Ala Glu Pro
755 760 765

Leu Leu Val Ser Ser Pro Glu His Pro Lys Arg Trp Gly Gln Val Ser
770 775 780

Glu Ala Tyr Val Ser Leu Leu Asp Leu Thr Pro Thr Ile Leu Asp Trp
785 790 795 800

Phe Ser Ile Pro Tyr Pro Ser Tyr Ala Ile Phe Gly Ser Lys Thr Ile
805 810 815

His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu Glu Ala Glu Pro Leu

820

825

830

Trp Ala Thr Val Phe Gly Ser Gln Ser His His Glu Val Thr Met Ser
 835 840 845

Tyr Pro Met Arg Ser Val Gln His Arg His Phe Arg Leu Val His Asn
 850 855 860

Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln Asp Phe Tyr Val Ser
 865 870 875 880

Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr Ala Gly Gln Pro Thr
 885 890 895

Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr Arg Ala Arg Trp Glu
 900 905 910

Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr Gln Asn Leu Ala Thr
 915 920 925

Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu Arg Asp Gln Leu Ala
 930 935 940

Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val Cys Ala Pro Asp Gly
 945 950 955 960

Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln Pro Leu His Asn Glu
 965 970 975

Leu

<210> 127

<211> 1027

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hSGSH, IgG4 HC-GS20-SGSH

<400> 127

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Arg Pro Arg Asn Ala Leu Leu Leu Leu Ala Asp Asp Gly Gly Phe
545 550 555 560

Glu Ser Gly Ala Tyr Asn Asn Ser Ala Ile Ala Thr Pro His Leu Asp

565

570

575

Ala Leu Ala Arg Arg Ser Leu Leu Phe Arg Asn Ala Phe Thr Ser Val
 580 585 590

Ser Ser Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Leu Pro Gln
 595 600 605

His Gln Asn Gly Met Tyr Gly Leu His Gln Asp Val His His Phe Asn
 610 615 620

Ser Phe Asp Lys Val Arg Ser Leu Pro Leu Leu Leu Ser Gln Ala Gly
 625 630 635 640

Val Arg Thr Gly Ile Ile Gly Lys Lys His Val Gly Pro Glu Thr Val
 645 650 655

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

Val Gly Arg Asn Ile Thr Arg Ile Lys Leu Leu Val Arg Lys Phe Leu
 675 680 685

Gln Thr Gln Asp Asp Arg Pro Phe Phe Leu Tyr Val Ala Phe His Asp
 690 695 700

Pro His Arg Cys Gly His Ser Gln Pro Gln Tyr Gly Thr Phe Cys Glu
 705 710 715 720

Lys Phe Gly Asn Gly Glu Ser Gly Met Gly Arg Ile Pro Asp Trp Thr
 725 730 735

Pro Gln Ala Tyr Asp Pro Leu Asp Val Leu Val Pro Tyr Phe Val Pro
 740 745 750

Asn Thr Pro Ala Ala Arg Ala Asp Leu Ala Ala Gln Tyr Thr Thr Val
 755 760 765

Gly Arg Met Asp Gln Gly Val Gly Leu Val Leu Gln Glu Leu Arg Asp
770 775 780

Ala Gly Val Leu Asn Asp Thr Leu Val Ile Phe Thr Ser Asp Asn Gly
785 790 795 800

Ile Pro Phe Pro Ser Gly Arg Thr Asn Leu Tyr Trp Pro Gly Thr Ala
805 810 815

Glu Pro Leu Leu Val Ser Ser Pro Glu His Pro Lys Arg Trp Gly Gln
820 825 830

Val Ser Glu Ala Tyr Val Ser Leu Leu Asp Leu Thr Pro Thr Ile Leu
835 840 845

Asp Trp Phe Ser Ile Pro Tyr Pro Ser Tyr Ala Ile Phe Gly Ser Lys
850 855 860

Thr Ile His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu Glu Ala Glu
865 870 875 880

Pro Leu Trp Ala Thr Val Phe Gly Ser Gln Ser His His Glu Val Thr
885 890 895

Met Ser Tyr Pro Met Arg Ser Val Gln His Arg His Phe Arg Leu Val
900 905 910

His Asn Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln Asp Phe Tyr
915 920 925

Val Ser Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr Ala Gly Gln
930 935 940

Pro Thr Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr Arg Ala Arg
945 950 955 960

Trp Glu Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr Gln Asn Leu
965 970 975

Ala Thr Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu Arg Asp Gln
980 985 990

Leu Ala Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val Cys Ala Pro
995 1000 1005

Asp Gly Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln Pro Leu
1010 1015 1020

His Asn Glu Leu
1025

<210> 128
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hSGSH, Fab HC-GS3-SGSH

<400> 128

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr

65		70		75		80	
Leu	Gln	Leu	Ser	Ser	Leu	Lys	Ala
			85				Ser
							Asp
							90
							Thr
							Ala
							Met
							Tyr
							95
							Tyr
							Cys
Ala	Arg	Ser	Gly	Asn	Tyr	Asp	Glu
			100				Val
							105
							Ala
							Tyr
							Trp
							Gly
							110
							Gln
							Gly
							Thr
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser
		115					120
							Thr
							Lys
							Gly
							Pro
							125
							Ser
							Val
							Phe
							Pro
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr
							135
							Ser
							Gly
							Gly
							Thr
							140
							Ala
							Ala
							Leu
							Gly
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro
							Glu
							150
							Pro
							Val
							155
							Thr
							Val
							Ser
							Trp
							Asn
							160
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val
							His
							170
							Thr
							Phe
							Pro
							Ala
							Val
							175
							Leu
							Gln
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser
							185
							Ser
							Val
							Val
							Thr
							Val
							190
							Pro
							Ser
							Ser
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile
							200
							Cys
							Asn
							Val
							Asn
							His
							205
							Lys
							Pro
							Ser
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val
							215
							Glu
							Pro
							Lys
							220
							Ser
							Cys
							Asp
							Lys
							Thr
His	Thr	Gly	Gly	Gly	Gly	Ser	Gly
							230
							Gly
							Gly
							235
							Ser
							Gly
							Gly
							Gly
							240
							Gly
							Phe
Ser	Arg	Pro	Arg	Asn	Ala	Leu	Leu
							245
							Leu
							Leu
							250
							Ala
							Asp
							Asp
							Gly
							255
							Gly
							Phe
Glu	Ser	Gly	Ala	Tyr	Asn	Asn	Ser
							260
							Ala
							265
							Ile
							Ala
							Thr
							Pro
							His
							270
							Leu
							Asp

Ala Leu Ala Arg Arg Ser Leu Leu Phe Arg Asn Ala Phe Thr Ser Val
275 280 285

Ser Ser Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Leu Pro Gln
290 295 300

His Gln Asn Gly Met Tyr Gly Leu His Gln Asp Val His His Phe Asn
305 310 315 320

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

Val Arg Thr Gly Ile Ile Gly Lys Lys His Val Gly Pro Glu Thr Val
340 345 350

Tyr Pro Phe Asp Phe Ala Tyr Thr Glu Glu Asn Gly Ser Val Leu Gln
355 360 365

Val Gly Arg Asn Ile Thr Arg Ile Lys Leu Leu Val Arg Lys Phe Leu
370 375 380

Gln Thr Gln Asp Asp Arg Pro Phe Phe Leu Tyr Val Ala Phe His Asp
385 390 395 400

Pro His Arg Cys Gly His Ser Gln Pro Gln Tyr Gly Thr Phe Cys Glu
405 410 415

Lys Phe Gly Asn Gly Glu Ser Gly Met Gly Arg Ile Pro Asp Trp Thr
420 425 430

Pro Gln Ala Tyr Asp Pro Leu Asp Val Leu Val Pro Tyr Phe Val Pro
435 440 445

Asn Thr Pro Ala Ala Arg Ala Asp Leu Ala Ala Gln Tyr Thr Thr Val
450 455 460

Gly Arg Met Asp Gln Gly Val Gly Leu Val Leu Gln Glu Leu Arg Asp
465 470 475 480

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

Ile Pro Phe Pro Ser Gly Arg Thr Asn Leu Tyr Trp Pro Gly Thr Ala
500 505 510

Glu Pro Leu Leu Val Ser Ser Pro Glu His Pro Lys Arg Trp Gly Gln
515 520 525

Val Ser Glu Ala Tyr Val Ser Leu Leu Asp Leu Thr Pro Thr Ile Leu
530 535 540

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

Thr Ile His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu Glu Ala Glu
565 570 575

Pro Leu Trp Ala Thr Val Phe Gly Ser Gln Ser His His Glu Val Thr
580 585 590

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

His Asn Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln Asp Phe Tyr
610 615 620

Val Ser Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr Ala Gly Gln
625 630 635 640

Pro Thr Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr Arg Ala Arg
645 650 655

Trp Glu Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr Gln Asn Leu
660 665 670

Ala Thr Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu Arg Asp Gln
675 680 685

Leu Ala Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val Cys Ala Pro
690 695 700

Asp Gly Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln Pro Leu His
705 710 715 720

Asn Glu Leu

<210> 129
<211> 994
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hSGSH, Tandem Fab HC-SGSH

<400> 129

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
260 265 270

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
275 280 285

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
290 295 300

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

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
325 330 335

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
340 345 350

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
370 375 380

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
385 390 395 400

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
405 410 415

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
420 425 430

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
435 440 445

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
450 455 460

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
465 470 475 480

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
485 490 495

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
500 505 510

Arg Pro Arg Asn Ala Leu Leu Leu Leu Ala Asp Asp Gly Gly Phe Glu
515 520 525

Ser Gly Ala Tyr Asn Asn Ser Ala Ile Ala Thr Pro His Leu Asp Ala
530 535 540

Leu Ala Arg Arg Ser Leu Leu Phe Arg Asn Ala Phe Thr Ser Val Ser
545 550 555 560

Ser Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Leu Pro Gln His
565 570 575

Gln Asn Gly Met Tyr Gly Leu His Gln Asp Val His His Phe Asn Ser
580 585 590

Phe Asp Lys Val Arg Ser Leu Pro Leu Leu Leu Ser Gln Ala Gly Val
595 600 605

Arg Thr Gly Ile Ile Gly Lys Lys His Val Gly Pro Glu Thr Val Tyr
610 615 620

Pro Phe Asp Phe Ala Tyr Thr Glu Glu Asn Gly Ser Val Leu Gln Val
625 630 635 640

Gly Arg Asn Ile Thr Arg Ile Lys Leu Leu Val Arg Lys Phe Leu Gln
645 650 655

Thr Gln Asp Asp Arg Pro Phe Phe Leu Tyr Val Ala Phe His Asp Pro

660

665

670

His Arg Cys Gly His Ser Gln Pro Gln Tyr Gly Thr Phe Cys Glu Lys
 675 680 685

Phe Gly Asn Gly Glu Ser Gly Met Gly Arg Ile Pro Asp Trp Thr Pro
 690 695 700

Gln Ala Tyr Asp Pro Leu Asp Val Leu Val Pro Tyr Phe Val Pro Asn
 705 710 715 720

Thr Pro Ala Ala Arg Ala Asp Leu Ala Ala Gln Tyr Thr Thr Val Gly
 725 730 735

Arg Met Asp Gln Gly Val Gly Leu Val Leu Gln Glu Leu Arg Asp Ala
 740 745 750

Gly Val Leu Asn Asp Thr Leu Val Ile Phe Thr Ser Asp Asn Gly Ile
 755 760 765

Pro Phe Pro Ser Gly Arg Thr Asn Leu Tyr Trp Pro Gly Thr Ala Glu
 770 775 780

Pro Leu Leu Val Ser Ser Pro Glu His Pro Lys Arg Trp Gly Gln Val
 785 790 795 800

Ser Glu Ala Tyr Val Ser Leu Leu Asp Leu Thr Pro Thr Ile Leu Asp
 805 810 815

Trp Phe Ser Ile Pro Tyr Pro Ser Tyr Ala Ile Phe Gly Ser Lys Thr
 820 825 830

Ile His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu Glu Ala Glu Pro
 835 840 845

Leu Trp Ala Thr Val Phe Gly Ser Gln Ser His His Glu Val Thr Met
 850 855 860

Ser Tyr Pro Met Arg Ser Val Gln His Arg His Phe Arg Leu Val His
865 870 875 880

Asn Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln Asp Phe Tyr Val
885 890 895

Ser Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr Ala Gly Gln Pro
900 905 910

Thr Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr Arg Ala Arg Trp
915 920 925

Glu Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr Gln Asn Leu Ala
930 935 940

Thr Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu Arg Asp Gln Leu
945 950 955 960

Ala Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val Cys Ala Pro Asp
965 970 975

Gly Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln Pro Leu His Asn
980 985 990

Glu Leu

<210> 130

<211> 944

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hGBA, IgG4 HC-GBA

<400> 130

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser

195

200

205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Ala
435 440 445

Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val
450 455 460

Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala
465 470 475 480

Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met
485 490 495

Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu
500 505 510

Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly Phe
515 520 525

Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu Ser
530 535 540

Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu Gly
545 550 555 560

Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
565 570 575

Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His
580 585 590

Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile
595 600 605

His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala Ser
610 615 620

Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn Gly
625 630 635 640

Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr Trp
645 650 655

Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys Leu
660 665 670

Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu Leu
675 680 685

Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg
690 695 700

Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His
705 710 715 720

His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro
725 730 735

His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val
740 745 750

His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys
755 760 765

Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe
770 775 780

Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg
785 790 795 800

Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr
805 810 815

Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu
820 825 830

Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro
835 840 845

Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe
850 855 860

Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln Arg
865 870 875 880

Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala Leu
885 890 895

Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser Ser
900 905 910

Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
915 920 925

Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg Gln
930 935 940

<210> 131

<211> 967

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hGBA, IgG4
HC-GS5-GBA

<400> 131

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly
465 470 475 480

Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe
485 490 495

Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser
500 505 510

Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala
515 520 525

Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys
530 535 540

Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala
545 550 555 560

Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys
565 570 575

Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
580 585 590

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
595 600 605

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
610 615 620

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
625 630 635 640

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
645 650 655

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly
660 665 670

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp
675 680 685

Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn
690 695 700

Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly
705 710 715 720

Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro
725 730 735

Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp
740 745 750

Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp
755 760 765

Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu

770

775

780

Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu
 785 790 795 800

Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys
 805 810 815

Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln
 820 825 830

Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp
 835 840 845

Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val
 850 855 860

Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr
 865 870 875 880

Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
 885 890 895

Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
 900 905 910

Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val
 915 920 925

Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp
 930 935 940

Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His
 945 950 955 960

Thr Tyr Leu Trp Arg Arg Gln
 965

<210> 132
<211> 992
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hGBA, IgG4
HC-GS10-GBA

<400> 132

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
485 490 495

Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val
500 505 510

Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala
515 520 525

Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met

530

535

540

Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu
 545 550 555 560

Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly Phe
 565 570 575

Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu Ser
 580 585 590

Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu Gly
 595 600 605

Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
 610 615 620

Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His
 625 630 635 640

Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile
 645 650 655

His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala Ser
 660 665 670

Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn Gly
 675 680 685

Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr Trp
 690 695 700

Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys Leu
 705 710 715 720

Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu Leu
 725 730 735

Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg
740 745 750

Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His
755 760 765

His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro
770 775 780

His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val
785 790 795 800

His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys
805 810 815

Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe
820 825 830

Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg
835 840 845

Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr
850 855 860

Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu
865 870 875 880

Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro
885 890 895

Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe
900 905 910

Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln Arg
915 920 925

Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala Leu
 930 935 940

Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser Ser
 945 950 955 960

Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
 965 970 975

Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg Gln
 980 985 990

<210> 133

<211> 1042

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hGBA, IgG4
 HC-GS20-GBA

<400> 133

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

275

280

285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

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

Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe
565 570 575

Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg
580 585 590

Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr
595 600 605

Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys
610 615 620

Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala
625 630 635 640

Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu
645 650 655

Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp
660 665 670

Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln
675 680 685

Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro
690 695 700

Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu
705 710 715 720

Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val
725 730 735

Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln
740 745 750

Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His
755 760 765

Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly
770 775 780

Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His
785 790 795 800

Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser
805 810 815

Thr His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu
820 825 830

Leu Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys
835 840 845

Tyr Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro
850 855 860

Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met
865 870 875 880

Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser
885 890 895

Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile
900 905 910

Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu
915 920 925

Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp
930 935 940

Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro
945 950 955 960

Met Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser
965 970 975

Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val
980 985 990

Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg
995 1000 1005

Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly
1010 1015 1020

Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu
1025 1030 1035

Trp Arg Arg Gln
1040

<210> 134

<211> 738
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of humanized anti-hTfR antibody No. 3N and hGBA, Fab HC-GS3-GBA

<400> 134

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val
245 250 255

Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe
260 265 270

Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg
275 280 285

Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr
290 295 300

Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys
305 310 315 320

Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala
325 330 335

Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu
340 345 350

Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp
355 360 365

Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln
370 375 380

Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro
385 390 395 400

Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu
405 410 415

Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val
420 425 430

Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln
435 440 445

Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His
450 455 460

Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly
465 470 475 480

Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His
485 490 495

Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser
500 505 510

Thr His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu
515 520 525

Leu Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys
530 535 540

Tyr Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro

545		550		555		560
Ala Lys Ala Thr	Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met					
	565			570		575
Leu Phe Ala Ser	Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser					
	580			585		590
Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile						
	595			600		605
Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu						
	610			615		620
Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp						
625				630		640
Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro						
	645			650		655
Met Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser						
	660			665		670
Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val						
	675			680		685
Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg						
	690			695		700
Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe						
705				710		720
Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg						
	725			730		735
Arg Gln						

<210> 135
<211> 1009
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hGBA, Tandem Fab HC-GBA

<400> 135

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
260 265 270

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
275 280 285

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
290 295 300

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

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
325 330 335

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys

340

345

350

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 355 360 365

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 370 375 380

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 385 390 395 400

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 405 410 415

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 420 425 430

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 435 440 445

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 450 455 460

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 465 470 475 480

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 500 505 510

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys
 515 520 525

Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
 530 535 540

Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg
545 550 555 560

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
565 570 575

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
580 585 590

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
595 600 605

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
610 615 620

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
625 630 635 640

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu
645 650 655

His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu
660 665 670

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala
675 680 685

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn
690 695 700

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
705 710 715 720

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
725 730 735

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
740 745 750

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
755 760 765

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
770 775 780

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
785 790 795 800

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
805 810 815

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala
820 825 830

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
835 840 845

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
850 855 860

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
865 870 875 880

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
885 890 895

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
900 905 910

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
915 920 925

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
930 935 940

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
945 950 955 960

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
965 970 975

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu
980 985 990

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg
995 1000 1005

Gln

<210> 136
<211> 991
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hTPP-1, IgG4
HC-TPP1

<400> 136

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe

50

55

60

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu Pro Pro Gly Trp Val
450 455 460

Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr Phe Ala
465 470 475 480

Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln Ala Val
485 490 495

Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr Leu Thr Leu Glu Asn
500 505 510

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

Lys Trp Leu Leu Ala Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr
530 535 540

Gln Asp Phe Leu Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu
545 550 555 560

Leu Pro Gly Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr
565 570 575

His Val Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala
580 585 590

Pro His Val Asp Phe Val Gly Gly Leu His His Phe Pro Pro Thr Ser
595 600 605

Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly Leu
610 615 620

His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn Leu Thr
625 630 635 640

Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln Ala Cys Ala
645 650 655

Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu Ala Gln Phe Met
660 665 670

Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala Ser Val Ala Arg Val
675 680 685

Val Gly Gln Gln Gly Arg Gly Arg Ala Gly Ile Glu Ala Ser Leu Asp
690 695 700

Val Gln Tyr Leu Met Ser Ala Gly Ala Asn Ile Ser Thr Trp Val Tyr
705 710 715 720

Ser Ser Pro Gly Arg His Glu Gly Gln Glu Pro Phe Leu Gln Trp Leu
725 730 735

Met Leu Leu Ser Asn Glu Ser Ala Leu Pro His Val His Thr Val Ser
740 745 750

Tyr Gly Asp Asp Glu Asp Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val
755 760 765

Asn Thr Glu Leu Met Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe
770 775 780

Ala Ser Gly Asp Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His
785 790 795 800

Gln Phe Arg Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val
805 810 815

Gly Gly Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val
820 825 830

Asp Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser

835	840	845
Tyr Gln Glu Glu Ala Val	Thr Lys Phe Leu Ser	Ser Ser Pro His Leu
850	855	860
Pro Pro Ser Ser Tyr Phe	Asn Ala Ser Gly Arg	Ala Tyr Pro Asp Val
865	870	875
Ala Ala Leu Ser Asp Gly	Tyr Trp Val Val Ser	Asn Arg Val Pro Ile
885	890	895
Pro Trp Val Ser Gly Thr	Ser Ala Ser Thr Pro	Val Phe Gly Gly Ile
900	905	910
Leu Ser Leu Ile Asn Glu	His Arg Ile Leu Ser	Gly Arg Pro Pro Leu
915	920	925
Gly Phe Leu Asn Pro Arg	Leu Tyr Gln Gln His	Gly Ala Gly Leu Phe
930	935	940
Asp Val Thr Arg Gly Cys	His Glu Ser Cys Leu	Asp Glu Glu Val Glu
945	950	955
Gly Gln Gly Phe Cys Ser	Gly Pro Gly Trp Asp	Pro Val Thr Gly Trp
965	970	975
Gly Thr Pro Asn Phe Pro	Ala Leu Leu Lys Thr	Leu Leu Asn Pro
980	985	990

<210> 137
 <211> 1014
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hTPP-1, IgG4
 GS5-TPP1

<400> 137

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg
465 470 475 480

Thr Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu
485 490 495

Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu
500 505 510

Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly
515 520 525

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

Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala Ala Gly Ala Gln
545 550 555 560

Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu Thr Cys Trp Leu Ser
565 570 575

Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly Ala Glu Phe His His Tyr

580

585

590

Val Gly Gly Pro Thr Glu Thr His Val Val Arg Ser Pro His Pro Tyr
 595 600 605

Gln Leu Pro Gln Ala Leu Ala Pro His Val Asp Phe Val Gly Gly Leu
 610 615 620

His His Phe Pro Pro Thr Ser Ser Leu Arg Gln Arg Pro Glu Pro Gln
 625 630 635 640

Val Thr Gly Thr Val Gly Leu His Leu Gly Val Thr Pro Ser Val Ile
 645 650 655

Arg Lys Arg Tyr Asn Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser
 660 665 670

Asn Asn Ser Gln Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp
 675 680 685

Ser Asp Leu Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His
 690 695 700

Gln Ala Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala
 705 710 715 720

Gly Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala
 725 730 735

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly Gln
 740 745 750

Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser Ala Leu
 755 760 765

Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp Ser Leu Ser
 770 775 780

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

Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp Ser Gly Ala Gly Cys
805 810 815

Trp Ser Val Ser Gly Arg His Gln Phe Arg Pro Thr Phe Pro Ala Ser
820 825 830

Ser Pro Tyr Val Thr Thr Val Gly Gly Thr Ser Phe Gln Glu Pro Phe
835 840 845

Leu Ile Thr Asn Glu Ile Val Asp Tyr Ile Ser Gly Gly Gly Phe Ser
850 855 860

Asn Val Phe Pro Arg Pro Ser Tyr Gln Glu Glu Ala Val Thr Lys Phe
865 870 875 880

Leu Ser Ser Ser Pro His Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser
885 890 895

Gly Arg Ala Tyr Pro Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val
900 905 910

Val Ser Asn Arg Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser
915 920 925

Thr Pro Val Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile
930 935 940

Leu Ser Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln
945 950 955 960

Gln His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
965 970 975

Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro Gly
980 985 990

Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Asn Phe Pro Ala Leu Leu
995 1000 1005

Lys Thr Leu Leu Asn Pro
1010

<210> 138

<211> 1039

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hTPP-1, IgG4
GS10-TPP1

<400> 138

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu

290

295

300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 485 490 495

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

Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr Phe Ala
515 520 525

Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln Ala Val
530 535 540

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

Val Ala Asp Leu Val Arg Pro Ser Pro Leu Thr Leu His Thr Val Gln
565 570 575

Lys Trp Leu Leu Ala Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr
580 585 590

Gln Asp Phe Leu Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu
595 600 605

Leu Pro Gly Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr
610 615 620

His Val Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala
625 630 635 640

Pro His Val Asp Phe Val Gly Gly Leu His His Phe Pro Pro Thr Ser
645 650 655

Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly Leu
660 665 670

His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn Leu Thr
675 680 685

Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln Ala Cys Ala
690 695 700

Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu Ala Gln Phe Met
705 710 715 720

Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala Ser Val Ala Arg Val
725 730 735

Val Gly Gln Gln Gly Arg Gly Arg Ala Gly Ile Glu Ala Ser Leu Asp
740 745 750

Val Gln Tyr Leu Met Ser Ala Gly Ala Asn Ile Ser Thr Trp Val Tyr
755 760 765

Ser Ser Pro Gly Arg His Glu Gly Gln Glu Pro Phe Leu Gln Trp Leu
770 775 780

Met Leu Leu Ser Asn Glu Ser Ala Leu Pro His Val His Thr Val Ser
785 790 795 800

Tyr Gly Asp Asp Glu Asp Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val
805 810 815

Asn Thr Glu Leu Met Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe
820 825 830

Ala Ser Gly Asp Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His
835 840 845

Gln Phe Arg Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val
850 855 860

Gly Gly Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val
865 870 875 880

Asp Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser
885 890 895

Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His Leu
900 905 910

Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro Asp Val
915 920 925

Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg Val Pro Ile
930 935 940

Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val Phe Gly Gly Ile
945 950 955 960

Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser Gly Arg Pro Pro Leu
965 970 975

Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln His Gly Ala Gly Leu Phe
980 985 990

Asp Val Thr Arg Gly Cys His Glu Ser Cys Leu Asp Glu Glu Val Glu
995 1000 1005

Gly Gln Gly Phe Cys Ser Gly Pro Gly Trp Asp Pro Val Thr Gly
1010 1015 1020

Trp Gly Thr Pro Asn Phe Pro Ala Leu Leu Lys Thr Leu Leu Asn
1025 1030 1035

Pro

<210> 139
<211> 1089
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hTPP-1, IgG4 GS20-TPP1

<400> 139

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

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

Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr
565 570 575

Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln
580 585 590

Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr Leu Thr Leu
595 600 605

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

Val Gln Lys Trp Leu Leu Ala Ala Gly Ala Gln Lys Cys His Ser Val
625 630 635 640

Ile Thr Gln Asp Phe Leu Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu
645 650 655

Leu Leu Leu Pro Gly Ala Glu Phe His His Tyr Val Gly Gly Pro Thr
660 665 670

Glu Thr His Val Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala
675 680 685

Leu Ala Pro His Val Asp Phe Val Gly Gly Leu His His Phe Pro Pro
690 695 700

Thr Ser Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val
705 710 715 720

Gly Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn
725 730 735

Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln Ala
740 745 750

Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu Ala Gln

755

760

765

Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala Ser Val Ala
 770 775 780

Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly Ile Glu Ala Ser
 785 790 795 800

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

Val Tyr Ser Ser Pro Gly Arg His Glu Gly Gln Glu Pro Phe Leu Gln
 820 825 830

Trp Leu Met Leu Leu Ser Asn Glu Ser Ala Leu Pro His Val His Thr
 835 840 845

Val Ser Tyr Gly Asp Asp Glu Asp Ser Leu Ser Ser Ala Tyr Ile Gln
 850 855 860

Arg Val Asn Thr Glu Leu Met Lys Ala Ala Ala Arg Gly Leu Thr Leu
 865 870 875 880

Leu Phe Ala Ser Gly Asp Ser Gly Ala Gly Cys Trp Ser Val Ser Gly
 885 890 895

Arg His Gln Phe Arg Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr
 900 905 910

Thr Val Gly Gly Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu
 915 920 925

Ile Val Asp Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg
 930 935 940

Pro Ser Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro
 945 950 955 960

His Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
965 970 975

Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg Val
980 985 990

Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val Phe Gly
995 1000 1005

Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser Gly Arg
1010 1015 1020

Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln His Gly
1025 1030 1035

Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser Cys Leu
1040 1045 1050

Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro Gly Trp
1055 1060 1065

Asp Pro Val Thr Gly Trp Gly Thr Pro Asn Phe Pro Ala Leu Leu
1070 1075 1080

Lys Thr Leu Leu Asn Pro
1085

<210> 140

<211> 785

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hTPP-1, Fab HC-GS3-TPP1

<400> 140

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195

200

205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 225 230 235 240

Ser Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu Pro Pro Gly
 245 250 255

Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr
 260 265 270

Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln
 275 280 285

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

Glu Asn Val Ala Asp Leu Val Arg Pro Ser Pro Leu Thr Leu His Thr
 305 310 315 320

Val Gln Lys Trp Leu Leu Ala Ala Gly Ala Gln Lys Cys His Ser Val
 325 330 335

Ile Thr Gln Asp Phe Leu Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu
 340 345 350

Leu Leu Leu Pro Gly Ala Glu Phe His His Tyr Val Gly Gly Pro Thr
 355 360 365

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

Leu Ala Pro His Val Asp Phe Val Gly Gly Leu His His Phe Pro Pro
 385 390 395 400

Thr Ser Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val
405 410 415

Gly Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn
420 425 430

Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln Ala
435 440 445

Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu Ala Gln
450 455 460

Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala Ser Val Ala
465 470 475 480

Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly Ile Glu Ala Ser
485 490 495

Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala Asn Ile Ser Thr Trp
500 505 510

Val Tyr Ser Ser Pro Gly Arg His Glu Gly Gln Glu Pro Phe Leu Gln
515 520 525

Trp Leu Met Leu Leu Ser Asn Glu Ser Ala Leu Pro His Val His Thr
530 535 540

Val Ser Tyr Gly Asp Asp Glu Asp Ser Leu Ser Ser Ala Tyr Ile Gln
545 550 555 560

Arg Val Asn Thr Glu Leu Met Lys Ala Ala Ala Arg Gly Leu Thr Leu
565 570 575

Leu Phe Ala Ser Gly Asp Ser Gly Ala Gly Cys Trp Ser Val Ser Gly
580 585 590

Arg His Gln Phe Arg Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr
595 600 605

Thr Val Gly Gly Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu
610 615 620

Ile Val Asp Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg
625 630 635 640

Pro Ser Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro
645 650 655

His Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
660 665 670

Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg Val
675 680 685

Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val Phe Gly
690 695 700

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

Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln His Gly Ala Gly
725 730 735

Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser Cys Leu Asp Glu Glu
740 745 750

Val Glu Gly Gln Gly Phe Cys Ser Gly Pro Gly Trp Asp Pro Val Thr
755 760 765

Gly Trp Gly Thr Pro Asn Phe Pro Ala Leu Leu Lys Thr Leu Leu Asn
770 775 780

Pro
785

<210> 141
<211> 1056
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hTPP-1, Tandem Fab
HC-TPP1

<400> 141

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130

135

140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
 225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 260 265 270

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 275 280 285

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 290 295 300

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

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 325 330 335

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
340 345 350

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
370 375 380

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
385 390 395 400

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
405 410 415

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
420 425 430

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
435 440 445

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
450 455 460

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
465 470 475 480

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
485 490 495

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
500 505 510

Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu Pro Pro Gly Trp
515 520 525

Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr Phe
530 535 540

Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln Ala
545 550 555 560

Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr Leu Thr Leu Glu
565 570 575

Asn Val Ala Asp Leu Val Arg Pro Ser Pro Leu Thr Leu His Thr Val
580 585 590

Gln Lys Trp Leu Leu Ala Ala Gly Ala Gln Lys Cys His Ser Val Ile
595 600 605

Thr Gln Asp Phe Leu Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu
610 615 620

Leu Leu Pro Gly Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu
625 630 635 640

Thr His Val Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu
645 650 655

Ala Pro His Val Asp Phe Val Gly Gly Leu His His Phe Pro Pro Thr
660 665 670

Ser Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly
675 680 685

Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn Leu
690 695 700

Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln Ala Cys
705 710 715 720

Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu Ala Gln Phe
725 730 735

Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala Ser Val Ala Arg
740 745 750

Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly Ile Glu Ala Ser Leu
755 760 765

Asp Val Gln Tyr Leu Met Ser Ala Gly Ala Asn Ile Ser Thr Trp Val
770 775 780

Tyr Ser Ser Pro Gly Arg His Glu Gly Gln Glu Pro Phe Leu Gln Trp
785 790 795 800

Leu Met Leu Leu Ser Asn Glu Ser Ala Leu Pro His Val His Thr Val
805 810 815

Ser Tyr Gly Asp Asp Glu Asp Ser Leu Ser Ser Ala Tyr Ile Gln Arg
820 825 830

Val Asn Thr Glu Leu Met Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu
835 840 845

Phe Ala Ser Gly Asp Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg
850 855 860

His Gln Phe Arg Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr
865 870 875 880

Val Gly Gly Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile
885 890 895

Val Asp Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro
900 905 910

Ser Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His

915

920

925

Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro Asp
 930 935 940

Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg Val Pro
 945 950 955 960

Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val Phe Gly Gly
 965 970 975

Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser Gly Arg Pro Pro
 980 985 990

Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln His Gly Ala Gly Leu
 995 1000 1005

Phe Asp Val Thr Arg Gly Cys His Glu Ser Cys Leu Asp Glu Glu
 1010 1015 1020

Val Glu Gly Gln Gly Phe Cys Ser Gly Pro Gly Trp Asp Pro Val
 1025 1030 1035

Thr Gly Trp Gly Thr Pro Asn Phe Pro Ala Leu Leu Lys Thr Leu
 1040 1045 1050

Leu Asn Pro
 1055

<210> 142

<211> 1167

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hNAGLU, IgG4
 HC-NAGLU

<400> 142

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Asp
435 440 445

Glu Ala Arg Glu Ala Ala Ala Val Arg Ala Leu Val Ala Arg Leu Leu
450 455 460

Gly Pro Gly Pro Ala Ala Asp Phe Ser Val Ser Val Glu Arg Ala Leu
465 470 475 480

Ala Ala Lys Pro Gly Leu Asp Thr Tyr Ser Leu Gly Gly Gly Gly Ala
485 490 495

Ala Arg Val Arg Val Arg Gly Ser Thr Gly Val Ala Ala Ala Ala Gly
500 505 510

Leu His Arg Tyr Leu Arg Asp Phe Cys Gly Cys His Val Ala Trp Ser
515 520 525

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

Leu Thr Glu Ala Thr Pro Asn Arg Tyr Arg Tyr Tyr Gln Asn Val Cys
545 550 555 560

Thr Gln Ser Tyr Ser Phe Val Trp Trp Asp Trp Ala Arg Trp Glu Arg
565 570 575

Glu Ile Asp Trp Met Ala Leu Asn Gly Ile Asn Leu Ala Leu Ala Trp

580

585

590

Ser Gly Gln Glu Ala Ile Trp Gln Arg Val Tyr Leu Ala Leu Gly Leu
 595 600 605

Thr Gln Ala Glu Ile Asn Glu Phe Phe Thr Gly Pro Ala Phe Leu Ala
 610 615 620

Trp Gly Arg Met Gly Asn Leu His Thr Trp Asp Gly Pro Leu Pro Pro
 625 630 635 640

Ser Trp His Ile Lys Gln Leu Tyr Leu Gln His Arg Val Leu Asp Gln
 645 650 655

Met Arg Ser Phe Gly Met Thr Pro Val Leu Pro Ala Phe Ala Gly His
 660 665 670

Val Pro Glu Ala Val Thr Arg Val Phe Pro Gln Val Asn Val Thr Lys
 675 680 685

Met Gly Ser Trp Gly His Phe Asn Cys Ser Tyr Ser Cys Ser Phe Leu
 690 695 700

Leu Ala Pro Glu Asp Pro Ile Phe Pro Ile Ile Gly Ser Leu Phe Leu
 705 710 715 720

Arg Glu Leu Ile Lys Glu Phe Gly Thr Asp His Ile Tyr Gly Ala Asp
 725 730 735

Thr Phe Asn Glu Met Gln Pro Pro Ser Ser Glu Pro Ser Tyr Leu Ala
 740 745 750

Ala Ala Thr Thr Ala Val Tyr Glu Ala Met Thr Ala Val Asp Thr Glu
 755 760 765

Ala Val Trp Leu Leu Gln Gly Trp Leu Phe Gln His Gln Pro Gln Phe
 770 775 780

Trp Gly Pro Ala Gln Ile Arg Ala Val Leu Gly Ala Val Pro Arg Gly
785 790 795 800

Arg Leu Leu Val Leu Asp Leu Phe Ala Glu Ser Gln Pro Val Tyr Thr
805 810 815

Arg Thr Ala Ser Phe Gln Gly Gln Pro Phe Ile Trp Cys Met Leu His
820 825 830

Asn Phe Gly Gly Asn His Gly Leu Phe Gly Ala Leu Glu Ala Val Asn
835 840 845

Gly Gly Pro Glu Ala Ala Arg Leu Phe Pro Asn Ser Thr Met Val Gly
850 855 860

Thr Gly Met Ala Pro Glu Gly Ile Ser Gln Asn Glu Val Val Tyr Ser
865 870 875 880

Leu Met Ala Glu Leu Gly Trp Arg Lys Asp Pro Val Pro Asp Leu Ala
885 890 895

Ala Trp Val Thr Ser Phe Ala Ala Arg Arg Tyr Gly Val Ser His Pro
900 905 910

Asp Ala Gly Ala Ala Trp Arg Leu Leu Arg Ser Val Tyr Asn Cys
915 920 925

Ser Gly Glu Ala Cys Arg Gly His Asn Arg Ser Pro Leu Val Arg Arg
930 935 940

Pro Ser Leu Gln Met Asn Thr Ser Ile Trp Tyr Asn Arg Ser Asp Val
945 950 955 960

Phe Glu Ala Trp Arg Leu Leu Leu Thr Ser Ala Pro Ser Leu Ala Thr
965 970 975

Ser Pro Ala Phe Arg Tyr Asp Leu Leu Asp Leu Thr Arg Gln Ala Val
980 985 990

Gln Glu Leu Val Ser Leu Tyr Tyr Glu Glu Ala Arg Ser Ala Tyr Leu
995 1000 1005

Ser Lys Glu Leu Ala Ser Leu Leu Arg Ala Gly Gly Val Leu Ala
1010 1015 1020

Tyr Glu Leu Leu Pro Ala Leu Asp Glu Val Leu Ala Ser Asp Ser
1025 1030 1035

Arg Phe Leu Leu Gly Ser Trp Leu Glu Gln Ala Arg Ala Ala Ala
1040 1045 1050

Val Ser Glu Ala Glu Ala Asp Phe Tyr Glu Gln Asn Ser Arg Tyr
1055 1060 1065

Gln Leu Thr Leu Trp Gly Pro Glu Gly Asn Ile Leu Asp Tyr Ala
1070 1075 1080

Asn Lys Gln Leu Ala Gly Leu Val Ala Asn Tyr Tyr Thr Pro Arg
1085 1090 1095

Trp Arg Leu Phe Leu Glu Ala Leu Val Asp Ser Val Ala Gln Gly
1100 1105 1110

Ile Pro Phe Gln Gln His Gln Phe Asp Lys Asn Val Phe Gln Leu
1115 1120 1125

Glu Gln Ala Phe Val Leu Ser Lys Gln Arg Tyr Pro Ser Gln Pro
1130 1135 1140

Arg Gly Asp Thr Val Asp Leu Ala Lys Lys Ile Phe Leu Lys Tyr
1145 1150 1155

Tyr Pro Arg Trp Val Ala Gly Ser Trp
1160 1165

<210> 143

<211> 1190

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hNAGLU, IgG4
HC-GS5-NAGLU

<400> 143

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

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

130

135

140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Asp Glu Ala Arg Glu Ala Ala Ala Val Arg
465 470 475 480

Ala Leu Val Ala Arg Leu Leu Gly Pro Gly Pro Ala Ala Asp Phe Ser
485 490 495

Val Ser Val Glu Arg Ala Leu Ala Ala Lys Pro Gly Leu Asp Thr Tyr
500 505 510

Ser Leu Gly Gly Gly Gly Ala Ala Arg Val Arg Val Arg Gly Ser Thr
515 520 525

Gly Val Ala Ala Ala Ala Gly Leu His Arg Tyr Leu Arg Asp Phe Cys
530 535 540

Gly Cys His Val Ala Trp Ser Gly Ser Gln Leu Arg Leu Pro Arg Pro
545 550 555 560

Leu Pro Ala Val Pro Gly Glu Leu Thr Glu Ala Thr Pro Asn Arg Tyr
565 570 575

Arg Tyr Tyr Gln Asn Val Cys Thr Gln Ser Tyr Ser Phe Val Trp Trp
580 585 590

Asp Trp Ala Arg Trp Glu Arg Glu Ile Asp Trp Met Ala Leu Asn Gly
595 600 605

Ile Asn Leu Ala Leu Ala Trp Ser Gly Gln Glu Ala Ile Trp Gln Arg
610 615 620

Val Tyr Leu Ala Leu Gly Leu Thr Gln Ala Glu Ile Asn Glu Phe Phe
625 630 635 640

Thr Gly Pro Ala Phe Leu Ala Trp Gly Arg Met Gly Asn Leu His Thr
645 650 655

Trp Asp Gly Pro Leu Pro Pro Ser Trp His Ile Lys Gln Leu Tyr Leu
660 665 670

Gln His Arg Val Leu Asp Gln Met Arg Ser Phe Gly Met Thr Pro Val
675 680 685

Leu Pro Ala Phe Ala Gly His Val Pro Glu Ala Val Thr Arg Val Phe
690 695 700

Pro Gln Val Asn Val Thr Lys Met Gly Ser Trp Gly His Phe Asn Cys
705 710 715 720

Ser Tyr Ser Cys Ser Phe Leu Leu Ala Pro Glu Asp Pro Ile Phe Pro
725 730 735

Ile Ile Gly Ser Leu Phe Leu Arg Glu Leu Ile Lys Glu Phe Gly Thr
740 745 750

Asp His Ile Tyr Gly Ala Asp Thr Phe Asn Glu Met Gln Pro Pro Ser
755 760 765

Ser Glu Pro Ser Tyr Leu Ala Ala Ala Thr Thr Ala Val Tyr Glu Ala
770 775 780

Met Thr Ala Val Asp Thr Glu Ala Val Trp Leu Leu Gln Gly Trp Leu
785 790 795 800

Phe Gln His Gln Pro Gln Phe Trp Gly Pro Ala Gln Ile Arg Ala Val
805 810 815

Leu Gly Ala Val Pro Arg Gly Arg Leu Leu Val Leu Asp Leu Phe Ala
820 825 830

Glu Ser Gln Pro Val Tyr Thr Arg Thr Ala Ser Phe Gln Gly Gln Pro
835 840 845

Phe Ile Trp Cys Met Leu His Asn Phe Gly Gly Asn His Gly Leu Phe
850 855 860

Gly Ala Leu Glu Ala Val Asn Gly Gly Pro Glu Ala Ala Arg Leu Phe
865 870 875 880

Pro Asn Ser Thr Met Val Gly Thr Gly Met Ala Pro Glu Gly Ile Ser
885 890 895

Gln Asn Glu Val Val Tyr Ser Leu Met Ala Glu Leu Gly Trp Arg Lys
900 905 910

Asp Pro Val Pro Asp Leu Ala Ala Trp Val Thr Ser Phe Ala Ala Arg

915

920

925

Arg Tyr Gly Val Ser His Pro Asp Ala Gly Ala Ala Trp Arg Leu Leu
 930 935 940

Leu Arg Ser Val Tyr Asn Cys Ser Gly Glu Ala Cys Arg Gly His Asn
 945 950 955 960

Arg Ser Pro Leu Val Arg Arg Pro Ser Leu Gln Met Asn Thr Ser Ile
 965 970 975

Trp Tyr Asn Arg Ser Asp Val Phe Glu Ala Trp Arg Leu Leu Leu Thr
 980 985 990

Ser Ala Pro Ser Leu Ala Thr Ser Pro Ala Phe Arg Tyr Asp Leu Leu
 995 1000 1005

Asp Leu Thr Arg Gln Ala Val Gln Glu Leu Val Ser Leu Tyr Tyr
 1010 1015 1020

Glu Glu Ala Arg Ser Ala Tyr Leu Ser Lys Glu Leu Ala Ser Leu
 1025 1030 1035

Leu Arg Ala Gly Gly Val Leu Ala Tyr Glu Leu Leu Pro Ala Leu
 1040 1045 1050

Asp Glu Val Leu Ala Ser Asp Ser Arg Phe Leu Leu Gly Ser Trp
 1055 1060 1065

Leu Glu Gln Ala Arg Ala Ala Ala Val Ser Glu Ala Glu Ala Asp
 1070 1075 1080

Phe Tyr Glu Gln Asn Ser Arg Tyr Gln Leu Thr Leu Trp Gly Pro
 1085 1090 1095

Glu Gly Asn Ile Leu Asp Tyr Ala Asn Lys Gln Leu Ala Gly Leu
 1100 1105 1110

Val Ala Asn Tyr Tyr Thr Pro Arg Trp Arg Leu Phe Leu Glu Ala
 1115 1120 1125

Leu Val Asp Ser Val Ala Gln Gly Ile Pro Phe Gln Gln His Gln
 1130 1135 1140

Phe Asp Lys Asn Val Phe Gln Leu Glu Gln Ala Phe Val Leu Ser
 1145 1150 1155

Lys Gln Arg Tyr Pro Ser Gln Pro Arg Gly Asp Thr Val Asp Leu
 1160 1165 1170

Ala Lys Lys Ile Phe Leu Lys Tyr Tyr Pro Arg Trp Val Ala Gly
 1175 1180 1185

Ser Trp
 1190

<210> 144
 <211> 1215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hNAGLU, IgG4
 HC-GS10-NAGLU

<400> 144

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly

435

440

445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 485 490 495

Glu Ala Arg Glu Ala Ala Ala Val Arg Ala Leu Val Ala Arg Leu Leu
 500 505 510

Gly Pro Gly Pro Ala Ala Asp Phe Ser Val Ser Val Glu Arg Ala Leu
 515 520 525

Ala Ala Lys Pro Gly Leu Asp Thr Tyr Ser Leu Gly Gly Gly Gly Ala
 530 535 540

Ala Arg Val Arg Val Arg Gly Ser Thr Gly Val Ala Ala Ala Ala Gly
 545 550 555 560

Leu His Arg Tyr Leu Arg Asp Phe Cys Gly Cys His Val Ala Trp Ser
 565 570 575

Gly Ser Gln Leu Arg Leu Pro Arg Pro Leu Pro Ala Val Pro Gly Glu
 580 585 590

Leu Thr Glu Ala Thr Pro Asn Arg Tyr Arg Tyr Tyr Gln Asn Val Cys
 595 600 605

Thr Gln Ser Tyr Ser Phe Val Trp Trp Asp Trp Ala Arg Trp Glu Arg
 610 615 620

Glu Ile Asp Trp Met Ala Leu Asn Gly Ile Asn Leu Ala Leu Ala Trp
 625 630 635 640

Ser Gly Gln Glu Ala Ile Trp Gln Arg Val Tyr Leu Ala Leu Gly Leu
645 650 655

Thr Gln Ala Glu Ile Asn Glu Phe Phe Thr Gly Pro Ala Phe Leu Ala
660 665 670

Trp Gly Arg Met Gly Asn Leu His Thr Trp Asp Gly Pro Leu Pro Pro
675 680 685

Ser Trp His Ile Lys Gln Leu Tyr Leu Gln His Arg Val Leu Asp Gln
690 695 700

Met Arg Ser Phe Gly Met Thr Pro Val Leu Pro Ala Phe Ala Gly His
705 710 715 720

Val Pro Glu Ala Val Thr Arg Val Phe Pro Gln Val Asn Val Thr Lys
725 730 735

Met Gly Ser Trp Gly His Phe Asn Cys Ser Tyr Ser Cys Ser Phe Leu
740 745 750

Leu Ala Pro Glu Asp Pro Ile Phe Pro Ile Ile Gly Ser Leu Phe Leu
755 760 765

Arg Glu Leu Ile Lys Glu Phe Gly Thr Asp His Ile Tyr Gly Ala Asp
770 775 780

Thr Phe Asn Glu Met Gln Pro Pro Ser Ser Glu Pro Ser Tyr Leu Ala
785 790 795 800

Ala Ala Thr Thr Ala Val Tyr Glu Ala Met Thr Ala Val Asp Thr Glu
805 810 815

Ala Val Trp Leu Leu Gln Gly Trp Leu Phe Gln His Gln Pro Gln Phe
820 825 830

Trp Gly Pro Ala Gln Ile Arg Ala Val Leu Gly Ala Val Pro Arg Gly
835 840 845

Arg Leu Leu Val Leu Asp Leu Phe Ala Glu Ser Gln Pro Val Tyr Thr
850 855 860

Arg Thr Ala Ser Phe Gln Gly Gln Pro Phe Ile Trp Cys Met Leu His
865 870 875 880

Asn Phe Gly Gly Asn His Gly Leu Phe Gly Ala Leu Glu Ala Val Asn
885 890 895

Gly Gly Pro Glu Ala Ala Arg Leu Phe Pro Asn Ser Thr Met Val Gly
900 905 910

Thr Gly Met Ala Pro Glu Gly Ile Ser Gln Asn Glu Val Val Tyr Ser
915 920 925

Leu Met Ala Glu Leu Gly Trp Arg Lys Asp Pro Val Pro Asp Leu Ala
930 935 940

Ala Trp Val Thr Ser Phe Ala Ala Arg Arg Tyr Gly Val Ser His Pro
945 950 955 960

Asp Ala Gly Ala Ala Trp Arg Leu Leu Leu Arg Ser Val Tyr Asn Cys
965 970 975

Ser Gly Glu Ala Cys Arg Gly His Asn Arg Ser Pro Leu Val Arg Arg
980 985 990

Pro Ser Leu Gln Met Asn Thr Ser Ile Trp Tyr Asn Arg Ser Asp Val
995 1000 1005

Phe Glu Ala Trp Arg Leu Leu Leu Thr Ser Ala Pro Ser Leu Ala
1010 1015 1020

Thr	Ser	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Leu	Asp	Leu	Thr	Arg	Gln
1025						1030					1035			
Ala	Val	Gln	Glu	Leu	Val	Ser	Leu	Tyr	Tyr	Glu	Glu	Ala	Arg	Ser
1040						1045					1050			
Ala	Tyr	Leu	Ser	Lys	Glu	Leu	Ala	Ser	Leu	Leu	Arg	Ala	Gly	Gly
1055						1060					1065			
Val	Leu	Ala	Tyr	Glu	Leu	Leu	Pro	Ala	Leu	Asp	Glu	Val	Leu	Ala
1070						1075					1080			
Ser	Asp	Ser	Arg	Phe	Leu	Leu	Gly	Ser	Trp	Leu	Glu	Gln	Ala	Arg
1085						1090					1095			
Ala	Ala	Ala	Val	Ser	Glu	Ala	Glu	Ala	Asp	Phe	Tyr	Glu	Gln	Asn
1100						1105					1110			
Ser	Arg	Tyr	Gln	Leu	Thr	Leu	Trp	Gly	Pro	Glu	Gly	Asn	Ile	Leu
1115						1120					1125			
Asp	Tyr	Ala	Asn	Lys	Gln	Leu	Ala	Gly	Leu	Val	Ala	Asn	Tyr	Tyr
1130						1135					1140			
Thr	Pro	Arg	Trp	Arg	Leu	Phe	Leu	Glu	Ala	Leu	Val	Asp	Ser	Val
1145						1150					1155			
Ala	Gln	Gly	Ile	Pro	Phe	Gln	Gln	His	Gln	Phe	Asp	Lys	Asn	Val
1160						1165					1170			
Phe	Gln	Leu	Glu	Gln	Ala	Phe	Val	Leu	Ser	Lys	Gln	Arg	Tyr	Pro
1175						1180					1185			
Ser	Gln	Pro	Arg	Gly	Asp	Thr	Val	Asp	Leu	Ala	Lys	Lys	Ile	Phe
1190						1195					1200			
Leu	Lys	Tyr	Tyr	Pro	Arg	Trp	Val	Ala	Gly	Ser	Trp			

1205

1210

1215

<210> 145

<211> 1265

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hNAGLU, IgG4
HC-GS20-NAGLU

<400> 145

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Asp Glu Ala Arg Glu Ala Ala Ala Val Arg Ala Leu Val Ala Arg
545 550 555 560

Leu Leu Gly Pro Gly Pro Ala Ala Asp Phe Ser Val Ser Val Glu Arg
565 570 575

Ala Leu Ala Ala Lys Pro Gly Leu Asp Thr Tyr Ser Leu Gly Gly Gly
580 585 590

Gly Ala Ala Arg Val Arg Val Arg Gly Ser Thr Gly Val Ala Ala Ala
595 600 605

Ala Gly Leu His Arg Tyr Leu Arg Asp Phe Cys Gly Cys His Val Ala
610 615 620

Trp Ser Gly Ser Gln Leu Arg Leu Pro Arg Pro Leu Pro Ala Val Pro
625 630 635 640

Gly Glu Leu Thr Glu Ala Thr Pro Asn Arg Tyr Arg Tyr Tyr Gln Asn
645 650 655

Val Cys Thr Gln Ser Tyr Ser Phe Val Trp Trp Asp Trp Ala Arg Trp
660 665 670

Glu Arg Glu Ile Asp Trp Met Ala Leu Asn Gly Ile Asn Leu Ala Leu
675 680 685

Ala Trp Ser Gly Gln Glu Ala Ile Trp Gln Arg Val Tyr Leu Ala Leu
690 695 700

Gly Leu Thr Gln Ala Glu Ile Asn Glu Phe Phe Thr Gly Pro Ala Phe
705 710 715 720

Leu Ala Trp Gly Arg Met Gly Asn Leu His Thr Trp Asp Gly Pro Leu

725

730

735

Pro Pro Ser Trp His Ile Lys Gln Leu Tyr Leu Gln His Arg Val Leu
 740 745 750

Asp Gln Met Arg Ser Phe Gly Met Thr Pro Val Leu Pro Ala Phe Ala
 755 760 765

Gly His Val Pro Glu Ala Val Thr Arg Val Phe Pro Gln Val Asn Val
 770 775 780

Thr Lys Met Gly Ser Trp Gly His Phe Asn Cys Ser Tyr Ser Cys Ser
 785 790 795 800

Phe Leu Leu Ala Pro Glu Asp Pro Ile Phe Pro Ile Ile Gly Ser Leu
 805 810 815

Phe Leu Arg Glu Leu Ile Lys Glu Phe Gly Thr Asp His Ile Tyr Gly
 820 825 830

Ala Asp Thr Phe Asn Glu Met Gln Pro Pro Ser Ser Glu Pro Ser Tyr
 835 840 845

Leu Ala Ala Ala Thr Thr Ala Val Tyr Glu Ala Met Thr Ala Val Asp
 850 855 860

Thr Glu Ala Val Trp Leu Leu Gln Gly Trp Leu Phe Gln His Gln Pro
 865 870 875 880

Gln Phe Trp Gly Pro Ala Gln Ile Arg Ala Val Leu Gly Ala Val Pro
 885 890 895

Arg Gly Arg Leu Leu Val Leu Asp Leu Phe Ala Glu Ser Gln Pro Val
 900 905 910

Tyr Thr Arg Thr Ala Ser Phe Gln Gly Gln Pro Phe Ile Trp Cys Met
 915 920 925

Leu His Asn Phe Gly Gly Asn His Gly Leu Phe Gly Ala Leu Glu Ala
930 935 940

Val Asn Gly Gly Pro Glu Ala Ala Arg Leu Phe Pro Asn Ser Thr Met
945 950 955 960

Val Gly Thr Gly Met Ala Pro Glu Gly Ile Ser Gln Asn Glu Val Val
965 970 975

Tyr Ser Leu Met Ala Glu Leu Gly Trp Arg Lys Asp Pro Val Pro Asp
980 985 990

Leu Ala Ala Trp Val Thr Ser Phe Ala Ala Arg Arg Tyr Gly Val Ser
995 1000 1005

His Pro Asp Ala Gly Ala Ala Trp Arg Leu Leu Leu Arg Ser Val
1010 1015 1020

Tyr Asn Cys Ser Gly Glu Ala Cys Arg Gly His Asn Arg Ser Pro
1025 1030 1035

Leu Val Arg Arg Pro Ser Leu Gln Met Asn Thr Ser Ile Trp Tyr
1040 1045 1050

Asn Arg Ser Asp Val Phe Glu Ala Trp Arg Leu Leu Leu Thr Ser
1055 1060 1065

Ala Pro Ser Leu Ala Thr Ser Pro Ala Phe Arg Tyr Asp Leu Leu
1070 1075 1080

Asp Leu Thr Arg Gln Ala Val Gln Glu Leu Val Ser Leu Tyr Tyr
1085 1090 1095

Glu Glu Ala Arg Ser Ala Tyr Leu Ser Lys Glu Leu Ala Ser Leu
1100 1105 1110

Leu Arg Ala Gly Gly Val Leu Ala Tyr Glu Leu Leu Pro Ala Leu
1115 1120 1125

Asp Glu Val Leu Ala Ser Asp Ser Arg Phe Leu Leu Gly Ser Trp
1130 1135 1140

Leu Glu Gln Ala Arg Ala Ala Ala Val Ser Glu Ala Glu Ala Asp
1145 1150 1155

Phe Tyr Glu Gln Asn Ser Arg Tyr Gln Leu Thr Leu Trp Gly Pro
1160 1165 1170

Glu Gly Asn Ile Leu Asp Tyr Ala Asn Lys Gln Leu Ala Gly Leu
1175 1180 1185

Val Ala Asn Tyr Tyr Thr Pro Arg Trp Arg Leu Phe Leu Glu Ala
1190 1195 1200

Leu Val Asp Ser Val Ala Gln Gly Ile Pro Phe Gln Gln His Gln
1205 1210 1215

Phe Asp Lys Asn Val Phe Gln Leu Glu Gln Ala Phe Val Leu Ser
1220 1225 1230

Lys Gln Arg Tyr Pro Ser Gln Pro Arg Gly Asp Thr Val Asp Leu
1235 1240 1245

Ala Lys Lys Ile Phe Leu Lys Tyr Tyr Pro Arg Trp Val Ala Gly
1250 1255 1260

Ser Trp
1265

<210> 146
<211> 961
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of humanized anti-hTfR antibody No. 3N and hNAGLU, Fab HC-GS3-NAGLU

<400> 146

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Asp Glu Ala Arg Glu Ala Ala Ala Val Arg Ala Leu Val Ala Arg
245 250 255

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

Ala Leu Ala Ala Lys Pro Gly Leu Asp Thr Tyr Ser Leu Gly Gly Gly
275 280 285

Gly Ala Ala Arg Val Arg Val Arg Gly Ser Thr Gly Val Ala Ala Ala
290 295 300

Ala Gly Leu His Arg Tyr Leu Arg Asp Phe Cys Gly Cys His Val Ala
305 310 315 320

Trp Ser Gly Ser Gln Leu Arg Leu Pro Arg Pro Leu Pro Ala Val Pro
325 330 335

Gly Glu Leu Thr Glu Ala Thr Pro Asn Arg Tyr Arg Tyr Tyr Gln Asn
340 345 350

Val Cys Thr Gln Ser Tyr Ser Phe Val Trp Trp Asp Trp Ala Arg Trp
355 360 365

Glu Arg Glu Ile Asp Trp Met Ala Leu Asn Gly Ile Asn Leu Ala Leu
370 375 380

Ala Trp Ser Gly Gln Glu Ala Ile Trp Gln Arg Val Tyr Leu Ala Leu
385 390 395 400

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

Leu Ala Trp Gly Arg Met Gly Asn Leu His Thr Trp Asp Gly Pro Leu
420 425 430

Pro Pro Ser Trp His Ile Lys Gln Leu Tyr Leu Gln His Arg Val Leu
435 440 445

Asp Gln Met Arg Ser Phe Gly Met Thr Pro Val Leu Pro Ala Phe Ala
450 455 460

Gly His Val Pro Glu Ala Val Thr Arg Val Phe Pro Gln Val Asn Val
465 470 475 480

Thr Lys Met Gly Ser Trp Gly His Phe Asn Cys Ser Tyr Ser Cys Ser
485 490 495

Phe Leu Leu Ala Pro Glu Asp Pro Ile Phe Pro Ile Ile Gly Ser Leu
500 505 510

Phe Leu Arg Glu Leu Ile Lys Glu Phe Gly Thr Asp His Ile Tyr Gly
515 520 525

Ala Asp Thr Phe Asn Glu Met Gln Pro Pro Ser Ser Glu Pro Ser Tyr
530 535 540

Leu Ala Ala Ala Thr Thr Ala Val Tyr Glu Ala Met Thr Ala Val Asp
545 550 555 560

Thr Glu Ala Val Trp Leu Leu Gln Gly Trp Leu Phe Gln His Gln Pro
565 570 575

Gln Phe Trp Gly Pro Ala Gln Ile Arg Ala Val Leu Gly Ala Val Pro
580 585 590

Arg Gly Arg Leu Leu Val Leu Asp Leu Phe Ala Glu Ser Gln Pro Val
595 600 605

Tyr Thr Arg Thr Ala Ser Phe Gln Gly Gln Pro Phe Ile Trp Cys Met
610 615 620

Leu His Asn Phe Gly Gly Asn His Gly Leu Phe Gly Ala Leu Glu Ala
625 630 635 640

Val Asn Gly Gly Pro Glu Ala Ala Arg Leu Phe Pro Asn Ser Thr Met
645 650 655

Val Gly Thr Gly Met Ala Pro Glu Gly Ile Ser Gln Asn Glu Val Val
660 665 670

Tyr Ser Leu Met Ala Glu Leu Gly Trp Arg Lys Asp Pro Val Pro Asp
675 680 685

Leu Ala Ala Trp Val Thr Ser Phe Ala Ala Arg Arg Tyr Gly Val Ser
690 695 700

His Pro Asp Ala Gly Ala Ala Trp Arg Leu Leu Leu Arg Ser Val Tyr
705 710 715 720

Asn Cys Ser Gly Glu Ala Cys Arg Gly His Asn Arg Ser Pro Leu Val
725 730 735

Arg Arg Pro Ser Leu Gln Met Asn Thr Ser Ile Trp Tyr Asn Arg Ser
740 745 750

Asp Val Phe Glu Ala Trp Arg Leu Leu Leu Thr Ser Ala Pro Ser Leu

755

760

765

Ala Thr Ser Pro Ala Phe Arg Tyr Asp Leu Leu Asp Leu Thr Arg Gln
 770 775 780

Ala Val Gln Glu Leu Val Ser Leu Tyr Tyr Glu Glu Ala Arg Ser Ala
 785 790 795 800

Tyr Leu Ser Lys Glu Leu Ala Ser Leu Leu Arg Ala Gly Gly Val Leu
 805 810 815

Ala Tyr Glu Leu Leu Pro Ala Leu Asp Glu Val Leu Ala Ser Asp Ser
 820 825 830

Arg Phe Leu Leu Gly Ser Trp Leu Glu Gln Ala Arg Ala Ala Ala Val
 835 840 845

Ser Glu Ala Glu Ala Asp Phe Tyr Glu Gln Asn Ser Arg Tyr Gln Leu
 850 855 860

Thr Leu Trp Gly Pro Glu Gly Asn Ile Leu Asp Tyr Ala Asn Lys Gln
 865 870 875 880

Leu Ala Gly Leu Val Ala Asn Tyr Tyr Thr Pro Arg Trp Arg Leu Phe
 885 890 895

Leu Glu Ala Leu Val Asp Ser Val Ala Gln Gly Ile Pro Phe Gln Gln
 900 905 910

His Gln Phe Asp Lys Asn Val Phe Gln Leu Glu Gln Ala Phe Val Leu
 915 920 925

Ser Lys Gln Arg Tyr Pro Ser Gln Pro Arg Gly Asp Thr Val Asp Leu
 930 935 940

Ala Lys Lys Ile Phe Leu Lys Tyr Tyr Pro Arg Trp Val Ala Gly Ser
 945 950 955 960

Trp

<210> 147
<211> 971
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hNAGLU, Fab HC-GS5-NAGLU

<400> 147

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Asp Glu Ala Arg Glu
245 250 255

Ala Ala Ala Val Arg Ala Leu Val Ala Arg Leu Leu Gly Pro Gly Pro
260 265 270

Ala Ala Asp Phe Ser Val Ser Val Glu Arg Ala Leu Ala Ala Lys Pro
275 280 285

Gly Leu Asp Thr Tyr Ser Leu Gly Gly Gly Gly Ala Ala Arg Val Arg
290 295 300

Val Arg Gly Ser Thr Gly Val Ala Ala Ala Ala Gly Leu His Arg Tyr
305 310 315 320

Leu Arg Asp Phe Cys Gly Cys His Val Ala Trp Ser Gly Ser Gln Leu

325

330

335

Arg Leu Pro Arg Pro Leu Pro Ala Val Pro Gly Glu Leu Thr Glu Ala
 340 345 350

Thr Pro Asn Arg Tyr Arg Tyr Tyr Gln Asn Val Cys Thr Gln Ser Tyr
 355 360 365

Ser Phe Val Trp Trp Asp Trp Ala Arg Trp Glu Arg Glu Ile Asp Trp
 370 375 380

Met Ala Leu Asn Gly Ile Asn Leu Ala Leu Ala Trp Ser Gly Gln Glu
 385 390 395 400

Ala Ile Trp Gln Arg Val Tyr Leu Ala Leu Gly Leu Thr Gln Ala Glu
 405 410 415

Ile Asn Glu Phe Phe Thr Gly Pro Ala Phe Leu Ala Trp Gly Arg Met
 420 425 430

Gly Asn Leu His Thr Trp Asp Gly Pro Leu Pro Pro Ser Trp His Ile
 435 440 445

Lys Gln Leu Tyr Leu Gln His Arg Val Leu Asp Gln Met Arg Ser Phe
 450 455 460

Gly Met Thr Pro Val Leu Pro Ala Phe Ala Gly His Val Pro Glu Ala
 465 470 475 480

Val Thr Arg Val Phe Pro Gln Val Asn Val Thr Lys Met Gly Ser Trp
 485 490 495

Gly His Phe Asn Cys Ser Tyr Ser Cys Ser Phe Leu Leu Ala Pro Glu
 500 505 510

Asp Pro Ile Phe Pro Ile Ile Gly Ser Leu Phe Leu Arg Glu Leu Ile
 515 520 525

Lys Glu Phe Gly Thr Asp His Ile Tyr Gly Ala Asp Thr Phe Asn Glu
530 535 540

Met Gln Pro Pro Ser Ser Glu Pro Ser Tyr Leu Ala Ala Ala Thr Thr
545 550 555 560

Ala Val Tyr Glu Ala Met Thr Ala Val Asp Thr Glu Ala Val Trp Leu
565 570 575

Leu Gln Gly Trp Leu Phe Gln His Gln Pro Gln Phe Trp Gly Pro Ala
580 585 590

Gln Ile Arg Ala Val Leu Gly Ala Val Pro Arg Gly Arg Leu Leu Val
595 600 605

Leu Asp Leu Phe Ala Glu Ser Gln Pro Val Tyr Thr Arg Thr Ala Ser
610 615 620

Phe Gln Gly Gln Pro Phe Ile Trp Cys Met Leu His Asn Phe Gly Gly
625 630 635 640

Asn His Gly Leu Phe Gly Ala Leu Glu Ala Val Asn Gly Gly Pro Glu
645 650 655

Ala Ala Arg Leu Phe Pro Asn Ser Thr Met Val Gly Thr Gly Met Ala
660 665 670

Pro Glu Gly Ile Ser Gln Asn Glu Val Val Tyr Ser Leu Met Ala Glu
675 680 685

Leu Gly Trp Arg Lys Asp Pro Val Pro Asp Leu Ala Ala Trp Val Thr
690 695 700

Ser Phe Ala Ala Arg Arg Tyr Gly Val Ser His Pro Asp Ala Gly Ala
705 710 715 720

Ala Trp Arg Leu Leu Leu Arg Ser Val Tyr Asn Cys Ser Gly Glu Ala
725 730 735

Cys Arg Gly His Asn Arg Ser Pro Leu Val Arg Arg Pro Ser Leu Gln
740 745 750

Met Asn Thr Ser Ile Trp Tyr Asn Arg Ser Asp Val Phe Glu Ala Trp
755 760 765

Arg Leu Leu Leu Thr Ser Ala Pro Ser Leu Ala Thr Ser Pro Ala Phe
770 775 780

Arg Tyr Asp Leu Leu Asp Leu Thr Arg Gln Ala Val Gln Glu Leu Val
785 790 795 800

Ser Leu Tyr Tyr Glu Glu Ala Arg Ser Ala Tyr Leu Ser Lys Glu Leu
805 810 815

Ala Ser Leu Leu Arg Ala Gly Gly Val Leu Ala Tyr Glu Leu Leu Pro
820 825 830

Ala Leu Asp Glu Val Leu Ala Ser Asp Ser Arg Phe Leu Leu Gly Ser
835 840 845

Trp Leu Glu Gln Ala Arg Ala Ala Ala Val Ser Glu Ala Glu Ala Asp
850 855 860

Phe Tyr Glu Gln Asn Ser Arg Tyr Gln Leu Thr Leu Trp Gly Pro Glu
865 870 875 880

Gly Asn Ile Leu Asp Tyr Ala Asn Lys Gln Leu Ala Gly Leu Val Ala
885 890 895

Asn Tyr Tyr Thr Pro Arg Trp Arg Leu Phe Leu Glu Ala Leu Val Asp
900 905 910

Ser Val Ala Gln Gly Ile Pro Phe Gln Gln His Gln Phe Asp Lys Asn
915 920 925

Val Phe Gln Leu Glu Gln Ala Phe Val Leu Ser Lys Gln Arg Tyr Pro
930 935 940

Ser Gln Pro Arg Gly Asp Thr Val Asp Leu Ala Lys Lys Ile Phe Leu
945 950 955 960

Lys Tyr Tyr Pro Arg Trp Val Ala Gly Ser Trp
965 970

<210> 148

<211> 996

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hNAGLU, Fab HC-GS10-NAGLU

<400> 148

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Asp Glu Ala Arg Glu Ala Ala Ala Val Arg Ala Leu
275 280 285

Val Ala Arg Leu Leu Gly Pro Gly Pro Ala Ala Asp Phe Ser Val Ser
290 295 300

Val Glu Arg Ala Leu Ala Ala Lys Pro Gly Leu Asp Thr Tyr Ser Leu
305 310 315 320

Gly Gly Gly Gly Ala Ala Arg Val Arg Val Arg Gly Ser Thr Gly Val
325 330 335

Ala Ala Ala Ala Gly Leu His Arg Tyr Leu Arg Asp Phe Cys Gly Cys
340 345 350

His Val Ala Trp Ser Gly Ser Gln Leu Arg Leu Pro Arg Pro Leu Pro
355 360 365

Ala Val Pro Gly Glu Leu Thr Glu Ala Thr Pro Asn Arg Tyr Arg Tyr
370 375 380

Tyr Gln Asn Val Cys Thr Gln Ser Tyr Ser Phe Val Trp Trp Asp Trp
385 390 395 400

Ala Arg Trp Glu Arg Glu Ile Asp Trp Met Ala Leu Asn Gly Ile Asn
405 410 415

Leu Ala Leu Ala Trp Ser Gly Gln Glu Ala Ile Trp Gln Arg Val Tyr
420 425 430

Leu Ala Leu Gly Leu Thr Gln Ala Glu Ile Asn Glu Phe Phe Thr Gly
435 440 445

Pro Ala Phe Leu Ala Trp Gly Arg Met Gly Asn Leu His Thr Trp Asp
450 455 460

Gly Pro Leu Pro Pro Ser Trp His Ile Lys Gln Leu Tyr Leu Gln His
465 470 475 480

Arg Val Leu Asp Gln Met Arg Ser Phe Gly Met Thr Pro Val Leu Pro
485 490 495

Ala Phe Ala Gly His Val Pro Glu Ala Val Thr Arg Val Phe Pro Gln
500 505 510

Val Asn Val Thr Lys Met Gly Ser Trp Gly His Phe Asn Cys Ser Tyr
515 520 525

Ser Cys Ser Phe Leu Leu Ala Pro Glu Asp Pro Ile Phe Pro Ile Ile
530 535 540

Gly Ser Leu Phe Leu Arg Glu Leu Ile Lys Glu Phe Gly Thr Asp His
545 550 555 560

Ile Tyr Gly Ala Asp Thr Phe Asn Glu Met Gln Pro Pro Ser Ser Glu
565 570 575

Pro Ser Tyr Leu Ala Ala Ala Thr Thr Ala Val Tyr Glu Ala Met Thr
580 585 590

Ala Val Asp Thr Glu Ala Val Trp Leu Leu Gln Gly Trp Leu Phe Gln
595 600 605

His Gln Pro Gln Phe Trp Gly Pro Ala Gln Ile Arg Ala Val Leu Gly
610 615 620

Ala Val Pro Arg Gly Arg Leu Leu Val Leu Asp Leu Phe Ala Glu Ser
625 630 635 640

Gln Pro Val Tyr Thr Arg Thr Ala Ser Phe Gln Gly Gln Pro Phe Ile
645 650 655

Trp Cys Met Leu His Asn Phe Gly Gly Asn His Gly Leu Phe Gly Ala
660 665 670

Leu Glu Ala Val Asn Gly Gly Pro Glu Ala Ala Arg Leu Phe Pro Asn

675

680

685

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

Glu Val Val Tyr Ser Leu Met Ala Glu Leu Gly Trp Arg Lys Asp Pro
 705 710 715 720

Val Pro Asp Leu Ala Ala Trp Val Thr Ser Phe Ala Ala Arg Arg Tyr
 725 730 735

Gly Val Ser His Pro Asp Ala Gly Ala Ala Trp Arg Leu Leu Leu Arg
 740 745 750

Ser Val Tyr Asn Cys Ser Gly Glu Ala Cys Arg Gly His Asn Arg Ser
 755 760 765

Pro Leu Val Arg Arg Pro Ser Leu Gln Met Asn Thr Ser Ile Trp Tyr
 770 775 780

Asn Arg Ser Asp Val Phe Glu Ala Trp Arg Leu Leu Leu Thr Ser Ala
 785 790 795 800

Pro Ser Leu Ala Thr Ser Pro Ala Phe Arg Tyr Asp Leu Leu Asp Leu
 805 810 815

Thr Arg Gln Ala Val Gln Glu Leu Val Ser Leu Tyr Tyr Glu Glu Ala
 820 825 830

Arg Ser Ala Tyr Leu Ser Lys Glu Leu Ala Ser Leu Leu Arg Ala Gly
 835 840 845

Gly Val Leu Ala Tyr Glu Leu Leu Pro Ala Leu Asp Glu Val Leu Ala
 850 855 860

Ser Asp Ser Arg Phe Leu Leu Gly Ser Trp Leu Glu Gln Ala Arg Ala
 865 870 875 880

Ala Ala Val Ser Glu Ala Glu Ala Asp Phe Tyr Glu Gln Asn Ser Arg
885 890 895

Tyr Gln Leu Thr Leu Trp Gly Pro Glu Gly Asn Ile Leu Asp Tyr Ala
900 905 910

Asn Lys Gln Leu Ala Gly Leu Val Ala Asn Tyr Tyr Thr Pro Arg Trp
915 920 925

Arg Leu Phe Leu Glu Ala Leu Val Asp Ser Val Ala Gln Gly Ile Pro
930 935 940

Phe Gln Gln His Gln Phe Asp Lys Asn Val Phe Gln Leu Glu Gln Ala
945 950 955 960

Phe Val Leu Ser Lys Gln Arg Tyr Pro Ser Gln Pro Arg Gly Asp Thr
965 970 975

Val Asp Leu Ala Lys Lys Ile Phe Leu Lys Tyr Tyr Pro Arg Trp Val
980 985 990

Ala Gly Ser Trp
995

<210> 149

<211> 1046

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hNAGLU, Fab HC-GS20-NAGLU

<400> 149

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr

210

215

220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 290 295 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 305 310 315 320

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

Ala Leu Val Ala Arg Leu Leu Gly Pro Gly Pro Ala Ala Asp Phe Ser
 340 345 350

Val Ser Val Glu Arg Ala Leu Ala Ala Lys Pro Gly Leu Asp Thr Tyr
 355 360 365

Ser Leu Gly Gly Gly Gly Ala Ala Arg Val Arg Val Arg Gly Ser Thr
 370 375 380

Gly Val Ala Ala Ala Ala Gly Leu His Arg Tyr Leu Arg Asp Phe Cys
 385 390 395 400

Gly Cys His Val Ala Trp Ser Gly Ser Gln Leu Arg Leu Pro Arg Pro
 405 410 415

Leu Pro Ala Val Pro Gly Glu Leu Thr Glu Ala Thr Pro Asn Arg Tyr
420 425 430

Arg Tyr Tyr Gln Asn Val Cys Thr Gln Ser Tyr Ser Phe Val Trp Trp
435 440 445

Asp Trp Ala Arg Trp Glu Arg Glu Ile Asp Trp Met Ala Leu Asn Gly
450 455 460

Ile Asn Leu Ala Leu Ala Trp Ser Gly Gln Glu Ala Ile Trp Gln Arg
465 470 475 480

Val Tyr Leu Ala Leu Gly Leu Thr Gln Ala Glu Ile Asn Glu Phe Phe
485 490 495

Thr Gly Pro Ala Phe Leu Ala Trp Gly Arg Met Gly Asn Leu His Thr
500 505 510

Trp Asp Gly Pro Leu Pro Pro Ser Trp His Ile Lys Gln Leu Tyr Leu
515 520 525

Gln His Arg Val Leu Asp Gln Met Arg Ser Phe Gly Met Thr Pro Val
530 535 540

Leu Pro Ala Phe Ala Gly His Val Pro Glu Ala Val Thr Arg Val Phe
545 550 555 560

Pro Gln Val Asn Val Thr Lys Met Gly Ser Trp Gly His Phe Asn Cys
565 570 575

Ser Tyr Ser Cys Ser Phe Leu Leu Ala Pro Glu Asp Pro Ile Phe Pro
580 585 590

Ile Ile Gly Ser Leu Phe Leu Arg Glu Leu Ile Lys Glu Phe Gly Thr
595 600 605

Asp His Ile Tyr Gly Ala Asp Thr Phe Asn Glu Met Gln Pro Pro Ser
610 615 620

Ser Glu Pro Ser Tyr Leu Ala Ala Ala Thr Thr Ala Val Tyr Glu Ala
625 630 635 640

Met Thr Ala Val Asp Thr Glu Ala Val Trp Leu Leu Gln Gly Trp Leu
645 650 655

Phe Gln His Gln Pro Gln Phe Trp Gly Pro Ala Gln Ile Arg Ala Val
660 665 670

Leu Gly Ala Val Pro Arg Gly Arg Leu Leu Val Leu Asp Leu Phe Ala
675 680 685

Glu Ser Gln Pro Val Tyr Thr Arg Thr Ala Ser Phe Gln Gly Gln Pro
690 695 700

Phe Ile Trp Cys Met Leu His Asn Phe Gly Gly Asn His Gly Leu Phe
705 710 715 720

Gly Ala Leu Glu Ala Val Asn Gly Gly Pro Glu Ala Ala Arg Leu Phe
725 730 735

Pro Asn Ser Thr Met Val Gly Thr Gly Met Ala Pro Glu Gly Ile Ser
740 745 750

Gln Asn Glu Val Val Tyr Ser Leu Met Ala Glu Leu Gly Trp Arg Lys
755 760 765

Asp Pro Val Pro Asp Leu Ala Ala Trp Val Thr Ser Phe Ala Ala Arg
770 775 780

Arg Tyr Gly Val Ser His Pro Asp Ala Gly Ala Ala Trp Arg Leu Leu
785 790 795 800

Leu Arg Ser Val Tyr Asn Cys Ser Gly Glu Ala Cys Arg Gly His Asn
805 810 815

Arg Ser Pro Leu Val Arg Arg Pro Ser Leu Gln Met Asn Thr Ser Ile
820 825 830

Trp Tyr Asn Arg Ser Asp Val Phe Glu Ala Trp Arg Leu Leu Leu Thr
835 840 845

Ser Ala Pro Ser Leu Ala Thr Ser Pro Ala Phe Arg Tyr Asp Leu Leu
850 855 860

Asp Leu Thr Arg Gln Ala Val Gln Glu Leu Val Ser Leu Tyr Tyr Glu
865 870 875 880

Glu Ala Arg Ser Ala Tyr Leu Ser Lys Glu Leu Ala Ser Leu Leu Arg
885 890 895

Ala Gly Gly Val Leu Ala Tyr Glu Leu Leu Pro Ala Leu Asp Glu Val
900 905 910

Leu Ala Ser Asp Ser Arg Phe Leu Leu Gly Ser Trp Leu Glu Gln Ala
915 920 925

Arg Ala Ala Ala Val Ser Glu Ala Glu Ala Asp Phe Tyr Glu Gln Asn
930 935 940

Ser Arg Tyr Gln Leu Thr Leu Trp Gly Pro Glu Gly Asn Ile Leu Asp
945 950 955 960

Tyr Ala Asn Lys Gln Leu Ala Gly Leu Val Ala Asn Tyr Tyr Thr Pro
965 970 975

Arg Trp Arg Leu Phe Leu Glu Ala Leu Val Asp Ser Val Ala Gln Gly
980 985 990

Ile Pro Phe Gln Gln His Gln Phe Asp Lys Asn Val Phe Gln Leu Glu

995

1000

1005

Gln Ala Phe Val Leu Ser Lys Gln Arg Tyr Pro Ser Gln Pro Arg
 1010 1015 1020

Gly Asp Thr Val Asp Leu Ala Lys Lys Ile Phe Leu Lys Tyr Tyr
 1025 1030 1035

Pro Arg Trp Val Ala Gly Ser Trp
 1040 1045

<210> 150

<211> 1076

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hGUSB, IgG4
 HC-GUSB

<400> 150

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser Arg Glu Cys Lys
450 455 460

Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe Ser Asp Asn Arg
465 470 475 480

Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro Leu Trp Glu Ser
485 490 495

Gly Pro Thr Val Asp Met Pro Val Pro Ser Ser Phe Asn Asp Ile Ser
500 505 510

Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val Trp Tyr Glu Arg
515 520 525

Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu Arg Thr Arg Val
530 535 540

Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala Ile Val Trp Val Asn
545 550 555 560

Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr Leu Pro Phe Glu Ala
565 570 575

Asp Ile Ser Asn Leu Val Gln Val Gly Pro Leu Pro Ser Arg Leu Arg
580 585 590

Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro Thr Thr Leu Pro Pro
595 600 605

Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys Tyr Pro Lys Gly Tyr
610 615 620

Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr Ala Gly Leu Gln
625 630 635 640

Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr Ile Asp Asp Ile
645 650 655

Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu Val Asn Tyr Gln
660 665 670

Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu Val Arg Leu Leu

675

680

685

Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr Gln Gly Gln
 690 695 700

Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr Leu Met His Glu
 705 710 715 720

Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln Leu Thr Ala Gln Thr
 725 730 735

Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu Pro Val Gly Ile Arg
 740 745 750

Thr Val Ala Val Thr Lys Ser Gln Phe Leu Ile Asn Gly Lys Pro Phe
 755 760 765

Tyr Phe His Gly Val Asn Lys His Glu Asp Ala Asp Ile Arg Gly Lys
 770 775 780

Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe Asn Leu Leu Arg Trp
 785 790 795 800

Leu Gly Ala Asn Ala Phe Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu
 805 810 815

Val Met Gln Met Cys Asp Arg Tyr Gly Ile Val Val Ile Asp Glu Cys
 820 825 830

Pro Gly Val Gly Leu Ala Leu Pro Gln Phe Phe Asn Asn Val Ser Leu
 835 840 845

His His His Met Gln Val Met Glu Glu Val Val Arg Arg Asp Lys Asn
 850 855 860

His Pro Ala Val Val Met Trp Ser Val Ala Asn Glu Pro Ala Ser His
 865 870 875 880

Leu Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala His Thr Lys
885 890 895

Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn Ser Asn Tyr
900 905 910

Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys Leu Asn Ser
915 920 925

Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu Ile Gln Leu
930 935 940

Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys Tyr Gln Lys Pro
945 950 955 960

Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile Ala Gly Phe His Gln
965 970 975

Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr Gln Lys Ser Leu Leu Glu
980 985 990

Gln Tyr His Leu Gly Leu Asp Gln Lys Arg Arg Lys Tyr Val Val Gly
995 1000 1005

Glu Leu Ile Trp Asn Phe Ala Asp Phe Met Thr Glu Gln Ser Pro
1010 1015 1020

Thr Arg Val Leu Gly Asn Lys Lys Gly Ile Phe Thr Arg Gln Arg
1025 1030 1035

Gln Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu Arg Tyr Trp Lys
1040 1045 1050

Ile Ala Asn Glu Thr Arg Tyr Pro His Ser Val Ala Lys Ser Gln
1055 1060 1065

Cys Leu Glu Asn Ser Leu Phe Thr
1070 1075

<210> 151
<211> 1099
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hGUSB, IgG4
HC-GS5-GUSB

<400> 151

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys

325

330

335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Leu Gln Gly Gly Met Leu Tyr Pro Gln Glu
 465 470 475 480

Ser Pro Ser Arg Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg
 485 490 495

Ala Asp Phe Ser Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr
 500 505 510

Arg Arg Pro Leu Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro
 515 520 525

Ser Ser Phe Asn Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val
530 535 540

Gly Trp Val Trp Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr
545 550 555 560

Gln Asp Leu Arg Thr Arg Val Val Leu Arg Ile Gly Ser Ala His Ser
565 570 575

Tyr Ala Ile Val Trp Val Asn Gly Val Asp Thr Leu Glu His Glu Gly
580 585 590

Gly Tyr Leu Pro Phe Glu Ala Asp Ile Ser Asn Leu Val Gln Val Gly
595 600 605

Pro Leu Pro Ser Arg Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu
610 615 620

Thr Pro Thr Thr Leu Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr
625 630 635 640

Ser Lys Tyr Pro Lys Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe
645 650 655

Phe Asn Tyr Ala Gly Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro
660 665 670

Thr Thr Tyr Ile Asp Asp Ile Thr Val Thr Thr Ser Val Glu Gln Asp
675 680 685

Ser Gly Leu Val Asn Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe
690 695 700

Lys Leu Glu Val Arg Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn
705 710 715 720

Gly Thr Gly Thr Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp
725 730 735

Trp Pro Tyr Leu Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu
740 745 750

Val Gln Leu Thr Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr
755 760 765

Thr Leu Pro Val Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe
770 775 780

Leu Ile Asn Gly Lys Pro Phe Tyr Phe His Gly Val Asn Lys His Glu
785 790 795 800

Asp Ala Asp Ile Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys
805 810 815

Asp Phe Asn Leu Leu Arg Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser
820 825 830

His Tyr Pro Tyr Ala Glu Glu Val Met Gln Met Cys Asp Arg Tyr Gly
835 840 845

Ile Val Val Ile Asp Glu Cys Pro Gly Val Gly Leu Ala Leu Pro Gln
850 855 860

Phe Phe Asn Asn Val Ser Leu His His His Met Gln Val Met Glu Glu
865 870 875 880

Val Val Arg Arg Asp Lys Asn His Pro Ala Val Val Met Trp Ser Val
885 890 895

Ala Asn Glu Pro Ala Ser His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys
900 905 910

Met Val Ile Ala His Thr Lys Ser Leu Asp Pro Ser Arg Pro Val Thr
915 920 925

Phe Val Ser Asn Ser Asn Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val
930 935 940

Asp Val Ile Cys Leu Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly
945 950 955 960

His Leu Glu Leu Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp
965 970 975

Tyr Lys Lys Tyr Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu
980 985 990

Thr Ile Ala Gly Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu
995 1000 1005

Tyr Gln Lys Ser Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln
1010 1015 1020

Lys Arg Arg Lys Tyr Val Val Gly Glu Leu Ile Trp Asn Phe Ala
1025 1030 1035

Asp Phe Met Thr Glu Gln Ser Pro Thr Arg Val Leu Gly Asn Lys
1040 1045 1050

Lys Gly Ile Phe Thr Arg Gln Arg Gln Pro Lys Ser Ala Ala Phe
1055 1060 1065

Leu Leu Arg Glu Arg Tyr Trp Lys Ile Ala Asn Glu Thr Arg Tyr
1070 1075 1080

Pro His Ser Val Ala Lys Ser Gln Cys Leu Glu Asn Ser Leu Phe
1085 1090 1095

Thr

<210> 152
<211> 1124
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hGUSB, IgG4
HC-GS10-GUSB

<400> 152

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu
485 490 495

Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser Arg Glu Cys Lys
500 505 510

Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe Ser Asp Asn Arg
515 520 525

Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro Leu Trp Glu Ser
530 535 540

Gly Pro Thr Val Asp Met Pro Val Pro Ser Ser Phe Asn Asp Ile Ser
545 550 555 560

Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val Trp Tyr Glu Arg
565 570 575

Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu Arg Thr Arg Val
580 585 590

Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala Ile Val Trp Val Asn
595 600 605

Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr Leu Pro Phe Glu Ala
610 615 620

Asp Ile Ser Asn Leu Val Gln Val Gly Pro Leu Pro Ser Arg Leu Arg
625 630 635 640

Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro Thr Thr Leu Pro Pro
645 650 655

Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys Tyr Pro Lys Gly Tyr
660 665 670

Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr Ala Gly Leu Gln
675 680 685

Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr Ile Asp Asp Ile
690 695 700

Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu Val Asn Tyr Gln
705 710 715 720

Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu Val Arg Leu Leu

725

730

735

Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr Gln Gly Gln
 740 745 750

Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr Leu Met His Glu
 755 760 765

Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln Leu Thr Ala Gln Thr
 770 775 780

Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu Pro Val Gly Ile Arg
 785 790 795 800

Thr Val Ala Val Thr Lys Ser Gln Phe Leu Ile Asn Gly Lys Pro Phe
 805 810 815

Tyr Phe His Gly Val Asn Lys His Glu Asp Ala Asp Ile Arg Gly Lys
 820 825 830

Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe Asn Leu Leu Arg Trp
 835 840 845

Leu Gly Ala Asn Ala Phe Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu
 850 855 860

Val Met Gln Met Cys Asp Arg Tyr Gly Ile Val Val Ile Asp Glu Cys
 865 870 875 880

Pro Gly Val Gly Leu Ala Leu Pro Gln Phe Phe Asn Asn Val Ser Leu
 885 890 895

His His His Met Gln Val Met Glu Glu Val Val Arg Arg Asp Lys Asn
 900 905 910

His Pro Ala Val Val Met Trp Ser Val Ala Asn Glu Pro Ala Ser His
 915 920 925

Leu Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala His Thr Lys
930 935 940

Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn Ser Asn Tyr
945 950 955 960

Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys Leu Asn Ser
965 970 975

Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu Ile Gln Leu
980 985 990

Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys Tyr Gln Lys Pro
995 1000 1005

Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile Ala Gly Phe His
1010 1015 1020

Gln Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr Gln Lys Ser Leu
1025 1030 1035

Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys Arg Arg Lys Tyr
1040 1045 1050

Val Val Gly Glu Leu Ile Trp Asn Phe Ala Asp Phe Met Thr Glu
1055 1060 1065

Gln Ser Pro Thr Arg Val Leu Gly Asn Lys Lys Gly Ile Phe Thr
1070 1075 1080

Arg Gln Arg Gln Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu Arg
1085 1090 1095

Tyr Trp Lys Ile Ala Asn Glu Thr Arg Tyr Pro His Ser Val Ala
1100 1105 1110

Lys Ser Gln Cys Leu Glu Asn Ser Leu Phe Thr
1115 1120

<210> 153
<211> 1174
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hGUSB, IgG4
HC-GS20-GUSB

<400> 153

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys

325

330

335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Leu Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser Arg Glu
545 550 555 560

Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe Ser Asp
565 570 575

Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro Leu Trp
580 585 590

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

Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val Trp Tyr
610 615 620

Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu Arg Thr
625 630 635 640

Arg Val Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala Ile Val Trp
645 650 655

Val Asn Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr Leu Pro Phe
660 665 670

Glu Ala Asp Ile Ser Asn Leu Val Gln Val Gly Pro Leu Pro Ser Arg
675 680 685

Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro Thr Thr Leu
690 695 700

Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys Tyr Pro Lys
705 710 715 720

Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr Ala Gly
725 730 735

Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr Ile Asp
740 745 750

Asp Ile Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu Val Asn
755 760 765

Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu Val Arg
770 775 780

Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr Gln
785 790 795 800

Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr Leu Met
805 810 815

His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln Leu Thr Ala
820 825 830

Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu Pro Val Gly
835 840 845

Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe Leu Ile Asn Gly Lys
850 855 860

Pro Phe Tyr Phe His Gly Val Asn Lys His Glu Asp Ala Asp Ile Arg
865 870 875 880

Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe Asn Leu Leu
885 890 895

Arg Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser His Tyr Pro Tyr Ala
900 905 910

Glu Glu Val Met Gln Met Cys Asp Arg Tyr Gly Ile Val Val Ile Asp
915 920 925

Glu Cys Pro Gly Val Gly Leu Ala Leu Pro Gln Phe Phe Asn Asn Val
930 935 940

Ser Leu His His His Met Gln Val Met Glu Glu Val Val Arg Arg Asp
945 950 955 960

Lys Asn His Pro Ala Val Val Met Trp Ser Val Ala Asn Glu Pro Ala
965 970 975

Ser His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala His
980 985 990

Thr Lys Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn Ser
995 1000 1005

Asn Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys
1010 1015 1020

Leu Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu
1025 1030 1035

Leu Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys
1040 1045 1050

Lys Tyr Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr
1055 1060 1065

Ile Ala Gly Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu
1070 1075 1080

Tyr Gln Lys Ser Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln
1085 1090 1095

Lys Arg Arg Lys Tyr Val Val Gly Glu Leu Ile Trp Asn Phe Ala

1100

1105

1110

Asp Phe Met Thr Glu Gln Ser Pro Thr Arg Val Leu Gly Asn Lys
 1115 1120 1125

Lys Gly Ile Phe Thr Arg Gln Arg Gln Pro Lys Ser Ala Ala Phe
 1130 1135 1140

Leu Leu Arg Glu Arg Tyr Trp Lys Ile Ala Asn Glu Thr Arg Tyr
 1145 1150 1155

Pro His Ser Val Ala Lys Ser Gln Cys Leu Glu Asn Ser Leu Phe
 1160 1165 1170

Thr

<210> 154

<211> 870

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
 humanized anti-hTfR antibody No. 3N and hGUSB, Fab HC-GS3-GUSB

<400> 154

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Leu Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser Arg Glu
245 250 255

Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe Ser Asp
260 265 270

Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro Leu Trp
275 280 285

Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro Ser Ser Phe Asn Asp
290 295 300

Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val Trp Tyr
305 310 315 320

Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu Arg Thr
325 330 335

Arg Val Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala Ile Val Trp
340 345 350

Val Asn Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr Leu Pro Phe
355 360 365

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

Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro Thr Thr Leu
385 390 395 400

Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys Tyr Pro Lys
405 410 415

Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr Ala Gly
420 425 430

Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr Ile Asp
435 440 445

Asp Ile Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu Val Asn

450

455

460

Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu Val Arg
 465 470 475 480

Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr Gln
 485 490 495

Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr Leu Met
 500 505 510

His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln Leu Thr Ala
 515 520 525

Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu Pro Val Gly
 530 535 540

Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe Leu Ile Asn Gly Lys
 545 550 555 560

Pro Phe Tyr Phe His Gly Val Asn Lys His Glu Asp Ala Asp Ile Arg
 565 570 575

Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe Asn Leu Leu
 580 585 590

Arg Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser His Tyr Pro Tyr Ala
 595 600 605

Glu Glu Val Met Gln Met Cys Asp Arg Tyr Gly Ile Val Val Ile Asp
 610 615 620

Glu Cys Pro Gly Val Gly Leu Ala Leu Pro Gln Phe Phe Asn Asn Val
 625 630 635 640

Ser Leu His His His Met Gln Val Met Glu Glu Val Val Arg Arg Asp
 645 650 655

Lys Asn His Pro Ala Val Val Met Trp Ser Val Ala Asn Glu Pro Ala
660 665 670

Ser His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala His
675 680 685

Thr Lys Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn Ser
690 695 700

Asn Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys Leu
705 710 715 720

Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu Ile
725 730 735

Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys Tyr Gln
740 745 750

Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile Ala Gly Phe
755 760 765

His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr Gln Lys Ser Leu
770 775 780

Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys Arg Arg Lys Tyr Val
785 790 795 800

Val Gly Glu Leu Ile Trp Asn Phe Ala Asp Phe Met Thr Glu Gln Ser
805 810 815

Pro Thr Arg Val Leu Gly Asn Lys Lys Gly Ile Phe Thr Arg Gln Arg
820 825 830

Gln Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu Arg Tyr Trp Lys Ile
835 840 845

Ala Asn Glu Thr Arg Tyr Pro His Ser Val Ala Lys Ser Gln Cys Leu
850 855 860

Glu Asn Ser Leu Phe Thr
865 870

<210> 155
<211> 880
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hGUSB, Fab HC-GS5-GUSB

<400> 155

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

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

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

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

115

120

125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Gln Gly Gly Met
 245 250 255

Leu Tyr Pro Gln Glu Ser Pro Ser Arg Glu Cys Lys Glu Leu Asp Gly
 260 265 270

Leu Trp Ser Phe Arg Ala Asp Phe Ser Asp Asn Arg Arg Arg Gly Phe
 275 280 285

Glu Glu Gln Trp Tyr Arg Arg Pro Leu Trp Glu Ser Gly Pro Thr Val
 290 295 300

Asp Met Pro Val Pro Ser Ser Phe Asn Asp Ile Ser Gln Asp Trp Arg
 305 310 315 320

Leu Arg His Phe Val Gly Trp Val Trp Tyr Glu Arg Glu Val Ile Leu
325 330 335

Pro Glu Arg Trp Thr Gln Asp Leu Arg Thr Arg Val Val Leu Arg Ile
340 345 350

Gly Ser Ala His Ser Tyr Ala Ile Val Trp Val Asn Gly Val Asp Thr
355 360 365

Leu Glu His Glu Gly Gly Tyr Leu Pro Phe Glu Ala Asp Ile Ser Asn
370 375 380

Leu Val Gln Val Gly Pro Leu Pro Ser Arg Leu Arg Ile Thr Ile Ala
385 390 395 400

Ile Asn Asn Thr Leu Thr Pro Thr Thr Leu Pro Pro Gly Thr Ile Gln
405 410 415

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

Thr Tyr Phe Asp Phe Phe Asn Tyr Ala Gly Leu Gln Arg Ser Val Leu
435 440 445

Leu Tyr Thr Thr Pro Thr Thr Tyr Ile Asp Asp Ile Thr Val Thr Thr
450 455 460

Ser Val Glu Gln Asp Ser Gly Leu Val Asn Tyr Gln Ile Ser Val Lys
465 470 475 480

Gly Ser Asn Leu Phe Lys Leu Glu Val Arg Leu Leu Asp Ala Glu Asn
485 490 495

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

Gly Val Ser Leu Trp Trp Pro Tyr Leu Met His Glu Arg Pro Ala Tyr
515 520 525

Leu Tyr Ser Leu Glu Val Gln Leu Thr Ala Gln Thr Ser Leu Gly Pro
530 535 540

Val Ser Asp Phe Tyr Thr Leu Pro Val Gly Ile Arg Thr Val Ala Val
545 550 555 560

Thr Lys Ser Gln Phe Leu Ile Asn Gly Lys Pro Phe Tyr Phe His Gly
565 570 575

Val Asn Lys His Glu Asp Ala Asp Ile Arg Gly Lys Gly Phe Asp Trp
580 585 590

Pro Leu Leu Val Lys Asp Phe Asn Leu Leu Arg Trp Leu Gly Ala Asn
595 600 605

Ala Phe Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu Val Met Gln Met
610 615 620

Cys Asp Arg Tyr Gly Ile Val Val Ile Asp Glu Cys Pro Gly Val Gly
625 630 635 640

Leu Ala Leu Pro Gln Phe Phe Asn Asn Val Ser Leu His His His Met
645 650 655

Gln Val Met Glu Glu Val Val Arg Arg Asp Lys Asn His Pro Ala Val
660 665 670

Val Met Trp Ser Val Ala Asn Glu Pro Ala Ser His Leu Glu Ser Ala
675 680 685

Gly Tyr Tyr Leu Lys Met Val Ile Ala His Thr Lys Ser Leu Asp Pro
690 695 700

Ser Arg Pro Val Thr Phe Val Ser Asn Ser Asn Tyr Ala Ala Asp Lys
705 710 715 720

Gly Ala Pro Tyr Val Asp Val Ile Cys Leu Asn Ser Tyr Tyr Ser Trp
725 730 735

Tyr His Asp Tyr Gly His Leu Glu Leu Ile Gln Leu Gln Leu Ala Thr
740 745 750

Gln Phe Glu Asn Trp Tyr Lys Lys Tyr Gln Lys Pro Ile Ile Gln Ser
755 760 765

Glu Tyr Gly Ala Glu Thr Ile Ala Gly Phe His Gln Asp Pro Pro Leu
770 775 780

Met Phe Thr Glu Glu Tyr Gln Lys Ser Leu Leu Glu Gln Tyr His Leu
785 790 795 800

Gly Leu Asp Gln Lys Arg Arg Lys Tyr Val Val Gly Glu Leu Ile Trp
805 810 815

Asn Phe Ala Asp Phe Met Thr Glu Gln Ser Pro Thr Arg Val Leu Gly
820 825 830

Asn Lys Lys Gly Ile Phe Thr Arg Gln Arg Gln Pro Lys Ser Ala Ala
835 840 845

Phe Leu Leu Arg Glu Arg Tyr Trp Lys Ile Ala Asn Glu Thr Arg Tyr
850 855 860

Pro His Ser Val Ala Lys Ser Gln Cys Leu Glu Asn Ser Leu Phe Thr
865 870 875 880

<210> 156
<211> 905
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of humanized anti-hTfR antibody No. 3N and hGUSB, Fab HC-GS10-GUSB

<400> 156

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

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

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

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

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Leu Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro
275 280 285

Ser Arg Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp
290 295 300

Phe Ser Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg
305 310 315 320

Pro Leu Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro Ser Ser
325 330 335

Phe Asn Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp
340 345 350

Val Trp Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp
355 360 365

Leu Arg Thr Arg Val Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala
370 375 380

Ile Val Trp Val Asn Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr
385 390 395 400

Leu Pro Phe Glu Ala Asp Ile Ser Asn Leu Val Gln Val Gly Pro Leu
405 410 415

Pro Ser Arg Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro
420 425 430

Thr Thr Leu Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys
435 440 445

Tyr Pro Lys Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn
450 455 460

Tyr Ala Gly Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr
465 470 475 480

Tyr Ile Asp Asp Ile Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly
485 490 495

Leu Val Asn Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu
500 505 510

Glu Val Arg Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr
515 520 525

Gly Thr Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro
530 535 540

Tyr Leu Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln
545 550 555 560

Leu Thr Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu

565

570

575

Pro Val Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe Leu Ile
 580 585 590

Asn Gly Lys Pro Phe Tyr Phe His Gly Val Asn Lys His Glu Asp Ala
 595 600 605

Asp Ile Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe
 610 615 620

Asn Leu Leu Arg Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser His Tyr
 625 630 635 640

Pro Tyr Ala Glu Glu Val Met Gln Met Cys Asp Arg Tyr Gly Ile Val
 645 650 655

Val Ile Asp Glu Cys Pro Gly Val Gly Leu Ala Leu Pro Gln Phe Phe
 660 665 670

Asn Asn Val Ser Leu His His His Met Gln Val Met Glu Glu Val Val
 675 680 685

Arg Arg Asp Lys Asn His Pro Ala Val Val Met Trp Ser Val Ala Asn
 690 695 700

Glu Pro Ala Ser His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val
 705 710 715 720

Ile Ala His Thr Lys Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val
 725 730 735

Ser Asn Ser Asn Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val
 740 745 750

Ile Cys Leu Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu
 755 760 765

Glu Leu Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys
770 775 780

Lys Tyr Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile
785 790 795 800

Ala Gly Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr Gln
805 810 815

Lys Ser Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys Arg Arg
820 825 830

Lys Tyr Val Val Gly Glu Leu Ile Trp Asn Phe Ala Asp Phe Met Thr
835 840 845

Glu Gln Ser Pro Thr Arg Val Leu Gly Asn Lys Lys Gly Ile Phe Thr
850 855 860

Arg Gln Arg Gln Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu Arg Tyr
865 870 875 880

Trp Lys Ile Ala Asn Glu Thr Arg Tyr Pro His Ser Val Ala Lys Ser
885 890 895

Gln Cys Leu Glu Asn Ser Leu Phe Thr
900 905

<210> 157

<211> 955

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hGUSB, Fab HC-GS20-GUSB

<400> 157

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195

200

205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 290 295 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 305 310 315 320

Ser Gly Gly Gly Gly Ser Leu Gln Gly Gly Met Leu Tyr Pro Gln Glu
 325 330 335

Ser Pro Ser Arg Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg
 340 345 350

Ala Asp Phe Ser Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr
 355 360 365

Arg Arg Pro Leu Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro
 370 375 380

Ser Ser Phe Asn Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val
 385 390 395 400

Gly Trp Val Trp Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr
405 410 415

Gln Asp Leu Arg Thr Arg Val Val Leu Arg Ile Gly Ser Ala His Ser
420 425 430

Tyr Ala Ile Val Trp Val Asn Gly Val Asp Thr Leu Glu His Glu Gly
435 440 445

Gly Tyr Leu Pro Phe Glu Ala Asp Ile Ser Asn Leu Val Gln Val Gly
450 455 460

Pro Leu Pro Ser Arg Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu
465 470 475 480

Thr Pro Thr Thr Leu Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr
485 490 495

Ser Lys Tyr Pro Lys Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe
500 505 510

Phe Asn Tyr Ala Gly Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro
515 520 525

Thr Thr Tyr Ile Asp Asp Ile Thr Val Thr Thr Ser Val Glu Gln Asp
530 535 540

Ser Gly Leu Val Asn Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe
545 550 555 560

Lys Leu Glu Val Arg Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn
565 570 575

Gly Thr Gly Thr Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp
580 585 590

Trp Pro Tyr Leu Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu
595 600 605

Val Gln Leu Thr Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr
610 615 620

Thr Leu Pro Val Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe
625 630 635 640

Leu Ile Asn Gly Lys Pro Phe Tyr Phe His Gly Val Asn Lys His Glu
645 650 655

Asp Ala Asp Ile Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys
660 665 670

Asp Phe Asn Leu Leu Arg Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser
675 680 685

His Tyr Pro Tyr Ala Glu Glu Val Met Gln Met Cys Asp Arg Tyr Gly
690 695 700

Ile Val Val Ile Asp Glu Cys Pro Gly Val Gly Leu Ala Leu Pro Gln
705 710 715 720

Phe Phe Asn Asn Val Ser Leu His His His Met Gln Val Met Glu Glu
725 730 735

Val Val Arg Arg Asp Lys Asn His Pro Ala Val Val Met Trp Ser Val
740 745 750

Ala Asn Glu Pro Ala Ser His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys
755 760 765

Met Val Ile Ala His Thr Lys Ser Leu Asp Pro Ser Arg Pro Val Thr
770 775 780

Phe Val Ser Asn Ser Asn Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val
785 790 795 800

Asp Val Ile Cys Leu Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly
805 810 815

His Leu Glu Leu Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp
820 825 830

Tyr Lys Lys Tyr Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu
835 840 845

Thr Ile Ala Gly Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu
850 855 860

Tyr Gln Lys Ser Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys
865 870 875 880

Arg Arg Lys Tyr Val Val Gly Glu Leu Ile Trp Asn Phe Ala Asp Phe
885 890 895

Met Thr Glu Gln Ser Pro Thr Arg Val Leu Gly Asn Lys Lys Gly Ile
900 905 910

Phe Thr Arg Gln Arg Gln Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu
915 920 925

Arg Tyr Trp Lys Ile Ala Asn Glu Thr Arg Tyr Pro His Ser Val Ala
930 935 940

Lys Ser Gln Cys Leu Glu Asn Ser Leu Phe Thr
945 950 955

<210> 158
<211> 1090
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hGALC, IgG4 HC-GALC

<400> 158

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Tyr
435 440 445

Val Leu Asp Asp Ser Asp Gly Leu Gly Arg Glu Phe Asp Gly Ile Gly
450 455 460

Ala Val Ser Gly Gly Gly Ala Thr Ser Arg Leu Leu Val Asn Tyr Pro
465 470 475 480

Glu Pro Tyr Arg Ser Gln Ile Leu Asp Tyr Leu Phe Lys Pro Asn Phe
485 490 495

Gly Ala Ser Leu His Ile Leu Lys Val Glu Ile Gly Gly Asp Gly Gln
500 505 510

Thr Thr Asp Gly Thr Glu Pro Ser His Met His Tyr Ala Leu Asp Glu
515 520 525

Asn Tyr Phe Arg Gly Tyr Glu Trp Trp Leu Met Lys Glu Ala Lys Lys
530 535 540

Arg Asn Pro Asn Ile Thr Leu Ile Gly Leu Pro Trp Ser Phe Pro Gly
545 550 555 560

Trp Leu Gly Lys Gly Phe Asp Trp Pro Tyr Val Asn Leu Gln Leu Thr
565 570 575

Ala Tyr Tyr Val Val Thr Trp Ile Val Gly Ala Lys Arg Tyr His Asp
580 585 590

Leu Asp Ile Asp Tyr Ile Gly Ile Trp Asn Glu Arg Ser Tyr Asn Ala
595 600 605

Asn Tyr Ile Lys Ile Leu Arg Lys Met Leu Asn Tyr Gln Gly Leu Gln
610 615 620

Arg Val Lys Ile Ile Ala Ser Asp Asn Leu Trp Glu Ser Ile Ser Ala
625 630 635 640

Ser Met Leu Leu Asp Ala Glu Leu Phe Lys Val Val Asp Val Ile Gly
645 650 655

Ala His Tyr Pro Gly Thr His Ser Ala Lys Asp Ala Lys Leu Thr Gly
660 665 670

Lys Lys Leu Trp Ser Ser Glu Asp Phe Ser Thr Leu Asn Ser Asp Met
675 680 685

Gly Ala Gly Cys Trp Gly Arg Ile Leu Asn Gln Asn Tyr Ile Asn Gly
690 695 700

Tyr Met Thr Ser Thr Ile Ala Trp Asn Leu Val Ala Ser Tyr Tyr Glu
705 710 715 720

Gln Leu Pro Tyr Gly Arg Cys Gly Leu Met Thr Ala Gln Glu Pro Trp
725 730 735

Ser Gly His Tyr Val Val Glu Ser Pro Val Trp Val Ser Ala His Thr
740 745 750

Thr Gln Phe Thr Gln Pro Gly Trp Tyr Tyr Leu Lys Thr Val Gly His

755

760

765

Leu Glu Lys Gly Gly Ser Tyr Val Ala Leu Thr Asp Gly Leu Gly Asn
 770 775 780

Leu Thr Ile Ile Ile Glu Thr Met Ser His Lys His Ser Lys Cys Ile
 785 790 795 800

Arg Pro Phe Leu Pro Tyr Phe Asn Val Ser Gln Gln Phe Ala Thr Phe
 805 810 815

Val Leu Lys Gly Ser Phe Ser Glu Ile Pro Glu Leu Gln Val Trp Tyr
 820 825 830

Thr Lys Leu Gly Lys Thr Ser Glu Arg Phe Leu Phe Lys Gln Leu Asp
 835 840 845

Ser Leu Trp Leu Leu Asp Ser Asp Gly Ser Phe Thr Leu Ser Leu His
 850 855 860

Glu Asp Glu Leu Phe Thr Leu Thr Thr Leu Thr Thr Gly Arg Lys Gly
 865 870 875 880

Ser Tyr Pro Leu Pro Pro Lys Ser Gln Pro Phe Pro Ser Thr Tyr Lys
 885 890 895

Asp Asp Phe Asn Val Asp Tyr Pro Phe Phe Ser Glu Ala Pro Asn Phe
 900 905 910

Ala Asp Gln Thr Gly Val Phe Glu Tyr Phe Thr Asn Ile Glu Asp Pro
 915 920 925

Gly Glu His His Phe Thr Leu Arg Gln Val Leu Asn Gln Arg Pro Ile
 930 935 940

Thr Trp Ala Ala Asp Ala Ser Asn Thr Ile Ser Ile Ile Gly Asp Tyr
 945 950 955 960

Asn Trp Thr Asn Leu Thr Ile Lys Cys Asp Val Tyr Ile Glu Thr Pro
965 970 975

Asp Thr Gly Gly Val Phe Ile Ala Gly Arg Val Asn Lys Gly Gly Ile
980 985 990

Leu Ile Arg Ser Ala Arg Gly Ile Phe Phe Trp Ile Phe Ala Asn Gly
995 1000 1005

Ser Tyr Arg Val Thr Gly Asp Leu Ala Gly Trp Ile Ile Tyr Ala
1010 1015 1020

Leu Gly Arg Val Glu Val Thr Ala Lys Lys Trp Tyr Thr Leu Thr
1025 1030 1035

Leu Thr Ile Lys Gly His Phe Thr Ser Gly Met Leu Asn Asp Lys
1040 1045 1050

Ser Leu Trp Thr Asp Ile Pro Val Asn Phe Pro Lys Asn Gly Trp
1055 1060 1065

Ala Ala Ile Gly Thr His Ser Phe Glu Phe Ala Gln Phe Asp Asn
1070 1075 1080

Phe Leu Val Glu Ala Thr Arg
1085 1090

<210> 159

<211> 1113

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hGALC, IgG4
HC-GS5-GALC

<400> 159

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Tyr Val Leu Asp Asp Ser Asp Gly Leu Gly
465 470 475 480

Arg Glu Phe Asp Gly Ile Gly Ala Val Ser Gly Gly Gly Ala Thr Ser
485 490 495

Arg Leu Leu Val Asn Tyr Pro Glu Pro Tyr Arg Ser Gln Ile Leu Asp
500 505 510

Tyr Leu Phe Lys Pro Asn Phe Gly Ala Ser Leu His Ile Leu Lys Val
515 520 525

Glu Ile Gly Gly Asp Gly Gln Thr Thr Asp Gly Thr Glu Pro Ser His
530 535 540

Met His Tyr Ala Leu Asp Glu Asn Tyr Phe Arg Gly Tyr Glu Trp Trp
545 550 555 560

Leu Met Lys Glu Ala Lys Lys Arg Asn Pro Asn Ile Thr Leu Ile Gly
565 570 575

Leu Pro Trp Ser Phe Pro Gly Trp Leu Gly Lys Gly Phe Asp Trp Pro
580 585 590

Tyr Val Asn Leu Gln Leu Thr Ala Tyr Tyr Val Val Thr Trp Ile Val
595 600 605

Gly Ala Lys Arg Tyr His Asp Leu Asp Ile Asp Tyr Ile Gly Ile Trp
610 615 620

Asn Glu Arg Ser Tyr Asn Ala Asn Tyr Ile Lys Ile Leu Arg Lys Met
625 630 635 640

Leu Asn Tyr Gln Gly Leu Gln Arg Val Lys Ile Ile Ala Ser Asp Asn
645 650 655

Leu Trp Glu Ser Ile Ser Ala Ser Met Leu Leu Asp Ala Glu Leu Phe
660 665 670

Lys Val Val Asp Val Ile Gly Ala His Tyr Pro Gly Thr His Ser Ala
675 680 685

Lys Asp Ala Lys Leu Thr Gly Lys Lys Leu Trp Ser Ser Glu Asp Phe
690 695 700

Ser Thr Leu Asn Ser Asp Met Gly Ala Gly Cys Trp Gly Arg Ile Leu
705 710 715 720

Asn Gln Asn Tyr Ile Asn Gly Tyr Met Thr Ser Thr Ile Ala Trp Asn
725 730 735

Leu Val Ala Ser Tyr Tyr Glu Gln Leu Pro Tyr Gly Arg Cys Gly Leu
740 745 750

Met Thr Ala Gln Glu Pro Trp Ser Gly His Tyr Val Val Glu Ser Pro
755 760 765

Val Trp Val Ser Ala His Thr Thr Gln Phe Thr Gln Pro Gly Trp Tyr
770 775 780

Tyr Leu Lys Thr Val Gly His Leu Glu Lys Gly Gly Ser Tyr Val Ala
785 790 795 800

Leu Thr Asp Gly Leu Gly Asn Leu Thr Ile Ile Ile Glu Thr Met Ser
805 810 815

His Lys His Ser Lys Cys Ile Arg Pro Phe Leu Pro Tyr Phe Asn Val
820 825 830

Ser Gln Gln Phe Ala Thr Phe Val Leu Lys Gly Ser Phe Ser Glu Ile
835 840 845

Pro Glu Leu Gln Val Trp Tyr Thr Lys Leu Gly Lys Thr Ser Glu Arg
850 855 860

Phe Leu Phe Lys Gln Leu Asp Ser Leu Trp Leu Leu Asp Ser Asp Gly
865 870 875 880

Ser Phe Thr Leu Ser Leu His Glu Asp Glu Leu Phe Thr Leu Thr Thr
885 890 895

Leu Thr Thr Gly Arg Lys Gly Ser Tyr Pro Leu Pro Pro Lys Ser Gln
900 905 910

Pro Phe Pro Ser Thr Tyr Lys Asp Asp Phe Asn Val Asp Tyr Pro Phe
915 920 925

Phe Ser Glu Ala Pro Asn Phe Ala Asp Gln Thr Gly Val Phe Glu Tyr
930 935 940

Phe Thr Asn Ile Glu Asp Pro Gly Glu His His Phe Thr Leu Arg Gln
945 950 955 960

Val Leu Asn Gln Arg Pro Ile Thr Trp Ala Ala Asp Ala Ser Asn Thr
965 970 975

Ile Ser Ile Ile Gly Asp Tyr Asn Trp Thr Asn Leu Thr Ile Lys Cys
980 985 990

Asp Val Tyr Ile Glu Thr Pro Asp Thr Gly Gly Val Phe Ile Ala Gly
995 1000 1005

Arg Val Asn Lys Gly Gly Ile Leu Ile Arg Ser Ala Arg Gly Ile
1010 1015 1020

Phe Phe Trp Ile Phe Ala Asn Gly Ser Tyr Arg Val Thr Gly Asp
1025 1030 1035

Leu Ala Gly Trp Ile Ile Tyr Ala Leu Gly Arg Val Glu Val Thr
1040 1045 1050

Ala Lys Lys Trp Tyr Thr Leu Thr Leu Thr Ile Lys Gly His Phe
1055 1060 1065

Thr Ser Gly Met Leu Asn Asp Lys Ser Leu Trp Thr Asp Ile Pro
1070 1075 1080

Val Asn Phe Pro Lys Asn Gly Trp Ala Ala Ile Gly Thr His Ser
1085 1090 1095

Phe Glu Phe Ala Gln Phe Asp Asn Phe Leu Val Glu Ala Thr Arg
1100 1105 1110

<210> 160

<211> 1138

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hGALC, IgG4
HC-GS10-GALC

<400> 160

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu

1	5	10	15
Ser	Leu	Lys	Ile
	20		
Ser	Cys	Lys	Gly
		25	
Ser	Gly	Tyr	Ser
			30
Phe	Met	Asn	Tyr
Trp	Leu	Gly	Trp
	35		
Val	Arg	Gln	Met
		40	
Pro	Gly	Lys	Gly
			45
Leu	Glu	Trp	Met
Gly	Asp	Ile	Tyr
	50		
Pro	Gly	Gly	Asp
		55	
Tyr	Pro	Thr	Tyr
			60
Ser	Glu	Lys	Phe
Lys	Val	Gln	Val
	65		
Thr	Ile	Ser	Ala
	70		
Asp	Lys	Ser	Ile
		75	
Ser	Thr	Ala	Tyr
			80
Leu	Gln	Leu	Ser
		85	
Ser	Leu	Lys	Ala
			90
Ser	Asp	Thr	Ala
			95
Met	Tyr	Tyr	Cys
Ala	Arg	Ser	Gly
		100	
Asn	Tyr	Asp	Glu
			105
Val	Ala	Tyr	Trp
			110
Gln	Gly	Thr	
Leu	Val	Thr	Val
	115		
Ser	Ser	Ala	Ser
			120
Thr	Lys	Gly	Pro
			125
Ser	Val	Phe	Pro
Leu	Ala	Pro	Cys
	130		
Ser	Arg	Ser	Thr
		135	
Ser	Glu	Ser	Thr
			140
Ala	Ala	Leu	Gly
Cys	Leu	Val	Lys
	145		
Asp	Tyr	Phe	Pro
		150	
Glu	Pro	Val	Thr
		155	
Val	Ser	Trp	Asn
			160
Ser	Gly	Ala	Leu
		165	
Ser	Gly	Val	His
			170
Thr	Phe	Pro	Ala
			175
Val	Leu	Gln	
Ser	Ser	Gly	Leu
		180	
Tyr	Ser	Leu	Ser
			185
Ser	Val	Val	Thr
			190
Pro	Ser	Ser	
Ser	Leu	Gly	Thr
	195		
Lys	Thr	Tyr	Thr
			200
Cys	Asn	Val	Asp
			205
His	Lys	Pro	Ser

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Tyr
485 490 495

Val Leu Asp Asp Ser Asp Gly Leu Gly Arg Glu Phe Asp Gly Ile Gly
500 505 510

Ala Val Ser Gly Gly Gly Ala Thr Ser Arg Leu Leu Val Asn Tyr Pro
515 520 525

Glu Pro Tyr Arg Ser Gln Ile Leu Asp Tyr Leu Phe Lys Pro Asn Phe
530 535 540

Gly Ala Ser Leu His Ile Leu Lys Val Glu Ile Gly Gly Asp Gly Gln
545 550 555 560

Thr Thr Asp Gly Thr Glu Pro Ser His Met His Tyr Ala Leu Asp Glu
565 570 575

Asn Tyr Phe Arg Gly Tyr Glu Trp Trp Leu Met Lys Glu Ala Lys Lys
580 585 590

Arg Asn Pro Asn Ile Thr Leu Ile Gly Leu Pro Trp Ser Phe Pro Gly
595 600 605

Trp Leu Gly Lys Gly Phe Asp Trp Pro Tyr Val Asn Leu Gln Leu Thr
610 615 620

Ala Tyr Tyr Val Val Thr Trp Ile Val Gly Ala Lys Arg Tyr His Asp
625 630 635 640

Leu Asp Ile Asp Tyr Ile Gly Ile Trp Asn Glu Arg Ser Tyr Asn Ala
645 650 655

Asn Tyr Ile Lys Ile Leu Arg Lys Met Leu Asn Tyr Gln Gly Leu Gln
660 665 670

Arg Val Lys Ile Ile Ala Ser Asp Asn Leu Trp Glu Ser Ile Ser Ala
675 680 685

Ser Met Leu Leu Asp Ala Glu Leu Phe Lys Val Val Asp Val Ile Gly
690 695 700

Ala His Tyr Pro Gly Thr His Ser Ala Lys Asp Ala Lys Leu Thr Gly
705 710 715 720

Lys Lys Leu Trp Ser Ser Glu Asp Phe Ser Thr Leu Asn Ser Asp Met
725 730 735

Gly Ala Gly Cys Trp Gly Arg Ile Leu Asn Gln Asn Tyr Ile Asn Gly
740 745 750

Tyr Met Thr Ser Thr Ile Ala Trp Asn Leu Val Ala Ser Tyr Tyr Glu
755 760 765

Gln Leu Pro Tyr Gly Arg Cys Gly Leu Met Thr Ala Gln Glu Pro Trp
770 775 780

Ser Gly His Tyr Val Val Glu Ser Pro Val Trp Val Ser Ala His Thr

785					790					795					800
Thr	Gln	Phe	Thr	Gln 805	Pro	Gly	Trp	Tyr	Tyr 810	Leu	Lys	Thr	Val	Gly 815	His
Leu	Glu	Lys	Gly 820	Gly	Ser	Tyr	Val	Ala 825	Leu	Thr	Asp	Gly	Leu 830	Gly	Asn
Leu	Thr	Ile 835	Ile	Ile	Glu	Thr	Met 840	Ser	His	Lys	His	Ser 845	Lys	Cys	Ile
Arg	Pro 850	Phe	Leu	Pro	Tyr	Phe 855	Asn	Val	Ser	Gln	Gln 860	Phe	Ala	Thr	Phe
Val 865	Leu	Lys	Gly	Ser 870	Phe	Ser	Glu	Ile	Pro	Glu 875	Leu	Gln	Val	Trp	Tyr 880
Thr	Lys	Leu	Gly	Lys 885	Thr	Ser	Glu	Arg	Phe 890	Leu	Phe	Lys	Gln	Leu 895	Asp
Ser	Leu	Trp	Leu 900	Leu	Asp	Ser	Asp	Gly 905	Ser	Phe	Thr	Leu	Ser 910	Leu	His
Glu	Asp	Glu 915	Leu	Phe	Thr	Leu	Thr 920	Thr	Leu	Thr	Thr	Gly 925	Arg	Lys	Gly
Ser	Tyr 930	Pro	Leu	Pro	Pro	Lys 935	Ser	Gln	Pro	Phe	Pro 940	Ser	Thr	Tyr	Lys
Asp 945	Asp	Phe	Asn	Val	Asp 950	Tyr	Pro	Phe	Phe	Ser 955	Glu	Ala	Pro	Asn	Phe 960
Ala	Asp	Gln	Thr	Gly 965	Val	Phe	Glu	Tyr	Phe 970	Thr	Asn	Ile	Glu	Asp 975	Pro
Gly	Glu	His	His 980	Phe	Thr	Leu	Arg	Gln 985	Val	Leu	Asn	Gln	Arg 990	Pro	Ile

Thr Trp Ala Ala Asp Ala Ser Asn Thr Ile Ser Ile Ile Gly Asp Tyr
995 1000 1005

Asn Trp Thr Asn Leu Thr Ile Lys Cys Asp Val Tyr Ile Glu Thr
1010 1015 1020

Pro Asp Thr Gly Gly Val Phe Ile Ala Gly Arg Val Asn Lys Gly
1025 1030 1035

Gly Ile Leu Ile Arg Ser Ala Arg Gly Ile Phe Phe Trp Ile Phe
1040 1045 1050

Ala Asn Gly Ser Tyr Arg Val Thr Gly Asp Leu Ala Gly Trp Ile
1055 1060 1065

Ile Tyr Ala Leu Gly Arg Val Glu Val Thr Ala Lys Lys Trp Tyr
1070 1075 1080

Thr Leu Thr Leu Thr Ile Lys Gly His Phe Thr Ser Gly Met Leu
1085 1090 1095

Asn Asp Lys Ser Leu Trp Thr Asp Ile Pro Val Asn Phe Pro Lys
1100 1105 1110

Asn Gly Trp Ala Ala Ile Gly Thr His Ser Phe Glu Phe Ala Gln
1115 1120 1125

Phe Asp Asn Phe Leu Val Glu Ala Thr Arg
1130 1135

<210> 161

<211> 1188

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of

humanized anti-hTfR antibody No. 3N (IgG4) and hGALC, IgG4
HC-GS20-GALC

<400> 161

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

370

375

380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
 405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
 435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 530 535 540

Ser Tyr Val Leu Asp Asp Ser Asp Gly Leu Gly Arg Glu Phe Asp Gly
 545 550 555 560

Ile Gly Ala Val Ser Gly Gly Gly Ala Thr Ser Arg Leu Leu Val Asn
 565 570 575

Tyr Pro Glu Pro Tyr Arg Ser Gln Ile Leu Asp Tyr Leu Phe Lys Pro
580 585 590

Asn Phe Gly Ala Ser Leu His Ile Leu Lys Val Glu Ile Gly Gly Asp
595 600 605

Gly Gln Thr Thr Asp Gly Thr Glu Pro Ser His Met His Tyr Ala Leu
610 615 620

Asp Glu Asn Tyr Phe Arg Gly Tyr Glu Trp Trp Leu Met Lys Glu Ala
625 630 635 640

Lys Lys Arg Asn Pro Asn Ile Thr Leu Ile Gly Leu Pro Trp Ser Phe
645 650 655

Pro Gly Trp Leu Gly Lys Gly Phe Asp Trp Pro Tyr Val Asn Leu Gln
660 665 670

Leu Thr Ala Tyr Tyr Val Val Thr Trp Ile Val Gly Ala Lys Arg Tyr
675 680 685

His Asp Leu Asp Ile Asp Tyr Ile Gly Ile Trp Asn Glu Arg Ser Tyr
690 695 700

Asn Ala Asn Tyr Ile Lys Ile Leu Arg Lys Met Leu Asn Tyr Gln Gly
705 710 715 720

Leu Gln Arg Val Lys Ile Ile Ala Ser Asp Asn Leu Trp Glu Ser Ile
725 730 735

Ser Ala Ser Met Leu Leu Asp Ala Glu Leu Phe Lys Val Val Asp Val
740 745 750

Ile Gly Ala His Tyr Pro Gly Thr His Ser Ala Lys Asp Ala Lys Leu
755 760 765

Thr Gly Lys Lys Leu Trp Ser Ser Glu Asp Phe Ser Thr Leu Asn Ser
770 775 780

Asp Met Gly Ala Gly Cys Trp Gly Arg Ile Leu Asn Gln Asn Tyr Ile
785 790 795 800

Asn Gly Tyr Met Thr Ser Thr Ile Ala Trp Asn Leu Val Ala Ser Tyr
805 810 815

Tyr Glu Gln Leu Pro Tyr Gly Arg Cys Gly Leu Met Thr Ala Gln Glu
820 825 830

Pro Trp Ser Gly His Tyr Val Val Glu Ser Pro Val Trp Val Ser Ala
835 840 845

His Thr Thr Gln Phe Thr Gln Pro Gly Trp Tyr Tyr Leu Lys Thr Val
850 855 860

Gly His Leu Glu Lys Gly Gly Ser Tyr Val Ala Leu Thr Asp Gly Leu
865 870 875 880

Gly Asn Leu Thr Ile Ile Ile Glu Thr Met Ser His Lys His Ser Lys
885 890 895

Cys Ile Arg Pro Phe Leu Pro Tyr Phe Asn Val Ser Gln Gln Phe Ala
900 905 910

Thr Phe Val Leu Lys Gly Ser Phe Ser Glu Ile Pro Glu Leu Gln Val
915 920 925

Trp Tyr Thr Lys Leu Gly Lys Thr Ser Glu Arg Phe Leu Phe Lys Gln
930 935 940

Leu Asp Ser Leu Trp Leu Leu Asp Ser Asp Gly Ser Phe Thr Leu Ser
945 950 955 960

Leu His Glu Asp Glu Leu Phe Thr Leu Thr Thr Leu Thr Thr Gly Arg
965 970 975

Lys Gly Ser Tyr Pro Leu Pro Pro Lys Ser Gln Pro Phe Pro Ser Thr
980 985 990

Tyr Lys Asp Asp Phe Asn Val Asp Tyr Pro Phe Phe Ser Glu Ala Pro
995 1000 1005

Asn Phe Ala Asp Gln Thr Gly Val Phe Glu Tyr Phe Thr Asn Ile
1010 1015 1020

Glu Asp Pro Gly Glu His His Phe Thr Leu Arg Gln Val Leu Asn
1025 1030 1035

Gln Arg Pro Ile Thr Trp Ala Ala Asp Ala Ser Asn Thr Ile Ser
1040 1045 1050

Ile Ile Gly Asp Tyr Asn Trp Thr Asn Leu Thr Ile Lys Cys Asp
1055 1060 1065

Val Tyr Ile Glu Thr Pro Asp Thr Gly Gly Val Phe Ile Ala Gly
1070 1075 1080

Arg Val Asn Lys Gly Gly Ile Leu Ile Arg Ser Ala Arg Gly Ile
1085 1090 1095

Phe Phe Trp Ile Phe Ala Asn Gly Ser Tyr Arg Val Thr Gly Asp
1100 1105 1110

Leu Ala Gly Trp Ile Ile Tyr Ala Leu Gly Arg Val Glu Val Thr
1115 1120 1125

Ala Lys Lys Trp Tyr Thr Leu Thr Leu Thr Ile Lys Gly His Phe
1130 1135 1140

Thr Ser Gly Met Leu Asn Asp Lys Ser Leu Trp Thr Asp Ile Pro

1145

1150

1155

Val Asn Phe Pro Lys Asn Gly Trp Ala Ala Ile Gly Thr His Ser
 1160 1165 1170

Phe Glu Phe Ala Gln Phe Asp Asn Phe Leu Val Glu Ala Thr Arg
 1175 1180 1185

<210> 162

<211> 884

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
 humanized anti-hTfR antibody No. 3N and hGALC, Fab HC-GS3-GALC

<400> 162

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
 50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Tyr Val Leu Asp Asp Ser Asp Gly Leu Gly Arg Glu Phe Asp Gly
245 250 255

Ile Gly Ala Val Ser Gly Gly Gly Ala Thr Ser Arg Leu Leu Val Asn
260 265 270

Tyr Pro Glu Pro Tyr Arg Ser Gln Ile Leu Asp Tyr Leu Phe Lys Pro
275 280 285

Asn Phe Gly Ala Ser Leu His Ile Leu Lys Val Glu Ile Gly Gly Asp
290 295 300

Gly Gln Thr Thr Asp Gly Thr Glu Pro Ser His Met His Tyr Ala Leu
305 310 315 320

Asp Glu Asn Tyr Phe Arg Gly Tyr Glu Trp Trp Leu Met Lys Glu Ala
325 330 335

Lys Lys Arg Asn Pro Asn Ile Thr Leu Ile Gly Leu Pro Trp Ser Phe
340 345 350

Pro Gly Trp Leu Gly Lys Gly Phe Asp Trp Pro Tyr Val Asn Leu Gln
355 360 365

Leu Thr Ala Tyr Tyr Val Val Thr Trp Ile Val Gly Ala Lys Arg Tyr
370 375 380

His Asp Leu Asp Ile Asp Tyr Ile Gly Ile Trp Asn Glu Arg Ser Tyr
385 390 395 400

Asn Ala Asn Tyr Ile Lys Ile Leu Arg Lys Met Leu Asn Tyr Gln Gly
405 410 415

Leu Gln Arg Val Lys Ile Ile Ala Ser Asp Asn Leu Trp Glu Ser Ile
420 425 430

Ser Ala Ser Met Leu Leu Asp Ala Glu Leu Phe Lys Val Val Asp Val
435 440 445

Ile Gly Ala His Tyr Pro Gly Thr His Ser Ala Lys Asp Ala Lys Leu
450 455 460

Thr Gly Lys Lys Leu Trp Ser Ser Glu Asp Phe Ser Thr Leu Asn Ser
465 470 475 480

Asp Met Gly Ala Gly Cys Trp Gly Arg Ile Leu Asn Gln Asn Tyr Ile
485 490 495

Asn Gly Tyr Met Thr Ser Thr Ile Ala Trp Asn Leu Val Ala Ser Tyr

500

505

510

Tyr Glu Gln Leu Pro Tyr Gly Arg Cys Gly Leu Met Thr Ala Gln Glu
 515 520 525

Pro Trp Ser Gly His Tyr Val Val Glu Ser Pro Val Trp Val Ser Ala
 530 535 540

His Thr Thr Gln Phe Thr Gln Pro Gly Trp Tyr Tyr Leu Lys Thr Val
 545 550 555 560

Gly His Leu Glu Lys Gly Gly Ser Tyr Val Ala Leu Thr Asp Gly Leu
 565 570 575

Gly Asn Leu Thr Ile Ile Ile Glu Thr Met Ser His Lys His Ser Lys
 580 585 590

Cys Ile Arg Pro Phe Leu Pro Tyr Phe Asn Val Ser Gln Gln Phe Ala
 595 600 605

Thr Phe Val Leu Lys Gly Ser Phe Ser Glu Ile Pro Glu Leu Gln Val
 610 615 620

Trp Tyr Thr Lys Leu Gly Lys Thr Ser Glu Arg Phe Leu Phe Lys Gln
 625 630 635 640

Leu Asp Ser Leu Trp Leu Leu Asp Ser Asp Gly Ser Phe Thr Leu Ser
 645 650 655

Leu His Glu Asp Glu Leu Phe Thr Leu Thr Thr Leu Thr Thr Gly Arg
 660 665 670

Lys Gly Ser Tyr Pro Leu Pro Pro Lys Ser Gln Pro Phe Pro Ser Thr
 675 680 685

Tyr Lys Asp Asp Phe Asn Val Asp Tyr Pro Phe Phe Ser Glu Ala Pro
 690 695 700

Asn Phe Ala Asp Gln Thr Gly Val Phe Glu Tyr Phe Thr Asn Ile Glu
705 710 715 720

Asp Pro Gly Glu His His Phe Thr Leu Arg Gln Val Leu Asn Gln Arg
725 730 735

Pro Ile Thr Trp Ala Ala Asp Ala Ser Asn Thr Ile Ser Ile Ile Gly
740 745 750

Asp Tyr Asn Trp Thr Asn Leu Thr Ile Lys Cys Asp Val Tyr Ile Glu
755 760 765

Thr Pro Asp Thr Gly Gly Val Phe Ile Ala Gly Arg Val Asn Lys Gly
770 775 780

Gly Ile Leu Ile Arg Ser Ala Arg Gly Ile Phe Phe Trp Ile Phe Ala
785 790 795 800

Asn Gly Ser Tyr Arg Val Thr Gly Asp Leu Ala Gly Trp Ile Ile Tyr
805 810 815

Ala Leu Gly Arg Val Glu Val Thr Ala Lys Lys Trp Tyr Thr Leu Thr
820 825 830

Leu Thr Ile Lys Gly His Phe Thr Ser Gly Met Leu Asn Asp Lys Ser
835 840 845

Leu Trp Thr Asp Ile Pro Val Asn Phe Pro Lys Asn Gly Trp Ala Ala
850 855 860

Ile Gly Thr His Ser Phe Glu Phe Ala Gln Phe Asp Asn Phe Leu Val
865 870 875 880

Glu Ala Thr Arg

<210> 163
<211> 894
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hGALC, Fab HC-GS5-GALC

<400> 163

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Tyr Val Leu Asp Asp
245 250 255

Ser Asp Gly Leu Gly Arg Glu Phe Asp Gly Ile Gly Ala Val Ser Gly
260 265 270

Gly Gly Ala Thr Ser Arg Leu Leu Val Asn Tyr Pro Glu Pro Tyr Arg
275 280 285

Ser Gln Ile Leu Asp Tyr Leu Phe Lys Pro Asn Phe Gly Ala Ser Leu
290 295 300

His Ile Leu Lys Val Glu Ile Gly Gly Asp Gly Gln Thr Thr Asp Gly
305 310 315 320

Thr Glu Pro Ser His Met His Tyr Ala Leu Asp Glu Asn Tyr Phe Arg
325 330 335

Gly Tyr Glu Trp Trp Leu Met Lys Glu Ala Lys Lys Arg Asn Pro Asn
340 345 350

Ile Thr Leu Ile Gly Leu Pro Trp Ser Phe Pro Gly Trp Leu Gly Lys
355 360 365

Gly Phe Asp Trp Pro Tyr Val Asn Leu Gln Leu Thr Ala Tyr Tyr Val
370 375 380

Val Thr Trp Ile Val Gly Ala Lys Arg Tyr His Asp Leu Asp Ile Asp
385 390 395 400

Tyr Ile Gly Ile Trp Asn Glu Arg Ser Tyr Asn Ala Asn Tyr Ile Lys
405 410 415

Ile Leu Arg Lys Met Leu Asn Tyr Gln Gly Leu Gln Arg Val Lys Ile
420 425 430

Ile Ala Ser Asp Asn Leu Trp Glu Ser Ile Ser Ala Ser Met Leu Leu
435 440 445

Asp Ala Glu Leu Phe Lys Val Val Asp Val Ile Gly Ala His Tyr Pro
450 455 460

Gly Thr His Ser Ala Lys Asp Ala Lys Leu Thr Gly Lys Lys Leu Trp
465 470 475 480

Ser Ser Glu Asp Phe Ser Thr Leu Asn Ser Asp Met Gly Ala Gly Cys
485 490 495

Trp Gly Arg Ile Leu Asn Gln Asn Tyr Ile Asn Gly Tyr Met Thr Ser
500 505 510

Thr Ile Ala Trp Asn Leu Val Ala Ser Tyr Tyr Glu Gln Leu Pro Tyr
515 520 525

Gly Arg Cys Gly Leu Met Thr Ala Gln Glu Pro Trp Ser Gly His Tyr
530 535 540

Val Val Glu Ser Pro Val Trp Val Ser Ala His Thr Thr Gln Phe Thr
 545 550 555 560

Gln Pro Gly Trp Tyr Tyr Leu Lys Thr Val Gly His Leu Glu Lys Gly
 565 570 575

Gly Ser Tyr Val Ala Leu Thr Asp Gly Leu Gly Asn Leu Thr Ile Ile
 580 585 590

Ile Glu Thr Met Ser His Lys His Ser Lys Cys Ile Arg Pro Phe Leu
 595 600 605

Pro Tyr Phe Asn Val Ser Gln Gln Phe Ala Thr Phe Val Leu Lys Gly
 610 615 620

Ser Phe Ser Glu Ile Pro Glu Leu Gln Val Trp Tyr Thr Lys Leu Gly
 625 630 635 640

Lys Thr Ser Glu Arg Phe Leu Phe Lys Gln Leu Asp Ser Leu Trp Leu
 645 650 655

Leu Asp Ser Asp Gly Ser Phe Thr Leu Ser Leu His Glu Asp Glu Leu
 660 665 670

Phe Thr Leu Thr Thr Leu Thr Thr Gly Arg Lys Gly Ser Tyr Pro Leu
 675 680 685

Pro Pro Lys Ser Gln Pro Phe Pro Ser Thr Tyr Lys Asp Asp Phe Asn
 690 695 700

Val Asp Tyr Pro Phe Phe Ser Glu Ala Pro Asn Phe Ala Asp Gln Thr
 705 710 715 720

Gly Val Phe Glu Tyr Phe Thr Asn Ile Glu Asp Pro Gly Glu His His
 725 730 735

Phe Thr Leu Arg Gln Val Leu Asn Gln Arg Pro Ile Thr Trp Ala Ala
740 745 750

Asp Ala Ser Asn Thr Ile Ser Ile Ile Gly Asp Tyr Asn Trp Thr Asn
755 760 765

Leu Thr Ile Lys Cys Asp Val Tyr Ile Glu Thr Pro Asp Thr Gly Gly
770 775 780

Val Phe Ile Ala Gly Arg Val Asn Lys Gly Gly Ile Leu Ile Arg Ser
785 790 795 800

Ala Arg Gly Ile Phe Phe Trp Ile Phe Ala Asn Gly Ser Tyr Arg Val
805 810 815

Thr Gly Asp Leu Ala Gly Trp Ile Ile Tyr Ala Leu Gly Arg Val Glu
820 825 830

Val Thr Ala Lys Lys Trp Tyr Thr Leu Thr Leu Thr Ile Lys Gly His
835 840 845

Phe Thr Ser Gly Met Leu Asn Asp Lys Ser Leu Trp Thr Asp Ile Pro
850 855 860

Val Asn Phe Pro Lys Asn Gly Trp Ala Ala Ile Gly Thr His Ser Phe
865 870 875 880

Glu Phe Ala Gln Phe Asp Asn Phe Leu Val Glu Ala Thr Arg
885 890

<210> 164

<211> 919

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hGALC, Fab HC-GS10-GALC

<400> 164

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Tyr Val Leu Asp Asp Ser Asp Gly Leu Gly Arg Glu
275 280 285

Phe Asp Gly Ile Gly Ala Val Ser Gly Gly Gly Ala Thr Ser Arg Leu
290 295 300

Leu Val Asn Tyr Pro Glu Pro Tyr Arg Ser Gln Ile Leu Asp Tyr Leu
305 310 315 320

Phe Lys Pro Asn Phe Gly Ala Ser Leu His Ile Leu Lys Val Glu Ile
325 330 335

Gly Gly Asp Gly Gln Thr Thr Asp Gly Thr Glu Pro Ser His Met His
340 345 350

Tyr Ala Leu Asp Glu Asn Tyr Phe Arg Gly Tyr Glu Trp Trp Leu Met
355 360 365

Lys Glu Ala Lys Lys Arg Asn Pro Asn Ile Thr Leu Ile Gly Leu Pro
370 375 380

Trp Ser Phe Pro Gly Trp Leu Gly Lys Gly Phe Asp Trp Pro Tyr Val
385 390 395 400

Asn Leu Gln Leu Thr Ala Tyr Tyr Val Val Thr Trp Ile Val Gly Ala
405 410 415

Lys Arg Tyr His Asp Leu Asp Ile Asp Tyr Ile Gly Ile Trp Asn Glu
420 425 430

Arg Ser Tyr Asn Ala Asn Tyr Ile Lys Ile Leu Arg Lys Met Leu Asn
435 440 445

Tyr Gln Gly Leu Gln Arg Val Lys Ile Ile Ala Ser Asp Asn Leu Trp
450 455 460

Glu Ser Ile Ser Ala Ser Met Leu Leu Asp Ala Glu Leu Phe Lys Val
465 470 475 480

Val Asp Val Ile Gly Ala His Tyr Pro Gly Thr His Ser Ala Lys Asp
485 490 495

Ala Lys Leu Thr Gly Lys Lys Leu Trp Ser Ser Glu Asp Phe Ser Thr
500 505 510

Leu Asn Ser Asp Met Gly Ala Gly Cys Trp Gly Arg Ile Leu Asn Gln
515 520 525

Asn Tyr Ile Asn Gly Tyr Met Thr Ser Thr Ile Ala Trp Asn Leu Val
530 535 540

Ala Ser Tyr Tyr Glu Gln Leu Pro Tyr Gly Arg Cys Gly Leu Met Thr
545 550 555 560

Ala Gln Glu Pro Trp Ser Gly His Tyr Val Val Glu Ser Pro Val Trp
565 570 575

Val Ser Ala His Thr Thr Gln Phe Thr Gln Pro Gly Trp Tyr Tyr Leu

580

585

590

Lys Thr Val Gly His Leu Glu Lys Gly Gly Ser Tyr Val Ala Leu Thr
 595 600 605

Asp Gly Leu Gly Asn Leu Thr Ile Ile Ile Glu Thr Met Ser His Lys
 610 615 620

His Ser Lys Cys Ile Arg Pro Phe Leu Pro Tyr Phe Asn Val Ser Gln
 625 630 635 640

Gln Phe Ala Thr Phe Val Leu Lys Gly Ser Phe Ser Glu Ile Pro Glu
 645 650 655

Leu Gln Val Trp Tyr Thr Lys Leu Gly Lys Thr Ser Glu Arg Phe Leu
 660 665 670

Phe Lys Gln Leu Asp Ser Leu Trp Leu Leu Asp Ser Asp Gly Ser Phe
 675 680 685

Thr Leu Ser Leu His Glu Asp Glu Leu Phe Thr Leu Thr Thr Leu Thr
 690 695 700

Thr Gly Arg Lys Gly Ser Tyr Pro Leu Pro Pro Lys Ser Gln Pro Phe
 705 710 715 720

Pro Ser Thr Tyr Lys Asp Asp Phe Asn Val Asp Tyr Pro Phe Phe Ser
 725 730 735

Glu Ala Pro Asn Phe Ala Asp Gln Thr Gly Val Phe Glu Tyr Phe Thr
 740 745 750

Asn Ile Glu Asp Pro Gly Glu His His Phe Thr Leu Arg Gln Val Leu
 755 760 765

Asn Gln Arg Pro Ile Thr Trp Ala Ala Asp Ala Ser Asn Thr Ile Ser
 770 775 780

Ile Ile Gly Asp Tyr Asn Trp Thr Asn Leu Thr Ile Lys Cys Asp Val
785 790 795 800

Tyr Ile Glu Thr Pro Asp Thr Gly Gly Val Phe Ile Ala Gly Arg Val
805 810 815

Asn Lys Gly Gly Ile Leu Ile Arg Ser Ala Arg Gly Ile Phe Phe Trp
820 825 830

Ile Phe Ala Asn Gly Ser Tyr Arg Val Thr Gly Asp Leu Ala Gly Trp
835 840 845

Ile Ile Tyr Ala Leu Gly Arg Val Glu Val Thr Ala Lys Lys Trp Tyr
850 855 860

Thr Leu Thr Leu Thr Ile Lys Gly His Phe Thr Ser Gly Met Leu Asn
865 870 875 880

Asp Lys Ser Leu Trp Thr Asp Ile Pro Val Asn Phe Pro Lys Asn Gly
885 890 895

Trp Ala Ala Ile Gly Thr His Ser Phe Glu Phe Ala Gln Phe Asp Asn
900 905 910

Phe Leu Val Glu Ala Thr Arg
915

<210> 165

<211> 969

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hGALC, Fab HC-GS20-GALC

<400> 165

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195

200

205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 290 295 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 305 310 315 320

Ser Gly Gly Gly Gly Ser Tyr Val Leu Asp Asp Ser Asp Gly Leu Gly
 325 330 335

Arg Glu Phe Asp Gly Ile Gly Ala Val Ser Gly Gly Gly Ala Thr Ser
 340 345 350

Arg Leu Leu Val Asn Tyr Pro Glu Pro Tyr Arg Ser Gln Ile Leu Asp
 355 360 365

Tyr Leu Phe Lys Pro Asn Phe Gly Ala Ser Leu His Ile Leu Lys Val
 370 375 380

Glu Ile Gly Gly Asp Gly Gln Thr Thr Asp Gly Thr Glu Pro Ser His
 385 390 395 400

Met His Tyr Ala Leu Asp Glu Asn Tyr Phe Arg Gly Tyr Glu Trp Trp
405 410 415

Leu Met Lys Glu Ala Lys Lys Arg Asn Pro Asn Ile Thr Leu Ile Gly
420 425 430

Leu Pro Trp Ser Phe Pro Gly Trp Leu Gly Lys Gly Phe Asp Trp Pro
435 440 445

Tyr Val Asn Leu Gln Leu Thr Ala Tyr Tyr Val Val Thr Trp Ile Val
450 455 460

Gly Ala Lys Arg Tyr His Asp Leu Asp Ile Asp Tyr Ile Gly Ile Trp
465 470 475 480

Asn Glu Arg Ser Tyr Asn Ala Asn Tyr Ile Lys Ile Leu Arg Lys Met
485 490 495

Leu Asn Tyr Gln Gly Leu Gln Arg Val Lys Ile Ile Ala Ser Asp Asn
500 505 510

Leu Trp Glu Ser Ile Ser Ala Ser Met Leu Leu Asp Ala Glu Leu Phe
515 520 525

Lys Val Val Asp Val Ile Gly Ala His Tyr Pro Gly Thr His Ser Ala
530 535 540

Lys Asp Ala Lys Leu Thr Gly Lys Lys Leu Trp Ser Ser Glu Asp Phe
545 550 555 560

Ser Thr Leu Asn Ser Asp Met Gly Ala Gly Cys Trp Gly Arg Ile Leu
565 570 575

Asn Gln Asn Tyr Ile Asn Gly Tyr Met Thr Ser Thr Ile Ala Trp Asn
580 585 590

Leu Val Ala Ser Tyr Tyr Glu Gln Leu Pro Tyr Gly Arg Cys Gly Leu
595 600 605

Met Thr Ala Gln Glu Pro Trp Ser Gly His Tyr Val Val Glu Ser Pro
610 615 620

Val Trp Val Ser Ala His Thr Thr Gln Phe Thr Gln Pro Gly Trp Tyr
625 630 635 640

Tyr Leu Lys Thr Val Gly His Leu Glu Lys Gly Gly Ser Tyr Val Ala
645 650 655

Leu Thr Asp Gly Leu Gly Asn Leu Thr Ile Ile Ile Glu Thr Met Ser
660 665 670

His Lys His Ser Lys Cys Ile Arg Pro Phe Leu Pro Tyr Phe Asn Val
675 680 685

Ser Gln Gln Phe Ala Thr Phe Val Leu Lys Gly Ser Phe Ser Glu Ile
690 695 700

Pro Glu Leu Gln Val Trp Tyr Thr Lys Leu Gly Lys Thr Ser Glu Arg
705 710 715 720

Phe Leu Phe Lys Gln Leu Asp Ser Leu Trp Leu Leu Asp Ser Asp Gly
725 730 735

Ser Phe Thr Leu Ser Leu His Glu Asp Glu Leu Phe Thr Leu Thr Thr
740 745 750

Leu Thr Thr Gly Arg Lys Gly Ser Tyr Pro Leu Pro Pro Lys Ser Gln
755 760 765

Pro Phe Pro Ser Thr Tyr Lys Asp Asp Phe Asn Val Asp Tyr Pro Phe
770 775 780

Phe Ser Glu Ala Pro Asn Phe Ala Asp Gln Thr Gly Val Phe Glu Tyr
785 790 795 800

Phe Thr Asn Ile Glu Asp Pro Gly Glu His His Phe Thr Leu Arg Gln
805 810 815

Val Leu Asn Gln Arg Pro Ile Thr Trp Ala Ala Asp Ala Ser Asn Thr
820 825 830

Ile Ser Ile Ile Gly Asp Tyr Asn Trp Thr Asn Leu Thr Ile Lys Cys
835 840 845

Asp Val Tyr Ile Glu Thr Pro Asp Thr Gly Gly Val Phe Ile Ala Gly
850 855 860

Arg Val Asn Lys Gly Gly Ile Leu Ile Arg Ser Ala Arg Gly Ile Phe
865 870 875 880

Phe Trp Ile Phe Ala Asn Gly Ser Tyr Arg Val Thr Gly Asp Leu Ala
885 890 895

Gly Trp Ile Ile Tyr Ala Leu Gly Arg Val Glu Val Thr Ala Lys Lys
900 905 910

Trp Tyr Thr Leu Thr Leu Thr Ile Lys Gly His Phe Thr Ser Gly Met
915 920 925

Leu Asn Asp Lys Ser Leu Trp Thr Asp Ile Pro Val Asn Phe Pro Lys
930 935 940

Asn Gly Trp Ala Ala Ile Gly Thr His Ser Phe Glu Phe Ala Gln Phe
945 950 955 960

Asp Asn Phe Leu Val Glu Ala Thr Arg
965

<210> 166

<211> 821
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hAC, IgG4 HC-AC

<400> 166

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Gln
435 440 445

His Ala Pro Pro Trp Thr Glu Asp Cys Arg Lys Ser Thr Tyr Pro Pro
450 455 460

Ser Gly Pro Thr Tyr Arg Gly Ala Val Pro Trp Tyr Thr Ile Asn Leu
465 470 475 480

Asp Leu Pro Pro Tyr Lys Arg Trp His Glu Leu Met Leu Asp Lys Ala
485 490 495

Pro Val Leu Lys Val Ile Val Asn Ser Leu Lys Asn Met Ile Asn Thr
500 505 510

Phe Val Pro Ser Gly Lys Ile Met Gln Val Val Asp Glu Lys Leu Pro
515 520 525

Gly Leu Leu Gly Asn Phe Pro Gly Pro Phe Glu Glu Glu Met Lys Gly
530 535 540

Ile Ala Ala Val Thr Asp Ile Pro Leu Gly Glu Ile Ile Ser Phe Asn

545		550		555		560
Ile Phe Tyr Glu	Leu Phe Thr Ile Cys Thr Ser Ile Val Ala Glu Asp					
	565		570			575
Lys Lys Gly His	Leu Ile His Gly Arg Asn Met Asp Phe Gly Val Phe					
	580		585			590
Leu Gly Trp Asn	Ile Asn Asn Asp Thr Trp Val Ile Thr Glu Gln Leu					
	595		600			605
Lys Pro Leu Thr Val	Asn Leu Asp Phe Gln Arg Asn Asn Lys Thr Val					
	610		615			620
Phe Lys Ala Ser Ser	Phe Ala Gly Tyr Val Gly Met Leu Thr Gly Phe					
625		630		635		640
Lys Pro Gly Leu Phe	Ser Leu Thr Leu Asn Glu Arg Phe Ser Ile Asn					
	645		650			655
Gly Gly Tyr Leu Gly	Ile Leu Glu Trp Ile Leu Gly Lys Lys Asp Val					
	660		665			670
Met Trp Ile Gly Phe	Leu Thr Arg Thr Val Leu Glu Asn Ser Thr Ser					
	675		680			685
Tyr Glu Glu Ala Lys	Asn Leu Leu Thr Lys Thr Lys Ile Leu Ala Pro					
	690		695			700
Ala Tyr Phe Ile Leu	Gly Gly Asn Gln Ser Gly Glu Gly Cys Val Ile					
705		710		715		720
Thr Arg Asp Arg	Lys Glu Ser Leu Asp Val Tyr Glu Leu Asp Ala Lys					
	725		730			735
Gln Gly Arg Trp Tyr	Val Val Gln Thr Asn Tyr Asp Arg Trp Lys His					
	740		745			750

Pro Phe Phe Leu Asp Asp Arg Arg Thr Pro Ala Lys Met Cys Leu Asn
755 760 765

Arg Thr Ser Gln Glu Asn Ile Ser Phe Glu Thr Met Tyr Asp Val Leu
770 775 780

Ser Thr Lys Pro Val Leu Asn Lys Leu Thr Val Tyr Thr Thr Leu Ile
785 790 795 800

Asp Val Thr Lys Gly Gln Phe Glu Thr Tyr Leu Arg Asp Cys Pro Asp
805 810 815

Pro Cys Ile Gly Trp
820

<210> 167

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hAC, IgG4
HC-GS5-AC

<400> 167

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

450

455

460

Ser Gly Gly Gly Gly Ser Gln His Ala Pro Pro Trp Thr Glu Asp Cys
 465 470 475 480

Arg Lys Ser Thr Tyr Pro Pro Ser Gly Pro Thr Tyr Arg Gly Ala Val
 485 490 495

Pro Trp Tyr Thr Ile Asn Leu Asp Leu Pro Pro Tyr Lys Arg Trp His
 500 505 510

Glu Leu Met Leu Asp Lys Ala Pro Val Leu Lys Val Ile Val Asn Ser
 515 520 525

Leu Lys Asn Met Ile Asn Thr Phe Val Pro Ser Gly Lys Ile Met Gln
 530 535 540

Val Val Asp Glu Lys Leu Pro Gly Leu Leu Gly Asn Phe Pro Gly Pro
 545 550 555 560

Phe Glu Glu Glu Met Lys Gly Ile Ala Ala Val Thr Asp Ile Pro Leu
 565 570 575

Gly Glu Ile Ile Ser Phe Asn Ile Phe Tyr Glu Leu Phe Thr Ile Cys
 580 585 590

Thr Ser Ile Val Ala Glu Asp Lys Lys Gly His Leu Ile His Gly Arg
 595 600 605

Asn Met Asp Phe Gly Val Phe Leu Gly Trp Asn Ile Asn Asn Asp Thr
 610 615 620

Trp Val Ile Thr Glu Gln Leu Lys Pro Leu Thr Val Asn Leu Asp Phe
 625 630 635 640

Gln Arg Asn Asn Lys Thr Val Phe Lys Ala Ser Ser Phe Ala Gly Tyr
 645 650 655

Val Gly Met Leu Thr Gly Phe Lys Pro Gly Leu Phe Ser Leu Thr Leu
660 665 670

Asn Glu Arg Phe Ser Ile Asn Gly Gly Tyr Leu Gly Ile Leu Glu Trp
675 680 685

Ile Leu Gly Lys Lys Asp Val Met Trp Ile Gly Phe Leu Thr Arg Thr
690 695 700

Val Leu Glu Asn Ser Thr Ser Tyr Glu Glu Ala Lys Asn Leu Leu Thr
705 710 715 720

Lys Thr Lys Ile Leu Ala Pro Ala Tyr Phe Ile Leu Gly Gly Asn Gln
725 730 735

Ser Gly Glu Gly Cys Val Ile Thr Arg Asp Arg Lys Glu Ser Leu Asp
740 745 750

Val Tyr Glu Leu Asp Ala Lys Gln Gly Arg Trp Tyr Val Val Gln Thr
755 760 765

Asn Tyr Asp Arg Trp Lys His Pro Phe Phe Leu Asp Asp Arg Arg Thr
770 775 780

Pro Ala Lys Met Cys Leu Asn Arg Thr Ser Gln Glu Asn Ile Ser Phe
785 790 795 800

Glu Thr Met Tyr Asp Val Leu Ser Thr Lys Pro Val Leu Asn Lys Leu
805 810 815

Thr Val Tyr Thr Thr Leu Ile Asp Val Thr Lys Gly Gln Phe Glu Thr
820 825 830

Tyr Leu Arg Asp Cys Pro Asp Pro Cys Ile Gly Trp
835 840

<210> 168
 <211> 869
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Amino acid sequence of fusion protein of the heavy chain of
 humanized anti-hTfR antibody No. 3N (IgG4) and hAC, IgG4
 HC-GS10-AC

<400> 168

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
 50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

340

345

350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
 405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
 435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 485 490 495

His Ala Pro Pro Trp Thr Glu Asp Cys Arg Lys Ser Thr Tyr Pro Pro
 500 505 510

Ser Gly Pro Thr Tyr Arg Gly Ala Val Pro Trp Tyr Thr Ile Asn Leu
 515 520 525

Asp Leu Pro Pro Tyr Lys Arg Trp His Glu Leu Met Leu Asp Lys Ala
 530 535 540

Pro Val Leu Lys Val Ile Val Asn Ser Leu Lys Asn Met Ile Asn Thr
545 550 555 560

Phe Val Pro Ser Gly Lys Ile Met Gln Val Val Asp Glu Lys Leu Pro
565 570 575

Gly Leu Leu Gly Asn Phe Pro Gly Pro Phe Glu Glu Glu Met Lys Gly
580 585 590

Ile Ala Ala Val Thr Asp Ile Pro Leu Gly Glu Ile Ile Ser Phe Asn
595 600 605

Ile Phe Tyr Glu Leu Phe Thr Ile Cys Thr Ser Ile Val Ala Glu Asp
610 615 620

Lys Lys Gly His Leu Ile His Gly Arg Asn Met Asp Phe Gly Val Phe
625 630 635 640

Leu Gly Trp Asn Ile Asn Asn Asp Thr Trp Val Ile Thr Glu Gln Leu
645 650 655

Lys Pro Leu Thr Val Asn Leu Asp Phe Gln Arg Asn Asn Lys Thr Val
660 665 670

Phe Lys Ala Ser Ser Phe Ala Gly Tyr Val Gly Met Leu Thr Gly Phe
675 680 685

Lys Pro Gly Leu Phe Ser Leu Thr Leu Asn Glu Arg Phe Ser Ile Asn
690 695 700

Gly Gly Tyr Leu Gly Ile Leu Glu Trp Ile Leu Gly Lys Lys Asp Val
705 710 715 720

Met Trp Ile Gly Phe Leu Thr Arg Thr Val Leu Glu Asn Ser Thr Ser
725 730 735

Tyr Glu Glu Ala Lys Asn Leu Leu Thr Lys Thr Lys Ile Leu Ala Pro
740 745 750

Ala Tyr Phe Ile Leu Gly Gly Asn Gln Ser Gly Glu Gly Cys Val Ile
755 760 765

Thr Arg Asp Arg Lys Glu Ser Leu Asp Val Tyr Glu Leu Asp Ala Lys
770 775 780

Gln Gly Arg Trp Tyr Val Val Gln Thr Asn Tyr Asp Arg Trp Lys His
785 790 795 800

Pro Phe Phe Leu Asp Asp Arg Arg Thr Pro Ala Lys Met Cys Leu Asn
805 810 815

Arg Thr Ser Gln Glu Asn Ile Ser Phe Glu Thr Met Tyr Asp Val Leu
820 825 830

Ser Thr Lys Pro Val Leu Asn Lys Leu Thr Val Tyr Thr Thr Leu Ile
835 840 845

Asp Val Thr Lys Gly Gln Phe Glu Thr Tyr Leu Arg Asp Cys Pro Asp
850 855 860

Pro Cys Ile Gly Trp
865

<210> 169
<211> 919
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hAC, IgG4
HC-GS20-AC

<400> 169

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser

195

200

205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Gln His Ala Pro Pro Trp Thr Glu Asp Cys Arg Lys Ser Thr Tyr
545 550 555 560

Pro Pro Ser Gly Pro Thr Tyr Arg Gly Ala Val Pro Trp Tyr Thr Ile
565 570 575

Asn Leu Asp Leu Pro Pro Tyr Lys Arg Trp His Glu Leu Met Leu Asp
580 585 590

Lys Ala Pro Val Leu Lys Val Ile Val Asn Ser Leu Lys Asn Met Ile
595 600 605

Asn Thr Phe Val Pro Ser Gly Lys Ile Met Gln Val Val Asp Glu Lys
610 615 620

Leu Pro Gly Leu Leu Gly Asn Phe Pro Gly Pro Phe Glu Glu Glu Met
625 630 635 640

Lys Gly Ile Ala Ala Val Thr Asp Ile Pro Leu Gly Glu Ile Ile Ser
645 650 655

Phe Asn Ile Phe Tyr Glu Leu Phe Thr Ile Cys Thr Ser Ile Val Ala
660 665 670

Glu Asp Lys Lys Gly His Leu Ile His Gly Arg Asn Met Asp Phe Gly
675 680 685

Val Phe Leu Gly Trp Asn Ile Asn Asn Asp Thr Trp Val Ile Thr Glu
690 695 700

Gln Leu Lys Pro Leu Thr Val Asn Leu Asp Phe Gln Arg Asn Asn Lys
705 710 715 720

Thr Val Phe Lys Ala Ser Ser Phe Ala Gly Tyr Val Gly Met Leu Thr
725 730 735

Gly Phe Lys Pro Gly Leu Phe Ser Leu Thr Leu Asn Glu Arg Phe Ser
740 745 750

Ile Asn Gly Gly Tyr Leu Gly Ile Leu Glu Trp Ile Leu Gly Lys Lys
755 760 765

Asp Val Met Trp Ile Gly Phe Leu Thr Arg Thr Val Leu Glu Asn Ser
770 775 780

Thr Ser Tyr Glu Glu Ala Lys Asn Leu Leu Thr Lys Thr Lys Ile Leu
785 790 795 800

Ala Pro Ala Tyr Phe Ile Leu Gly Gly Asn Gln Ser Gly Glu Gly Cys
805 810 815

Val Ile Thr Arg Asp Arg Lys Glu Ser Leu Asp Val Tyr Glu Leu Asp
820 825 830

Ala Lys Gln Gly Arg Trp Tyr Val Val Gln Thr Asn Tyr Asp Arg Trp
835 840 845

Lys His Pro Phe Phe Leu Asp Asp Arg Arg Thr Pro Ala Lys Met Cys
850 855 860

Leu Asn Arg Thr Ser Gln Glu Asn Ile Ser Phe Glu Thr Met Tyr Asp
865 870 875 880

Val Leu Ser Thr Lys Pro Val Leu Asn Lys Leu Thr Val Tyr Thr Thr
885 890 895

Leu Ile Asp Val Thr Lys Gly Gln Phe Glu Thr Tyr Leu Arg Asp Cys
900 905 910

Pro Asp Pro Cys Ile Gly Trp
915

<210> 170

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hAC, Fab HC-GS3-AC

<400> 170

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gln His Ala Pro Pro Trp Thr Glu Asp Cys Arg Lys Ser Thr Tyr
245 250 255

Pro Pro Ser Gly Pro Thr Tyr Arg Gly Ala Val Pro Trp Tyr Thr Ile
260 265 270

Asn Leu Asp Leu Pro Pro Tyr Lys Arg Trp His Glu Leu Met Leu Asp
275 280 285

Lys Ala Pro Val Leu Lys Val Ile Val Asn Ser Leu Lys Asn Met Ile
290 295 300

Asn Thr Phe Val Pro Ser Gly Lys Ile Met Gln Val Val Asp Glu Lys
305 310 315 320

Leu Pro Gly Leu Leu Gly Asn Phe Pro Gly Pro Phe Glu Glu Glu Met
325 330 335

Lys Gly Ile Ala Ala Val Thr Asp Ile Pro Leu Gly Glu Ile Ile Ser
340 345 350

Phe Asn Ile Phe Tyr Glu Leu Phe Thr Ile Cys Thr Ser Ile Val Ala
355 360 365

Glu Asp Lys Lys Gly His Leu Ile His Gly Arg Asn Met Asp Phe Gly
370 375 380

Val Phe Leu Gly Trp Asn Ile Asn Asn Asp Thr Trp Val Ile Thr Glu
385 390 395 400

Gln Leu Lys Pro Leu Thr Val Asn Leu Asp Phe Gln Arg Asn Asn Lys
405 410 415

Thr Val Phe Lys Ala Ser Ser Phe Ala Gly Tyr Val Gly Met Leu Thr
420 425 430

Gly Phe Lys Pro Gly Leu Phe Ser Leu Thr Leu Asn Glu Arg Phe Ser
435 440 445

Ile Asn Gly Gly Tyr Leu Gly Ile Leu Glu Trp Ile Leu Gly Lys Lys
450 455 460

Asp Val Met Trp Ile Gly Phe Leu Thr Arg Thr Val Leu Glu Asn Ser
465 470 475 480

Thr Ser Tyr Glu Glu Ala Lys Asn Leu Leu Thr Lys Thr Lys Ile Leu
485 490 495

Ala Pro Ala Tyr Phe Ile Leu Gly Gly Asn Gln Ser Gly Glu Gly Cys
500 505 510

Val Ile Thr Arg Asp Arg Lys Glu Ser Leu Asp Val Tyr Glu Leu Asp
515 520 525

Ala Lys Gln Gly Arg Trp Tyr Val Val Gln Thr Asn Tyr Asp Arg Trp
530 535 540

Lys His Pro Phe Phe Leu Asp Asp Arg Arg Thr Pro Ala Lys Met Cys
545 550 555 560

Leu Asn Arg Thr Ser Gln Glu Asn Ile Ser Phe Glu Thr Met Tyr Asp
565 570 575

Val Leu Ser Thr Lys Pro Val Leu Asn Lys Leu Thr Val Tyr Thr Thr
580 585 590

Leu Ile Asp Val Thr Lys Gly Gln Phe Glu Thr Tyr Leu Arg Asp Cys

595

600

605

Pro Asp Pro Cys Ile Gly Trp
610 615

<210> 171

<211> 625

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hAC, Fab HC-GS5-AC

<400> 171

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln His Ala Pro Pro
245 250 255

Trp Thr Glu Asp Cys Arg Lys Ser Thr Tyr Pro Pro Ser Gly Pro Thr
260 265 270

Tyr Arg Gly Ala Val Pro Trp Tyr Thr Ile Asn Leu Asp Leu Pro Pro
275 280 285

Tyr Lys Arg Trp His Glu Leu Met Leu Asp Lys Ala Pro Val Leu Lys
290 295 300

Val Ile Val Asn Ser Leu Lys Asn Met Ile Asn Thr Phe Val Pro Ser
305 310 315 320

Gly Lys Ile Met Gln Val Val Asp Glu Lys Leu Pro Gly Leu Leu Gly
325 330 335

Asn Phe Pro Gly Pro Phe Glu Glu Glu Met Lys Gly Ile Ala Ala Val
340 345 350

Thr Asp Ile Pro Leu Gly Glu Ile Ile Ser Phe Asn Ile Phe Tyr Glu
355 360 365

Leu Phe Thr Ile Cys Thr Ser Ile Val Ala Glu Asp Lys Lys Gly His
370 375 380

Leu Ile His Gly Arg Asn Met Asp Phe Gly Val Phe Leu Gly Trp Asn
385 390 395 400

Ile Asn Asn Asp Thr Trp Val Ile Thr Glu Gln Leu Lys Pro Leu Thr
405 410 415

Val Asn Leu Asp Phe Gln Arg Asn Asn Lys Thr Val Phe Lys Ala Ser
420 425 430

Ser Phe Ala Gly Tyr Val Gly Met Leu Thr Gly Phe Lys Pro Gly Leu
435 440 445

Phe Ser Leu Thr Leu Asn Glu Arg Phe Ser Ile Asn Gly Gly Tyr Leu
450 455 460

Gly Ile Leu Glu Trp Ile Leu Gly Lys Lys Asp Val Met Trp Ile Gly
465 470 475 480

Phe Leu Thr Arg Thr Val Leu Glu Asn Ser Thr Ser Tyr Glu Glu Ala
485 490 495

Lys Asn Leu Leu Thr Lys Thr Lys Ile Leu Ala Pro Ala Tyr Phe Ile
500 505 510

Leu Gly Gly Asn Gln Ser Gly Glu Gly Cys Val Ile Thr Arg Asp Arg

515

520

525

Lys Glu Ser Leu Asp Val Tyr Glu Leu Asp Ala Lys Gln Gly Arg Trp
 530 535 540

Tyr Val Val Gln Thr Asn Tyr Asp Arg Trp Lys His Pro Phe Phe Leu
 545 550 555 560

Asp Asp Arg Arg Thr Pro Ala Lys Met Cys Leu Asn Arg Thr Ser Gln
 565 570 575

Glu Asn Ile Ser Phe Glu Thr Met Tyr Asp Val Leu Ser Thr Lys Pro
 580 585 590

Val Leu Asn Lys Leu Thr Val Tyr Thr Thr Leu Ile Asp Val Thr Lys
 595 600 605

Gly Gln Phe Glu Thr Tyr Leu Arg Asp Cys Pro Asp Pro Cys Ile Gly
 610 615 620

Trp
 625

<210> 172
 <211> 650
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of fusion protein of the Fab heavy chain of
 humanized anti-hTfR antibody No. 3N and hAC, Fab HC-GS10-AC

<400> 172

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gln His Ala Pro Pro Trp Thr Glu Asp Cys Arg Lys
275 280 285

Ser Thr Tyr Pro Pro Ser Gly Pro Thr Tyr Arg Gly Ala Val Pro Trp
290 295 300

Tyr Thr Ile Asn Leu Asp Leu Pro Pro Tyr Lys Arg Trp His Glu Leu
305 310 315 320

Met Leu Asp Lys Ala Pro Val Leu Lys Val Ile Val Asn Ser Leu Lys
325 330 335

Asn Met Ile Asn Thr Phe Val Pro Ser Gly Lys Ile Met Gln Val Val
340 345 350

Asp Glu Lys Leu Pro Gly Leu Leu Gly Asn Phe Pro Gly Pro Phe Glu
355 360 365

Glu Glu Met Lys Gly Ile Ala Ala Val Thr Asp Ile Pro Leu Gly Glu
370 375 380

Ile Ile Ser Phe Asn Ile Phe Tyr Glu Leu Phe Thr Ile Cys Thr Ser
385 390 395 400

Ile Val Ala Glu Asp Lys Lys Gly His Leu Ile His Gly Arg Asn Met
405 410 415

Asp Phe Gly Val Phe Leu Gly Trp Asn Ile Asn Asn Asp Thr Trp Val

420

425

430

Ile Thr Glu Gln Leu Lys Pro Leu Thr Val Asn Leu Asp Phe Gln Arg
 435 440 445

Asn Asn Lys Thr Val Phe Lys Ala Ser Ser Phe Ala Gly Tyr Val Gly
 450 455 460

Met Leu Thr Gly Phe Lys Pro Gly Leu Phe Ser Leu Thr Leu Asn Glu
 465 470 475 480

Arg Phe Ser Ile Asn Gly Gly Tyr Leu Gly Ile Leu Glu Trp Ile Leu
 485 490 495

Gly Lys Lys Asp Val Met Trp Ile Gly Phe Leu Thr Arg Thr Val Leu
 500 505 510

Glu Asn Ser Thr Ser Tyr Glu Glu Ala Lys Asn Leu Leu Thr Lys Thr
 515 520 525

Lys Ile Leu Ala Pro Ala Tyr Phe Ile Leu Gly Gly Asn Gln Ser Gly
 530 535 540

Glu Gly Cys Val Ile Thr Arg Asp Arg Lys Glu Ser Leu Asp Val Tyr
 545 550 555 560

Glu Leu Asp Ala Lys Gln Gly Arg Trp Tyr Val Val Gln Thr Asn Tyr
 565 570 575

Asp Arg Trp Lys His Pro Phe Phe Leu Asp Asp Arg Arg Thr Pro Ala
 580 585 590

Lys Met Cys Leu Asn Arg Thr Ser Gln Glu Asn Ile Ser Phe Glu Thr
 595 600 605

Met Tyr Asp Val Leu Ser Thr Lys Pro Val Leu Asn Lys Leu Thr Val
 610 615 620

Tyr Thr Thr Leu Ile Asp Val Thr Lys Gly Gln Phe Glu Thr Tyr Leu
625 630 635 640

Arg Asp Cys Pro Asp Pro Cys Ile Gly Trp
645 650

<210> 173
<211> 700
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of fusion protein of the Fab heavy chain of
humanized anti-hTfR antibody No. 3N and hAC, Fab HC-GS20-AC

<400> 173

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
290 295 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

305					310					315					320	
Ser	Gly	Gly	Gly	Gly	Ser	Gln	His	Ala	Pro	Pro	Trp	Thr	Glu	Asp	Cys	
				325					330					335		
Arg	Lys	Ser	Thr	Tyr	Pro	Pro	Ser	Gly	Pro	Thr	Tyr	Arg	Gly	Ala	Val	
				340					345					350		
Pro	Trp	Tyr	Thr	Ile	Asn	Leu	Asp	Leu	Pro	Pro	Tyr	Lys	Arg	Trp	His	
				355					360					365		
Glu	Leu	Met	Leu	Asp	Lys	Ala	Pro	Val	Leu	Lys	Val	Ile	Val	Asn	Ser	
				370					375					380		
Leu	Lys	Asn	Met	Ile	Asn	Thr	Phe	Val	Pro	Ser	Gly	Lys	Ile	Met	Gln	
				385					390					395		
Val	Val	Asp	Glu	Lys	Leu	Pro	Gly	Leu	Leu	Gly	Asn	Phe	Pro	Gly	Pro	
				405					410					415		
Phe	Glu	Glu	Glu	Met	Lys	Gly	Ile	Ala	Ala	Val	Thr	Asp	Ile	Pro	Leu	
				420					425					430		
Gly	Glu	Ile	Ile	Ser	Phe	Asn	Ile	Phe	Tyr	Glu	Leu	Phe	Thr	Ile	Cys	
				435					440					445		
Thr	Ser	Ile	Val	Ala	Glu	Asp	Lys	Lys	Gly	His	Leu	Ile	His	Gly	Arg	
				450					455					460		
Asn	Met	Asp	Phe	Gly	Val	Phe	Leu	Gly	Trp	Asn	Ile	Asn	Asn	Asp	Thr	
				465					470					475		
Trp	Val	Ile	Thr	Glu	Gln	Leu	Lys	Pro	Leu	Thr	Val	Asn	Leu	Asp	Phe	
				485					490					495		
Gln	Arg	Asn	Asn	Lys	Thr	Val	Phe	Lys	Ala	Ser	Ser	Phe	Ala	Gly	Tyr	
				500					505					510		

Val Gly Met Leu Thr Gly Phe Lys Pro Gly Leu Phe Ser Leu Thr Leu
515 520 525

Asn Glu Arg Phe Ser Ile Asn Gly Gly Tyr Leu Gly Ile Leu Glu Trp
530 535 540

Ile Leu Gly Lys Lys Asp Val Met Trp Ile Gly Phe Leu Thr Arg Thr
545 550 555 560

Val Leu Glu Asn Ser Thr Ser Tyr Glu Glu Ala Lys Asn Leu Leu Thr
565 570 575

Lys Thr Lys Ile Leu Ala Pro Ala Tyr Phe Ile Leu Gly Gly Asn Gln
580 585 590

Ser Gly Glu Gly Cys Val Ile Thr Arg Asp Arg Lys Glu Ser Leu Asp
595 600 605

Val Tyr Glu Leu Asp Ala Lys Gln Gly Arg Trp Tyr Val Val Gln Thr
610 615 620

Asn Tyr Asp Arg Trp Lys His Pro Phe Phe Leu Asp Asp Arg Arg Thr
625 630 635 640

Pro Ala Lys Met Cys Leu Asn Arg Thr Ser Gln Glu Asn Ile Ser Phe
645 650 655

Glu Thr Met Tyr Asp Val Leu Ser Thr Lys Pro Val Leu Asn Lys Leu
660 665 670

Thr Val Tyr Thr Thr Leu Ile Asp Val Thr Lys Gly Gln Phe Glu Thr
675 680 685

Tyr Leu Arg Asp Cys Pro Asp Pro Cys Ile Gly Trp
690 695 700

<210> 174
<211> 882
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino FUCA1id sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hFUCA1, IgG4
HC-FUCA1

<400> 174

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

340

345

350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
 405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Gln
 435 440 445

Pro Pro Arg Arg Tyr Thr Pro Asp Trp Pro Ser Leu Asp Ser Arg Pro
 450 455 460

Leu Pro Ala Trp Phe Asp Glu Ala Lys Phe Gly Val Phe Ile His Trp
 465 470 475 480

Gly Val Phe Ser Val Pro Ala Trp Gly Ser Glu Trp Phe Trp Trp His
 485 490 495

Trp Gln Gly Glu Gly Arg Pro Gln Tyr Gln Arg Phe Met Arg Asp Asn
 500 505 510

Tyr Pro Pro Gly Phe Ser Tyr Ala Asp Phe Gly Pro Gln Phe Thr Ala
 515 520 525

Arg Phe Phe His Pro Glu Glu Trp Ala Asp Leu Phe Gln Ala Ala Gly
 530 535 540

Ala Lys Tyr Val Val Leu Thr Thr Lys His His Glu Gly Phe Thr Asn
545 550 555 560

Trp Pro Ser Pro Val Ser Trp Asn Trp Asn Ser Lys Asp Val Gly Pro
565 570 575

His Arg Asp Leu Val Gly Glu Leu Gly Thr Ala Leu Arg Lys Arg Asn
580 585 590

Ile Arg Tyr Gly Leu Tyr His Ser Leu Leu Glu Trp Phe His Pro Leu
595 600 605

Tyr Leu Leu Asp Lys Lys Asn Gly Phe Lys Thr Gln His Phe Val Ser
610 615 620

Ala Lys Thr Met Pro Glu Leu Tyr Asp Leu Val Asn Ser Tyr Lys Pro
625 630 635 640

Asp Leu Ile Trp Ser Asp Gly Glu Trp Glu Cys Pro Asp Thr Tyr Trp
645 650 655

Asn Ser Thr Asn Phe Leu Ser Trp Leu Tyr Asn Asp Ser Pro Val Lys
660 665 670

Asp Glu Val Val Val Asn Asp Arg Trp Gly Gln Asn Cys Ser Cys His
675 680 685

His Gly Gly Tyr Tyr Asn Cys Glu Asp Lys Phe Lys Pro Gln Ser Leu
690 695 700

Pro Asp His Lys Trp Glu Met Cys Thr Ser Ile Asp Lys Phe Ser Trp
705 710 715 720

Gly Tyr Arg Arg Asp Met Ala Leu Ser Asp Val Thr Glu Glu Ser Glu
725 730 735

Ile Ile Ser Glu Leu Val Gln Thr Val Ser Leu Gly Gly Asn Tyr Leu
740 745 750

Leu Asn Ile Gly Pro Thr Lys Asp Gly Leu Ile Val Pro Ile Phe Gln
755 760 765

Glu Arg Leu Leu Ala Val Gly Lys Trp Leu Ser Ile Asn Gly Glu Ala
770 775 780

Ile Tyr Ala Ser Lys Pro Trp Arg Val Gln Trp Glu Lys Asn Thr Thr
785 790 795 800

Ser Val Trp Tyr Thr Ser Lys Gly Ser Ala Val Tyr Ala Ile Phe Leu
805 810 815

His Trp Pro Glu Asn Gly Val Leu Asn Leu Glu Ser Pro Ile Thr Thr
820 825 830

Ser Thr Thr Lys Ile Thr Met Leu Gly Ile Gln Gly Asp Leu Lys Trp
835 840 845

Ser Thr Asp Pro Asp Lys Gly Leu Phe Ile Ser Leu Pro Gln Leu Pro
850 855 860

Pro Ser Ala Val Pro Ala Glu Phe Ala Trp Thr Ile Lys Leu Thr Gly
865 870 875 880

Val Lys

<210> 175

<211> 905

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino FUCA1id sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hFUCA1, IgG4

HC-GS5-FUCA1

<400> 175

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

180

185

190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gln Pro Pro Arg Arg Tyr Thr Pro Asp Trp
465 470 475 480

Pro Ser Leu Asp Ser Arg Pro Leu Pro Ala Trp Phe Asp Glu Ala Lys
485 490 495

Phe Gly Val Phe Ile His Trp Gly Val Phe Ser Val Pro Ala Trp Gly
500 505 510

Ser Glu Trp Phe Trp Trp His Trp Gln Gly Glu Gly Arg Pro Gln Tyr
515 520 525

Gln Arg Phe Met Arg Asp Asn Tyr Pro Pro Gly Phe Ser Tyr Ala Asp
530 535 540

Phe Gly Pro Gln Phe Thr Ala Arg Phe Phe His Pro Glu Glu Trp Ala
545 550 555 560

Asp Leu Phe Gln Ala Ala Gly Ala Lys Tyr Val Val Leu Thr Thr Lys
565 570 575

His His Glu Gly Phe Thr Asn Trp Pro Ser Pro Val Ser Trp Asn Trp
580 585 590

Asn Ser Lys Asp Val Gly Pro His Arg Asp Leu Val Gly Glu Leu Gly
595 600 605

Thr Ala Leu Arg Lys Arg Asn Ile Arg Tyr Gly Leu Tyr His Ser Leu
610 615 620

Leu Glu Trp Phe His Pro Leu Tyr Leu Leu Asp Lys Lys Asn Gly Phe
625 630 635 640

Lys Thr Gln His Phe Val Ser Ala Lys Thr Met Pro Glu Leu Tyr Asp
645 650 655

Leu Val Asn Ser Tyr Lys Pro Asp Leu Ile Trp Ser Asp Gly Glu Trp
660 665 670

Glu Cys Pro Asp Thr Tyr Trp Asn Ser Thr Asn Phe Leu Ser Trp Leu
675 680 685

Tyr Asn Asp Ser Pro Val Lys Asp Glu Val Val Val Asn Asp Arg Trp
690 695 700

Gly Gln Asn Cys Ser Cys His His Gly Gly Tyr Tyr Asn Cys Glu Asp
705 710 715 720

Lys Phe Lys Pro Gln Ser Leu Pro Asp His Lys Trp Glu Met Cys Thr
725 730 735

Ser Ile Asp Lys Phe Ser Trp Gly Tyr Arg Arg Asp Met Ala Leu Ser
740 745 750

Asp Val Thr Glu Glu Ser Glu Ile Ile Ser Glu Leu Val Gln Thr Val
755 760 765

Ser Leu Gly Gly Asn Tyr Leu Leu Asn Ile Gly Pro Thr Lys Asp Gly
770 775 780

Leu Ile Val Pro Ile Phe Gln Glu Arg Leu Leu Ala Val Gly Lys Trp
785 790 795 800

Leu Ser Ile Asn Gly Glu Ala Ile Tyr Ala Ser Lys Pro Trp Arg Val
805 810 815

Gln Trp Glu Lys Asn Thr Thr Ser Val Trp Tyr Thr Ser Lys Gly Ser
820 825 830

Ala Val Tyr Ala Ile Phe Leu His Trp Pro Glu Asn Gly Val Leu Asn
835 840 845

Leu Glu Ser Pro Ile Thr Thr Ser Thr Thr Lys Ile Thr Met Leu Gly
850 855 860

Ile Gln Gly Asp Leu Lys Trp Ser Thr Asp Pro Asp Lys Gly Leu Phe
865 870 875 880

Ile Ser Leu Pro Gln Leu Pro Pro Ser Ala Val Pro Ala Glu Phe Ala
885 890 895

Trp Thr Ile Lys Leu Thr Gly Val Lys
900 905

<210> 176

<211> 930

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino FUCA1id sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hFUCA1, IgG4
HC-GS10-FUCA1

<400> 176

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu

1	5	10	15
Ser	Leu	Lys	Ile
	20		
Ser	Cys	Lys	Gly
		25	
Ser	Gly	Tyr	Ser
			30
Phe	Met	Asn	Tyr
Trp	Leu	Gly	Trp
	35		
Val	Arg	Gln	Met
		40	
Pro	Gly	Lys	Gly
			45
Leu	Glu	Trp	Met
Gly	Asp	Ile	Tyr
	50		
Pro	Gly	Gly	Asp
		55	
Tyr	Pro	Thr	Tyr
			60
Ser	Glu	Lys	Phe
Lys	Val	Gln	Val
	65		
Thr	Ile	Ser	Ala
	70		
Asp	Lys	Ser	Ile
		75	
Ser	Thr	Ala	Tyr
			80
Leu	Gln	Leu	Ser
		85	
Ser	Leu	Lys	Ala
			90
Ser	Asp	Thr	Ala
			95
Met	Tyr	Tyr	Cys
Ala	Arg	Ser	Gly
		100	
Asn	Tyr	Asp	Glu
			105
Val	Ala	Tyr	Trp
			110
Gln	Gly	Thr	
Leu	Val	Thr	Val
	115		
Ser	Ser	Ala	Ser
			120
Thr	Lys	Gly	Pro
			125
Ser	Val	Phe	Pro
Leu	Ala	Pro	Cys
	130		
Ser	Arg	Ser	Thr
		135	
Ser	Glu	Ser	Thr
			140
Ala	Ala	Leu	Gly
Cys	Leu	Val	Lys
	145		
Asp	Tyr	Phe	Pro
		150	
Glu	Pro	Val	Thr
		155	
Val	Ser	Trp	Asn
			160
Ser	Gly	Ala	Leu
		165	
Ser	Gly	Val	His
			170
Thr	Phe	Pro	Ala
			175
Val	Leu	Gln	
Ser	Ser	Gly	Leu
		180	
Tyr	Ser	Leu	Ser
			185
Ser	Val	Val	Thr
			190
Pro	Ser	Ser	
Ser	Leu	Gly	Thr
	195		
Lys	Thr	Tyr	Thr
			200
Cys	Asn	Val	Asp
			205
His	Lys	Pro	Ser

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
485 490 495

Pro Pro Arg Arg Tyr Thr Pro Asp Trp Pro Ser Leu Asp Ser Arg Pro
500 505 510

Leu Pro Ala Trp Phe Asp Glu Ala Lys Phe Gly Val Phe Ile His Trp
515 520 525

Gly Val Phe Ser Val Pro Ala Trp Gly Ser Glu Trp Phe Trp Trp His
530 535 540

Trp Gln Gly Glu Gly Arg Pro Gln Tyr Gln Arg Phe Met Arg Asp Asn
545 550 555 560

Tyr Pro Pro Gly Phe Ser Tyr Ala Asp Phe Gly Pro Gln Phe Thr Ala
565 570 575

Arg Phe Phe His Pro Glu Glu Trp Ala Asp Leu Phe Gln Ala Ala Gly
580 585 590

Ala Lys Tyr Val Val Leu Thr Thr Lys His His Glu Gly Phe Thr Asn
595 600 605

Trp Pro Ser Pro Val Ser Trp Asn Trp Asn Ser Lys Asp Val Gly Pro
610 615 620

His Arg Asp Leu Val Gly Glu Leu Gly Thr Ala Leu Arg Lys Arg Asn
625 630 635 640

Ile Arg Tyr Gly Leu Tyr His Ser Leu Leu Glu Trp Phe His Pro Leu
645 650 655

Tyr Leu Leu Asp Lys Lys Asn Gly Phe Lys Thr Gln His Phe Val Ser
660 665 670

Ala Lys Thr Met Pro Glu Leu Tyr Asp Leu Val Asn Ser Tyr Lys Pro
675 680 685

Asp Leu Ile Trp Ser Asp Gly Glu Trp Glu Cys Pro Asp Thr Tyr Trp
690 695 700

Asn Ser Thr Asn Phe Leu Ser Trp Leu Tyr Asn Asp Ser Pro Val Lys
705 710 715 720

Asp Glu Val Val Val Asn Asp Arg Trp Gly Gln Asn Cys Ser Cys His
725 730 735

His Gly Gly Tyr Tyr Asn Cys Glu Asp Lys Phe Lys Pro Gln Ser Leu
740 745 750

Pro Asp His Lys Trp Glu Met Cys Thr Ser Ile Asp Lys Phe Ser Trp
755 760 765

Gly Tyr Arg Arg Asp Met Ala Leu Ser Asp Val Thr Glu Glu Ser Glu
770 775 780

Ile Ile Ser Glu Leu Val Gln Thr Val Ser Leu Gly Gly Asn Tyr Leu

<400> 177

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Gln Pro Pro Arg Arg Tyr Thr Pro Asp Trp Pro Ser Leu Asp Ser
545 550 555 560

Arg Pro Leu Pro Ala Trp Phe Asp Glu Ala Lys Phe Gly Val Phe Ile
565 570 575

His Trp Gly Val Phe Ser Val Pro Ala Trp Gly Ser Glu Trp Phe Trp

580

585

590

Trp His Trp Gln Gly Glu Gly Arg Pro Gln Tyr Gln Arg Phe Met Arg
 595 600 605

Asp Asn Tyr Pro Pro Gly Phe Ser Tyr Ala Asp Phe Gly Pro Gln Phe
 610 615 620

Thr Ala Arg Phe Phe His Pro Glu Glu Trp Ala Asp Leu Phe Gln Ala
 625 630 635 640

Ala Gly Ala Lys Tyr Val Val Leu Thr Thr Lys His His Glu Gly Phe
 645 650 655

Thr Asn Trp Pro Ser Pro Val Ser Trp Asn Trp Asn Ser Lys Asp Val
 660 665 670

Gly Pro His Arg Asp Leu Val Gly Glu Leu Gly Thr Ala Leu Arg Lys
 675 680 685

Arg Asn Ile Arg Tyr Gly Leu Tyr His Ser Leu Leu Glu Trp Phe His
 690 695 700

Pro Leu Tyr Leu Leu Asp Lys Lys Asn Gly Phe Lys Thr Gln His Phe
 705 710 715 720

Val Ser Ala Lys Thr Met Pro Glu Leu Tyr Asp Leu Val Asn Ser Tyr
 725 730 735

Lys Pro Asp Leu Ile Trp Ser Asp Gly Glu Trp Glu Cys Pro Asp Thr
 740 745 750

Tyr Trp Asn Ser Thr Asn Phe Leu Ser Trp Leu Tyr Asn Asp Ser Pro
 755 760 765

Val Lys Asp Glu Val Val Val Asn Asp Arg Trp Gly Gln Asn Cys Ser
 770 775 780

Cys His His Gly Gly Tyr Tyr Asn Cys Glu Asp Lys Phe Lys Pro Gln
785 790 795 800

Ser Leu Pro Asp His Lys Trp Glu Met Cys Thr Ser Ile Asp Lys Phe
805 810 815

Ser Trp Gly Tyr Arg Arg Asp Met Ala Leu Ser Asp Val Thr Glu Glu
820 825 830

Ser Glu Ile Ile Ser Glu Leu Val Gln Thr Val Ser Leu Gly Gly Asn
835 840 845

Tyr Leu Leu Asn Ile Gly Pro Thr Lys Asp Gly Leu Ile Val Pro Ile
850 855 860

Phe Gln Glu Arg Leu Leu Ala Val Gly Lys Trp Leu Ser Ile Asn Gly
865 870 875 880

Glu Ala Ile Tyr Ala Ser Lys Pro Trp Arg Val Gln Trp Glu Lys Asn
885 890 895

Thr Thr Ser Val Trp Tyr Thr Ser Lys Gly Ser Ala Val Tyr Ala Ile
900 905 910

Phe Leu His Trp Pro Glu Asn Gly Val Leu Asn Leu Glu Ser Pro Ile
915 920 925

Thr Thr Ser Thr Thr Lys Ile Thr Met Leu Gly Ile Gln Gly Asp Leu
930 935 940

Lys Trp Ser Thr Asp Pro Asp Lys Gly Leu Phe Ile Ser Leu Pro Gln
945 950 955 960

Leu Pro Pro Ser Ala Val Pro Ala Glu Phe Ala Trp Thr Ile Lys Leu
965 970 975

Thr Gly Val Lys
980

<210> 178

<211> 676

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino FUCA1id sequence of fusion protein of the Fab heavy chain
of humanized anti-hTfR antibody No. 3N and hFUCA1, Fab
HC-GS3-FUCA1

<400> 178

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gln Pro Pro Arg Arg Tyr Thr Pro Asp Trp Pro Ser Leu Asp Ser
245 250 255

Arg Pro Leu Pro Ala Trp Phe Asp Glu Ala Lys Phe Gly Val Phe Ile
260 265 270

His Trp Gly Val Phe Ser Val Pro Ala Trp Gly Ser Glu Trp Phe Trp
275 280 285

Trp His Trp Gln Gly Glu Gly Arg Pro Gln Tyr Gln Arg Phe Met Arg
290 295 300

Asp Asn Tyr Pro Pro Gly Phe Ser Tyr Ala Asp Phe Gly Pro Gln Phe
305 310 315 320

Thr Ala Arg Phe Phe His Pro Glu Glu Trp Ala Asp Leu Phe Gln Ala

325

330

335

Ala Gly Ala Lys Tyr Val Val Leu Thr Thr Lys His His Glu Gly Phe
 340 345 350

Thr Asn Trp Pro Ser Pro Val Ser Trp Asn Trp Asn Ser Lys Asp Val
 355 360 365

Gly Pro His Arg Asp Leu Val Gly Glu Leu Gly Thr Ala Leu Arg Lys
 370 375 380

Arg Asn Ile Arg Tyr Gly Leu Tyr His Ser Leu Leu Glu Trp Phe His
 385 390 395 400

Pro Leu Tyr Leu Leu Asp Lys Lys Asn Gly Phe Lys Thr Gln His Phe
 405 410 415

Val Ser Ala Lys Thr Met Pro Glu Leu Tyr Asp Leu Val Asn Ser Tyr
 420 425 430

Lys Pro Asp Leu Ile Trp Ser Asp Gly Glu Trp Glu Cys Pro Asp Thr
 435 440 445

Tyr Trp Asn Ser Thr Asn Phe Leu Ser Trp Leu Tyr Asn Asp Ser Pro
 450 455 460

Val Lys Asp Glu Val Val Val Asn Asp Arg Trp Gly Gln Asn Cys Ser
 465 470 475 480

Cys His His Gly Gly Tyr Tyr Asn Cys Glu Asp Lys Phe Lys Pro Gln
 485 490 495

Ser Leu Pro Asp His Lys Trp Glu Met Cys Thr Ser Ile Asp Lys Phe
 500 505 510

Ser Trp Gly Tyr Arg Arg Asp Met Ala Leu Ser Asp Val Thr Glu Glu
 515 520 525

Ser Glu Ile Ile Ser Glu Leu Val Gln Thr Val Ser Leu Gly Gly Asn
530 535 540

Tyr Leu Leu Asn Ile Gly Pro Thr Lys Asp Gly Leu Ile Val Pro Ile
545 550 555 560

Phe Gln Glu Arg Leu Leu Ala Val Gly Lys Trp Leu Ser Ile Asn Gly
565 570 575

Glu Ala Ile Tyr Ala Ser Lys Pro Trp Arg Val Gln Trp Glu Lys Asn
580 585 590

Thr Thr Ser Val Trp Tyr Thr Ser Lys Gly Ser Ala Val Tyr Ala Ile
595 600 605

Phe Leu His Trp Pro Glu Asn Gly Val Leu Asn Leu Glu Ser Pro Ile
610 615 620

Thr Thr Ser Thr Thr Lys Ile Thr Met Leu Gly Ile Gln Gly Asp Leu
625 630 635 640

Lys Trp Ser Thr Asp Pro Asp Lys Gly Leu Phe Ile Ser Leu Pro Gln
645 650 655

Leu Pro Pro Ser Ala Val Pro Ala Glu Phe Ala Trp Thr Ile Lys Leu
660 665 670

Thr Gly Val Lys
675

<210> 179

<211> 686

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino FUCA1id sequence of fusion protein of the Fab heavy chain

of humanized anti-hTfR antibody No. 3N and hFUCA1, Fab
HC-GS5-FUCA1

<400> 179

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Pro Pro Arg Arg
245 250 255

Tyr Thr Pro Asp Trp Pro Ser Leu Asp Ser Arg Pro Leu Pro Ala Trp
260 265 270

Phe Asp Glu Ala Lys Phe Gly Val Phe Ile His Trp Gly Val Phe Ser
275 280 285

Val Pro Ala Trp Gly Ser Glu Trp Phe Trp Trp His Trp Gln Gly Glu
290 295 300

Gly Arg Pro Gln Tyr Gln Arg Phe Met Arg Asp Asn Tyr Pro Pro Gly
305 310 315 320

Phe Ser Tyr Ala Asp Phe Gly Pro Gln Phe Thr Ala Arg Phe Phe His
325 330 335

Pro Glu Glu Trp Ala Asp Leu Phe Gln Ala Ala Gly Ala Lys Tyr Val
340 345 350

Val Leu Thr Thr Lys His His Glu Gly Phe Thr Asn Trp Pro Ser Pro
355 360 365

Val Ser Trp Asn Trp Asn Ser Lys Asp Val Gly Pro His Arg Asp Leu

370

375

380

Val Gly Glu Leu Gly Thr Ala Leu Arg Lys Arg Asn Ile Arg Tyr Gly
 385 390 395 400

Leu Tyr His Ser Leu Leu Glu Trp Phe His Pro Leu Tyr Leu Leu Asp
 405 410 415

Lys Lys Asn Gly Phe Lys Thr Gln His Phe Val Ser Ala Lys Thr Met
 420 425 430

Pro Glu Leu Tyr Asp Leu Val Asn Ser Tyr Lys Pro Asp Leu Ile Trp
 435 440 445

Ser Asp Gly Glu Trp Glu Cys Pro Asp Thr Tyr Trp Asn Ser Thr Asn
 450 455 460

Phe Leu Ser Trp Leu Tyr Asn Asp Ser Pro Val Lys Asp Glu Val Val
 465 470 475 480

Val Asn Asp Arg Trp Gly Gln Asn Cys Ser Cys His His Gly Gly Tyr
 485 490 495

Tyr Asn Cys Glu Asp Lys Phe Lys Pro Gln Ser Leu Pro Asp His Lys
 500 505 510

Trp Glu Met Cys Thr Ser Ile Asp Lys Phe Ser Trp Gly Tyr Arg Arg
 515 520 525

Asp Met Ala Leu Ser Asp Val Thr Glu Glu Ser Glu Ile Ile Ser Glu
 530 535 540

Leu Val Gln Thr Val Ser Leu Gly Gly Asn Tyr Leu Leu Asn Ile Gly
 545 550 555 560

Pro Thr Lys Asp Gly Leu Ile Val Pro Ile Phe Gln Glu Arg Leu Leu
 565 570 575

Ala Val Gly Lys Trp Leu Ser Ile Asn Gly Glu Ala Ile Tyr Ala Ser
580 585 590

Lys Pro Trp Arg Val Gln Trp Glu Lys Asn Thr Thr Ser Val Trp Tyr
595 600 605

Thr Ser Lys Gly Ser Ala Val Tyr Ala Ile Phe Leu His Trp Pro Glu
610 615 620

Asn Gly Val Leu Asn Leu Glu Ser Pro Ile Thr Thr Ser Thr Thr Lys
625 630 635 640

Ile Thr Met Leu Gly Ile Gln Gly Asp Leu Lys Trp Ser Thr Asp Pro
645 650 655

Asp Lys Gly Leu Phe Ile Ser Leu Pro Gln Leu Pro Pro Ser Ala Val
660 665 670

Pro Ala Glu Phe Ala Trp Thr Ile Lys Leu Thr Gly Val Lys
675 680 685

<210> 180

<211> 711

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino FUCA1id sequence of fusion protein of the Fab heavy chain
of humanized anti-hTfR antibody No. 3N and hFUCA1, Fab
HC-GS10-FUCA1

<400> 180

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gln Pro Pro Arg Arg Tyr Thr Pro Asp Trp Pro Ser
275 280 285

Leu Asp Ser Arg Pro Leu Pro Ala Trp Phe Asp Glu Ala Lys Phe Gly
290 295 300

Val Phe Ile His Trp Gly Val Phe Ser Val Pro Ala Trp Gly Ser Glu
305 310 315 320

Trp Phe Trp Trp His Trp Gln Gly Glu Gly Arg Pro Gln Tyr Gln Arg
325 330 335

Phe Met Arg Asp Asn Tyr Pro Pro Gly Phe Ser Tyr Ala Asp Phe Gly
340 345 350

Pro Gln Phe Thr Ala Arg Phe Phe His Pro Glu Glu Trp Ala Asp Leu
355 360 365

Phe Gln Ala Ala Gly Ala Lys Tyr Val Val Leu Thr Thr Lys His His
370 375 380

Glu Gly Phe Thr Asn Trp Pro Ser Pro Val Ser Trp Asn Trp Asn Ser
385 390 395 400

Lys Asp Val Gly Pro His Arg Asp Leu Val Gly Glu Leu Gly Thr Ala
405 410 415

Leu Arg Lys Arg Asn Ile Arg Tyr Gly Leu Tyr His Ser Leu Leu Glu

420

425

430

Trp Phe His Pro Leu Tyr Leu Leu Asp Lys Lys Asn Gly Phe Lys Thr
 435 440 445

Gln His Phe Val Ser Ala Lys Thr Met Pro Glu Leu Tyr Asp Leu Val
 450 455 460

Asn Ser Tyr Lys Pro Asp Leu Ile Trp Ser Asp Gly Glu Trp Glu Cys
 465 470 475 480

Pro Asp Thr Tyr Trp Asn Ser Thr Asn Phe Leu Ser Trp Leu Tyr Asn
 485 490 495

Asp Ser Pro Val Lys Asp Glu Val Val Val Asn Asp Arg Trp Gly Gln
 500 505 510

Asn Cys Ser Cys His His Gly Gly Tyr Tyr Asn Cys Glu Asp Lys Phe
 515 520 525

Lys Pro Gln Ser Leu Pro Asp His Lys Trp Glu Met Cys Thr Ser Ile
 530 535 540

Asp Lys Phe Ser Trp Gly Tyr Arg Arg Asp Met Ala Leu Ser Asp Val
 545 550 555 560

Thr Glu Glu Ser Glu Ile Ile Ser Glu Leu Val Gln Thr Val Ser Leu
 565 570 575

Gly Gly Asn Tyr Leu Leu Asn Ile Gly Pro Thr Lys Asp Gly Leu Ile
 580 585 590

Val Pro Ile Phe Gln Glu Arg Leu Leu Ala Val Gly Lys Trp Leu Ser
 595 600 605

Ile Asn Gly Glu Ala Ile Tyr Ala Ser Lys Pro Trp Arg Val Gln Trp
 610 615 620

Glu Lys Asn Thr Thr Ser Val Trp Tyr Thr Ser Lys Gly Ser Ala Val
625 630 635 640

Tyr Ala Ile Phe Leu His Trp Pro Glu Asn Gly Val Leu Asn Leu Glu
645 650 655

Ser Pro Ile Thr Thr Ser Thr Thr Lys Ile Thr Met Leu Gly Ile Gln
660 665 670

Gly Asp Leu Lys Trp Ser Thr Asp Pro Asp Lys Gly Leu Phe Ile Ser
675 680 685

Leu Pro Gln Leu Pro Pro Ser Ala Val Pro Ala Glu Phe Ala Trp Thr
690 695 700

Ile Lys Leu Thr Gly Val Lys
705 710

<210> 181

<211> 761

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino FUCA1id sequence of fusion protein of the Fab heavy chain
of humanized anti-hTfR antibody No. 3N and hFUCA1, Fab
HC-GS20-FUCA1

<400> 181

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
290 295 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305 310 315 320

Ser Gly Gly Gly Gly Ser Gln Pro Pro Arg Arg Tyr Thr Pro Asp Trp
325 330 335

Pro Ser Leu Asp Ser Arg Pro Leu Pro Ala Trp Phe Asp Glu Ala Lys
340 345 350

Phe Gly Val Phe Ile His Trp Gly Val Phe Ser Val Pro Ala Trp Gly
355 360 365

Ser Glu Trp Phe Trp Trp His Trp Gln Gly Glu Gly Arg Pro Gln Tyr
370 375 380

Gln Arg Phe Met Arg Asp Asn Tyr Pro Pro Gly Phe Ser Tyr Ala Asp
385 390 395 400

Phe Gly Pro Gln Phe Thr Ala Arg Phe Phe His Pro Glu Glu Trp Ala
405 410 415

Asp Leu Phe Gln Ala Ala Gly Ala Lys Tyr Val Val Leu Thr Thr Lys
420 425 430

His His Glu Gly Phe Thr Asn Trp Pro Ser Pro Val Ser Trp Asn Trp

435

440

445

Asn Ser Lys Asp Val Gly Pro His Arg Asp Leu Val Gly Glu Leu Gly
 450 455 460

Thr Ala Leu Arg Lys Arg Asn Ile Arg Tyr Gly Leu Tyr His Ser Leu
 465 470 475 480

Leu Glu Trp Phe His Pro Leu Tyr Leu Leu Asp Lys Lys Asn Gly Phe
 485 490 495

Lys Thr Gln His Phe Val Ser Ala Lys Thr Met Pro Glu Leu Tyr Asp
 500 505 510

Leu Val Asn Ser Tyr Lys Pro Asp Leu Ile Trp Ser Asp Gly Glu Trp
 515 520 525

Glu Cys Pro Asp Thr Tyr Trp Asn Ser Thr Asn Phe Leu Ser Trp Leu
 530 535 540

Tyr Asn Asp Ser Pro Val Lys Asp Glu Val Val Val Asn Asp Arg Trp
 545 550 555 560

Gly Gln Asn Cys Ser Cys His His Gly Gly Tyr Tyr Asn Cys Glu Asp
 565 570 575

Lys Phe Lys Pro Gln Ser Leu Pro Asp His Lys Trp Glu Met Cys Thr
 580 585 590

Ser Ile Asp Lys Phe Ser Trp Gly Tyr Arg Arg Asp Met Ala Leu Ser
 595 600 605

Asp Val Thr Glu Glu Ser Glu Ile Ile Ser Glu Leu Val Gln Thr Val
 610 615 620

Ser Leu Gly Gly Asn Tyr Leu Leu Asn Ile Gly Pro Thr Lys Asp Gly
 625 630 635 640

Leu Ile Val Pro Ile Phe Gln Glu Arg Leu Leu Ala Val Gly Lys Trp
645 650 655

Leu Ser Ile Asn Gly Glu Ala Ile Tyr Ala Ser Lys Pro Trp Arg Val
660 665 670

Gln Trp Glu Lys Asn Thr Thr Ser Val Trp Tyr Thr Ser Lys Gly Ser
675 680 685

Ala Val Tyr Ala Ile Phe Leu His Trp Pro Glu Asn Gly Val Leu Asn
690 695 700

Leu Glu Ser Pro Ile Thr Thr Ser Thr Thr Lys Ile Thr Met Leu Gly
705 710 715 720

Ile Gln Gly Asp Leu Lys Trp Ser Thr Asp Pro Asp Lys Gly Leu Phe
725 730 735

Ile Ser Leu Pro Gln Leu Pro Pro Ser Ala Val Pro Ala Glu Phe Ala
740 745 750

Trp Thr Ile Lys Leu Thr Gly Val Lys
755 760

<210> 182

<211> 1409

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino LAMANid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hLAMAN, IgG4
HC-LAMAN

<400> 182

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln

405

410

415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Ser Gly
 435 440 445

Gly Tyr Glu Thr Cys Pro Thr Val Gln Pro Asn Met Leu Asn Val His
 450 455 460

Leu Leu Pro His Thr His Asp Asp Val Gly Trp Leu Lys Thr Val Asp
 465 470 475 480

Gln Tyr Phe Tyr Gly Ile Lys Asn Asp Ile Gln His Ala Gly Val Gln
 485 490 495

Tyr Ile Leu Asp Ser Val Ile Ser Ala Leu Leu Ala Asp Pro Thr Arg
 500 505 510

Arg Phe Ile Tyr Val Glu Ile Ala Phe Phe Ser Arg Trp Trp His Gln
 515 520 525

Gln Thr Asn Ala Thr Gln Glu Val Val Arg Asp Leu Val Arg Gln Gly
 530 535 540

Arg Leu Glu Phe Ala Asn Gly Gly Trp Val Met Asn Asp Glu Ala Ala
 545 550 555 560

Thr His Tyr Gly Ala Ile Val Asp Gln Met Thr Leu Gly Leu Arg Phe
 565 570 575

Leu Glu Asp Thr Phe Gly Asn Asp Gly Arg Pro Arg Val Ala Trp His
 580 585 590

Ile Asp Pro Phe Gly His Ser Arg Glu Gln Ala Ser Leu Phe Ala Gln
 595 600 605

Met Gly Phe Asp Gly Phe Phe Phe Gly Arg Leu Asp Tyr Gln Asp Lys
610 615 620

Trp Val Arg Met Gln Lys Leu Glu Met Glu Gln Val Trp Arg Ala Ser
625 630 635 640

Thr Ser Leu Lys Pro Pro Thr Ala Asp Leu Phe Thr Gly Val Leu Pro
645 650 655

Asn Gly Tyr Asn Pro Pro Arg Asn Leu Cys Trp Asp Val Leu Cys Val
660 665 670

Asp Gln Pro Leu Val Glu Asp Pro Arg Ser Pro Glu Tyr Asn Ala Lys
675 680 685

Glu Leu Val Asp Tyr Phe Leu Asn Val Ala Thr Ala Gln Gly Arg Tyr
690 695 700

Tyr Arg Thr Asn His Thr Val Met Thr Met Gly Ser Asp Phe Gln Tyr
705 710 715 720

Glu Asn Ala Asn Met Trp Phe Lys Asn Leu Asp Lys Leu Ile Arg Leu
725 730 735

Val Asn Ala Gln Gln Ala Lys Gly Ser Ser Val His Val Leu Tyr Ser
740 745 750

Thr Pro Ala Cys Tyr Leu Trp Glu Leu Asn Lys Ala Asn Leu Thr Trp
755 760 765

Ser Val Lys His Asp Asp Phe Phe Pro Tyr Ala Asp Gly Pro His Gln
770 775 780

Phe Trp Thr Gly Tyr Phe Ser Ser Arg Pro Ala Leu Lys Arg Tyr Glu
785 790 795 800

Arg Leu Ser Tyr Asn Phe Leu Gln Val Cys Asn Gln Leu Glu Ala Leu
805 810 815

Val Gly Leu Ala Ala Asn Val Gly Pro Tyr Gly Ser Gly Asp Ser Ala
820 825 830

Pro Leu Asn Glu Ala Met Ala Val Leu Gln His His Asp Ala Val Ser
835 840 845

Gly Thr Ser Arg Gln His Val Ala Asn Asp Tyr Ala Arg Gln Leu Ala
850 855 860

Ala Gly Trp Gly Pro Cys Glu Val Leu Leu Ser Asn Ala Leu Ala Arg
865 870 875 880

Leu Arg Gly Phe Lys Asp His Phe Thr Phe Cys Gln Gln Leu Asn Ile
885 890 895

Ser Ile Cys Pro Leu Ser Gln Thr Ala Ala Arg Phe Gln Val Ile Val
900 905 910

Tyr Asn Pro Leu Gly Arg Lys Val Asn Trp Met Val Arg Leu Pro Val
915 920 925

Ser Glu Gly Val Phe Val Val Lys Asp Pro Asn Gly Arg Thr Val Pro
930 935 940

Ser Asp Val Val Ile Phe Pro Ser Ser Asp Ser Gln Ala His Pro Pro
945 950 955 960

Glu Leu Leu Phe Ser Ala Ser Leu Pro Ala Leu Gly Phe Ser Thr Tyr
965 970 975

Ser Val Ala Gln Val Pro Arg Trp Lys Pro Gln Ala Arg Ala Pro Gln
980 985 990

Pro Ile Pro Arg Arg Ser Trp Ser Pro Ala Leu Thr Ile Glu Asn Glu
 995 1000 1005

His Ile Arg Ala Thr Phe Asp Pro Asp Thr Gly Leu Leu Met Glu
 1010 1015 1020

Ile Met Asn Met Asn Gln Gln Leu Leu Leu Pro Val Arg Gln Thr
 1025 1030 1035

Phe Phe Trp Tyr Asn Ala Ser Ile Gly Asp Asn Glu Ser Asp Gln
 1040 1045 1050

Ala Ser Gly Ala Tyr Ile Phe Arg Pro Asn Gln Gln Lys Pro Leu
 1055 1060 1065

Pro Val Ser Arg Trp Ala Gln Ile His Leu Val Lys Thr Pro Leu
 1070 1075 1080

Val Gln Glu Val His Gln Asn Phe Ser Ala Trp Cys Ser Gln Val
 1085 1090 1095

Val Arg Leu Tyr Pro Gly Gln Arg His Leu Glu Leu Glu Trp Ser
 1100 1105 1110

Val Gly Pro Ile Pro Val Gly Asp Thr Trp Gly Lys Glu Val Ile
 1115 1120 1125

Ser Arg Phe Asp Thr Pro Leu Glu Thr Lys Gly Arg Phe Tyr Thr
 1130 1135 1140

Asp Ser Asn Gly Arg Glu Ile Leu Glu Arg Arg Arg Asp Tyr Arg
 1145 1150 1155

Pro Thr Trp Lys Leu Asn Gln Thr Glu Pro Val Ala Gly Asn Tyr
 1160 1165 1170

Tyr Pro Val Asn Thr Arg Ile Tyr Ile Thr Asp Gly Asn Met Gln

1175		1180		1185
Leu Thr Val Leu Thr Asp Arg Ser Gln Gly Gly Ser Ser Leu Arg	1190	1195	1200	
Asp Gly Ser Leu Glu Leu Met Val His Arg Arg Leu Leu Lys Asp	1205	1210	1215	
Asp Gly Arg Gly Val Ser Glu Pro Leu Met Glu Asn Gly Ser Gly	1220	1225	1230	
Ala Trp Val Arg Gly Arg His Leu Val Leu Leu Asp Thr Ala Gln	1235	1240	1245	
Ala Ala Ala Ala Gly His Arg Leu Leu Ala Glu Gln Glu Val Leu	1250	1255	1260	
Ala Pro Gln Val Val Leu Ala Pro Gly Gly Gly Ala Ala Tyr Asn	1265	1270	1275	
Leu Gly Ala Pro Pro Arg Thr Gln Phe Ser Gly Leu Arg Arg Asp	1280	1285	1290	
Leu Pro Pro Ser Val His Leu Leu Thr Leu Ala Ser Trp Gly Pro	1295	1300	1305	
Glu Met Val Leu Leu Arg Leu Glu His Gln Phe Ala Val Gly Glu	1310	1315	1320	
Asp Ser Gly Arg Asn Leu Ser Ala Pro Val Thr Leu Asn Leu Arg	1325	1330	1335	
Asp Leu Phe Ser Thr Phe Thr Ile Thr Arg Leu Gln Glu Thr Thr	1340	1345	1350	
Leu Val Ala Asn Gln Leu Arg Glu Ala Ala Ser Arg Leu Lys Trp	1355	1360	1365	

Thr Thr Asn Thr Gly Pro Thr Pro His Gln Thr Pro Tyr Gln Leu
1370 1375 1380

Asp Pro Ala Asn Ile Thr Leu Glu Pro Met Glu Ile Arg Thr Phe
1385 1390 1395

Leu Ala Ser Val Gln Trp Lys Glu Val Asp Gly
1400 1405

<210> 183

<211> 1432

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino LAMANid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hLAMAN, IgG4
HC-GS5-LAMAN

<400> 183

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Tyr Glu Thr Cys Pro Thr Val Gln
465 470 475 480

Pro Asn Met Leu Asn Val His Leu Leu Pro His Thr His Asp Asp Val

485

490

495

Gly Trp Leu Lys Thr Val Asp Gln Tyr Phe Tyr Gly Ile Lys Asn Asp
 500 505 510

Ile Gln His Ala Gly Val Gln Tyr Ile Leu Asp Ser Val Ile Ser Ala
 515 520 525

Leu Leu Ala Asp Pro Thr Arg Arg Phe Ile Tyr Val Glu Ile Ala Phe
 530 535 540

Phe Ser Arg Trp Trp His Gln Gln Thr Asn Ala Thr Gln Glu Val Val
 545 550 555 560

Arg Asp Leu Val Arg Gln Gly Arg Leu Glu Phe Ala Asn Gly Gly Trp
 565 570 575

Val Met Asn Asp Glu Ala Ala Thr His Tyr Gly Ala Ile Val Asp Gln
 580 585 590

Met Thr Leu Gly Leu Arg Phe Leu Glu Asp Thr Phe Gly Asn Asp Gly
 595 600 605

Arg Pro Arg Val Ala Trp His Ile Asp Pro Phe Gly His Ser Arg Glu
 610 615 620

Gln Ala Ser Leu Phe Ala Gln Met Gly Phe Asp Gly Phe Phe Phe Gly
 625 630 635 640

Arg Leu Asp Tyr Gln Asp Lys Trp Val Arg Met Gln Lys Leu Glu Met
 645 650 655

Glu Gln Val Trp Arg Ala Ser Thr Ser Leu Lys Pro Pro Thr Ala Asp
 660 665 670

Leu Phe Thr Gly Val Leu Pro Asn Gly Tyr Asn Pro Pro Arg Asn Leu
 675 680 685

Cys Trp Asp Val Leu Cys Val Asp Gln Pro Leu Val Glu Asp Pro Arg
690 695 700

Ser Pro Glu Tyr Asn Ala Lys Glu Leu Val Asp Tyr Phe Leu Asn Val
705 710 715 720

Ala Thr Ala Gln Gly Arg Tyr Tyr Arg Thr Asn His Thr Val Met Thr
725 730 735

Met Gly Ser Asp Phe Gln Tyr Glu Asn Ala Asn Met Trp Phe Lys Asn
740 745 750

Leu Asp Lys Leu Ile Arg Leu Val Asn Ala Gln Gln Ala Lys Gly Ser
755 760 765

Ser Val His Val Leu Tyr Ser Thr Pro Ala Cys Tyr Leu Trp Glu Leu
770 775 780

Asn Lys Ala Asn Leu Thr Trp Ser Val Lys His Asp Asp Phe Phe Pro
785 790 795 800

Tyr Ala Asp Gly Pro His Gln Phe Trp Thr Gly Tyr Phe Ser Ser Arg
805 810 815

Pro Ala Leu Lys Arg Tyr Glu Arg Leu Ser Tyr Asn Phe Leu Gln Val
820 825 830

Cys Asn Gln Leu Glu Ala Leu Val Gly Leu Ala Ala Asn Val Gly Pro
835 840 845

Tyr Gly Ser Gly Asp Ser Ala Pro Leu Asn Glu Ala Met Ala Val Leu
850 855 860

Gln His His Asp Ala Val Ser Gly Thr Ser Arg Gln His Val Ala Asn
865 870 875 880

Asp Tyr Ala Arg Gln Leu Ala Ala Gly Trp Gly Pro Cys Glu Val Leu
885 890 895

Leu Ser Asn Ala Leu Ala Arg Leu Arg Gly Phe Lys Asp His Phe Thr
900 905 910

Phe Cys Gln Gln Leu Asn Ile Ser Ile Cys Pro Leu Ser Gln Thr Ala
915 920 925

Ala Arg Phe Gln Val Ile Val Tyr Asn Pro Leu Gly Arg Lys Val Asn
930 935 940

Trp Met Val Arg Leu Pro Val Ser Glu Gly Val Phe Val Val Lys Asp
945 950 955 960

Pro Asn Gly Arg Thr Val Pro Ser Asp Val Val Ile Phe Pro Ser Ser
965 970 975

Asp Ser Gln Ala His Pro Pro Glu Leu Leu Phe Ser Ala Ser Leu Pro
980 985 990

Ala Leu Gly Phe Ser Thr Tyr Ser Val Ala Gln Val Pro Arg Trp Lys
995 1000 1005

Pro Gln Ala Arg Ala Pro Gln Pro Ile Pro Arg Arg Ser Trp Ser
1010 1015 1020

Pro Ala Leu Thr Ile Glu Asn Glu His Ile Arg Ala Thr Phe Asp
1025 1030 1035

Pro Asp Thr Gly Leu Leu Met Glu Ile Met Asn Met Asn Gln Gln
1040 1045 1050

Leu Leu Leu Pro Val Arg Gln Thr Phe Phe Trp Tyr Asn Ala Ser
1055 1060 1065

Ile Gly Asp Asn Glu Ser Asp Gln Ala Ser Gly Ala Tyr Ile Phe
1070 1075 1080

Arg Pro Asn Gln Gln Lys Pro Leu Pro Val Ser Arg Trp Ala Gln
1085 1090 1095

Ile His Leu Val Lys Thr Pro Leu Val Gln Glu Val His Gln Asn
1100 1105 1110

Phe Ser Ala Trp Cys Ser Gln Val Val Arg Leu Tyr Pro Gly Gln
1115 1120 1125

Arg His Leu Glu Leu Glu Trp Ser Val Gly Pro Ile Pro Val Gly
1130 1135 1140

Asp Thr Trp Gly Lys Glu Val Ile Ser Arg Phe Asp Thr Pro Leu
1145 1150 1155

Glu Thr Lys Gly Arg Phe Tyr Thr Asp Ser Asn Gly Arg Glu Ile
1160 1165 1170

Leu Glu Arg Arg Arg Asp Tyr Arg Pro Thr Trp Lys Leu Asn Gln
1175 1180 1185

Thr Glu Pro Val Ala Gly Asn Tyr Tyr Pro Val Asn Thr Arg Ile
1190 1195 1200

Tyr Ile Thr Asp Gly Asn Met Gln Leu Thr Val Leu Thr Asp Arg
1205 1210 1215

Ser Gln Gly Gly Ser Ser Leu Arg Asp Gly Ser Leu Glu Leu Met
1220 1225 1230

Val His Arg Arg Leu Leu Lys Asp Asp Gly Arg Gly Val Ser Glu
1235 1240 1245

Pro Leu Met Glu Asn Gly Ser Gly Ala Trp Val Arg Gly Arg His

1250		1255		1260
Leu Val	Leu Leu Asp Thr	Ala	Gln Ala Ala Ala	Ala Gly His Arg
1265		1270		1275
Leu Leu	Ala Glu Gln Glu	Val	Leu Ala Pro Gln	Val Val Leu Ala
1280		1285		1290
Pro Gly	Gly Gly Ala Ala	Tyr	Asn Leu Gly Ala	Pro Pro Arg Thr
1295		1300		1305
Gln Phe	Ser Gly Leu Arg	Arg	Asp Leu Pro Pro	Ser Val His Leu
1310		1315		1320
Leu Thr	Leu Ala Ser Trp	Gly	Pro Glu Met Val	Leu Leu Arg Leu
1325		1330		1335
Glu His	Gln Phe Ala Val	Gly	Glu Asp Ser Gly	Arg Asn Leu Ser
1340		1345		1350
Ala Pro	Val Thr Leu Asn	Leu	Arg Asp Leu Phe	Ser Thr Phe Thr
1355		1360		1365
Ile Thr	Arg Leu Gln Glu	Thr	Thr Leu Val Ala	Asn Gln Leu Arg
1370		1375		1380
Glu Ala	Ala Ser Arg Leu	Lys	Trp Thr Thr Asn	Thr Gly Pro Thr
1385		1390		1395
Pro His	Gln Thr Pro Tyr	Gln	Leu Asp Pro Ala	Asn Ile Thr Leu
1400		1405		1410
Glu Pro	Met Glu Ile Arg	Thr	Phe Leu Ala Ser	Val Gln Trp Lys
1415		1420		1425
Glu Val	Asp Gly			
1430				

<210> 184
<211> 1457
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino LAMANid sequence of fusion protein of the heavy chain of
humanized anti-hTfR antibody No. 3N (IgG4) and hLAMAN, IgG4
HC-GS10-LAMAN

<400> 184

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Tyr Glu Thr Cys Pro Thr Val Gln Pro Asn Met Leu Asn Val His
500 505 510

Leu Leu Pro His Thr His Asp Asp Val Gly Trp Leu Lys Thr Val Asp
515 520 525

Gln Tyr Phe Tyr Gly Ile Lys Asn Asp Ile Gln His Ala Gly Val Gln

530

535

540

Tyr Ile Leu Asp Ser Val Ile Ser Ala Leu Leu Ala Asp Pro Thr Arg
 545 550 555 560

Arg Phe Ile Tyr Val Glu Ile Ala Phe Phe Ser Arg Trp Trp His Gln
 565 570 575

Gln Thr Asn Ala Thr Gln Glu Val Val Arg Asp Leu Val Arg Gln Gly
 580 585 590

Arg Leu Glu Phe Ala Asn Gly Gly Trp Val Met Asn Asp Glu Ala Ala
 595 600 605

Thr His Tyr Gly Ala Ile Val Asp Gln Met Thr Leu Gly Leu Arg Phe
 610 615 620

Leu Glu Asp Thr Phe Gly Asn Asp Gly Arg Pro Arg Val Ala Trp His
 625 630 635 640

Ile Asp Pro Phe Gly His Ser Arg Glu Gln Ala Ser Leu Phe Ala Gln
 645 650 655

Met Gly Phe Asp Gly Phe Phe Phe Gly Arg Leu Asp Tyr Gln Asp Lys
 660 665 670

Trp Val Arg Met Gln Lys Leu Glu Met Glu Gln Val Trp Arg Ala Ser
 675 680 685

Thr Ser Leu Lys Pro Pro Thr Ala Asp Leu Phe Thr Gly Val Leu Pro
 690 695 700

Asn Gly Tyr Asn Pro Pro Arg Asn Leu Cys Trp Asp Val Leu Cys Val
 705 710 715 720

Asp Gln Pro Leu Val Glu Asp Pro Arg Ser Pro Glu Tyr Asn Ala Lys
 725 730 735

Glu Leu Val Asp Tyr Phe Leu Asn Val Ala Thr Ala Gln Gly Arg Tyr
740 745 750

Tyr Arg Thr Asn His Thr Val Met Thr Met Gly Ser Asp Phe Gln Tyr
755 760 765

Glu Asn Ala Asn Met Trp Phe Lys Asn Leu Asp Lys Leu Ile Arg Leu
770 775 780

Val Asn Ala Gln Gln Ala Lys Gly Ser Ser Val His Val Leu Tyr Ser
785 790 795 800

Thr Pro Ala Cys Tyr Leu Trp Glu Leu Asn Lys Ala Asn Leu Thr Trp
805 810 815

Ser Val Lys His Asp Asp Phe Phe Pro Tyr Ala Asp Gly Pro His Gln
820 825 830

Phe Trp Thr Gly Tyr Phe Ser Ser Arg Pro Ala Leu Lys Arg Tyr Glu
835 840 845

Arg Leu Ser Tyr Asn Phe Leu Gln Val Cys Asn Gln Leu Glu Ala Leu
850 855 860

Val Gly Leu Ala Ala Asn Val Gly Pro Tyr Gly Ser Gly Asp Ser Ala
865 870 875 880

Pro Leu Asn Glu Ala Met Ala Val Leu Gln His His Asp Ala Val Ser
885 890 895

Gly Thr Ser Arg Gln His Val Ala Asn Asp Tyr Ala Arg Gln Leu Ala
900 905 910

Ala Gly Trp Gly Pro Cys Glu Val Leu Leu Ser Asn Ala Leu Ala Arg
915 920 925

Leu Arg Gly Phe Lys Asp His Phe Thr Phe Cys Gln Gln Leu Asn Ile
930 935 940

Ser Ile Cys Pro Leu Ser Gln Thr Ala Ala Arg Phe Gln Val Ile Val
945 950 955 960

Tyr Asn Pro Leu Gly Arg Lys Val Asn Trp Met Val Arg Leu Pro Val
965 970 975

Ser Glu Gly Val Phe Val Val Lys Asp Pro Asn Gly Arg Thr Val Pro
980 985 990

Ser Asp Val Val Ile Phe Pro Ser Ser Asp Ser Gln Ala His Pro Pro
995 1000 1005

Glu Leu Leu Phe Ser Ala Ser Leu Pro Ala Leu Gly Phe Ser Thr
1010 1015 1020

Tyr Ser Val Ala Gln Val Pro Arg Trp Lys Pro Gln Ala Arg Ala
1025 1030 1035

Pro Gln Pro Ile Pro Arg Arg Ser Trp Ser Pro Ala Leu Thr Ile
1040 1045 1050

Glu Asn Glu His Ile Arg Ala Thr Phe Asp Pro Asp Thr Gly Leu
1055 1060 1065

Leu Met Glu Ile Met Asn Met Asn Gln Gln Leu Leu Leu Pro Val
1070 1075 1080

Arg Gln Thr Phe Phe Trp Tyr Asn Ala Ser Ile Gly Asp Asn Glu
1085 1090 1095

Ser Asp Gln Ala Ser Gly Ala Tyr Ile Phe Arg Pro Asn Gln Gln
1100 1105 1110

Lys Pro Leu Pro Val Ser Arg Trp Ala Gln Ile His Leu Val Lys
1115 1120 1125

Thr Pro Leu Val Gln Glu Val His Gln Asn Phe Ser Ala Trp Cys
1130 1135 1140

Ser Gln Val Val Arg Leu Tyr Pro Gly Gln Arg His Leu Glu Leu
1145 1150 1155

Glu Trp Ser Val Gly Pro Ile Pro Val Gly Asp Thr Trp Gly Lys
1160 1165 1170

Glu Val Ile Ser Arg Phe Asp Thr Pro Leu Glu Thr Lys Gly Arg
1175 1180 1185

Phe Tyr Thr Asp Ser Asn Gly Arg Glu Ile Leu Glu Arg Arg Arg
1190 1195 1200

Asp Tyr Arg Pro Thr Trp Lys Leu Asn Gln Thr Glu Pro Val Ala
1205 1210 1215

Gly Asn Tyr Tyr Pro Val Asn Thr Arg Ile Tyr Ile Thr Asp Gly
1220 1225 1230

Asn Met Gln Leu Thr Val Leu Thr Asp Arg Ser Gln Gly Gly Ser
1235 1240 1245

Ser Leu Arg Asp Gly Ser Leu Glu Leu Met Val His Arg Arg Leu
1250 1255 1260

Leu Lys Asp Asp Gly Arg Gly Val Ser Glu Pro Leu Met Glu Asn
1265 1270 1275

Gly Ser Gly Ala Trp Val Arg Gly Arg His Leu Val Leu Leu Asp
1280 1285 1290

Thr Ala Gln Ala Ala Ala Ala Gly His Arg Leu Leu Ala Glu Gln

1295

1300

1305

Glu Val Leu Ala Pro Gln Val Val Leu Ala Pro Gly Gly Gly Ala
 1310 1315 1320

Ala Tyr Asn Leu Gly Ala Pro Pro Arg Thr Gln Phe Ser Gly Leu
 1325 1330 1335

Arg Arg Asp Leu Pro Pro Ser Val His Leu Leu Thr Leu Ala Ser
 1340 1345 1350

Trp Gly Pro Glu Met Val Leu Leu Arg Leu Glu His Gln Phe Ala
 1355 1360 1365

Val Gly Glu Asp Ser Gly Arg Asn Leu Ser Ala Pro Val Thr Leu
 1370 1375 1380

Asn Leu Arg Asp Leu Phe Ser Thr Phe Thr Ile Thr Arg Leu Gln
 1385 1390 1395

Glu Thr Thr Leu Val Ala Asn Gln Leu Arg Glu Ala Ala Ser Arg
 1400 1405 1410

Leu Lys Trp Thr Thr Asn Thr Gly Pro Thr Pro His Gln Thr Pro
 1415 1420 1425

Tyr Gln Leu Asp Pro Ala Asn Ile Thr Leu Glu Pro Met Glu Ile
 1430 1435 1440

Arg Thr Phe Leu Ala Ser Val Gln Trp Lys Glu Val Asp Gly
 1445 1450 1455

<210> 185

<211> 1507

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino LAMANid sequence of fusion protein of the heavy chain of humanized anti-hTfR antibody No. 3N (IgG4) and hLAMAN, IgG4 HC-GS20-LAMAN

<400> 185

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
485 490 495

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Gly Gly Tyr Glu Thr Cys Pro Thr Val Gln Pro Asn Met Leu Asn
545 550 555 560

Val His Leu Leu Pro His Thr His Asp Asp Val Gly Trp Leu Lys Thr

565

570

575

Val Asp Gln Tyr Phe Tyr Gly Ile Lys Asn Asp Ile Gln His Ala Gly
 580 585 590

Val Gln Tyr Ile Leu Asp Ser Val Ile Ser Ala Leu Leu Ala Asp Pro
 595 600 605

Thr Arg Arg Phe Ile Tyr Val Glu Ile Ala Phe Phe Ser Arg Trp Trp
 610 615 620

His Gln Gln Thr Asn Ala Thr Gln Glu Val Val Arg Asp Leu Val Arg
 625 630 635 640

Gln Gly Arg Leu Glu Phe Ala Asn Gly Gly Trp Val Met Asn Asp Glu
 645 650 655

Ala Ala Thr His Tyr Gly Ala Ile Val Asp Gln Met Thr Leu Gly Leu
 660 665 670

Arg Phe Leu Glu Asp Thr Phe Gly Asn Asp Gly Arg Pro Arg Val Ala
 675 680 685

Trp His Ile Asp Pro Phe Gly His Ser Arg Glu Gln Ala Ser Leu Phe
 690 695 700

Ala Gln Met Gly Phe Asp Gly Phe Phe Phe Gly Arg Leu Asp Tyr Gln
 705 710 715 720

Asp Lys Trp Val Arg Met Gln Lys Leu Glu Met Glu Gln Val Trp Arg
 725 730 735

Ala Ser Thr Ser Leu Lys Pro Pro Thr Ala Asp Leu Phe Thr Gly Val
 740 745 750

Leu Pro Asn Gly Tyr Asn Pro Pro Arg Asn Leu Cys Trp Asp Val Leu
 755 760 765

Cys Val Asp Gln Pro Leu Val Glu Asp Pro Arg Ser Pro Glu Tyr Asn
770 775 780

Ala Lys Glu Leu Val Asp Tyr Phe Leu Asn Val Ala Thr Ala Gln Gly
785 790 795 800

Arg Tyr Tyr Arg Thr Asn His Thr Val Met Thr Met Gly Ser Asp Phe
805 810 815

Gln Tyr Glu Asn Ala Asn Met Trp Phe Lys Asn Leu Asp Lys Leu Ile
820 825 830

Arg Leu Val Asn Ala Gln Gln Ala Lys Gly Ser Ser Val His Val Leu
835 840 845

Tyr Ser Thr Pro Ala Cys Tyr Leu Trp Glu Leu Asn Lys Ala Asn Leu
850 855 860

Thr Trp Ser Val Lys His Asp Asp Phe Phe Pro Tyr Ala Asp Gly Pro
865 870 875 880

His Gln Phe Trp Thr Gly Tyr Phe Ser Ser Arg Pro Ala Leu Lys Arg
885 890 895

Tyr Glu Arg Leu Ser Tyr Asn Phe Leu Gln Val Cys Asn Gln Leu Glu
900 905 910

Ala Leu Val Gly Leu Ala Ala Asn Val Gly Pro Tyr Gly Ser Gly Asp
915 920 925

Ser Ala Pro Leu Asn Glu Ala Met Ala Val Leu Gln His His Asp Ala
930 935 940

Val Ser Gly Thr Ser Arg Gln His Val Ala Asn Asp Tyr Ala Arg Gln
945 950 955 960

Leu Ala Ala Gly Trp Gly Pro Cys Glu Val Leu Leu Ser Asn Ala Leu
965 970 975

Ala Arg Leu Arg Gly Phe Lys Asp His Phe Thr Phe Cys Gln Gln Leu
980 985 990

Asn Ile Ser Ile Cys Pro Leu Ser Gln Thr Ala Ala Arg Phe Gln Val
995 1000 1005

Ile Val Tyr Asn Pro Leu Gly Arg Lys Val Asn Trp Met Val Arg
1010 1015 1020

Leu Pro Val Ser Glu Gly Val Phe Val Val Lys Asp Pro Asn Gly
1025 1030 1035

Arg Thr Val Pro Ser Asp Val Val Ile Phe Pro Ser Ser Asp Ser
1040 1045 1050

Gln Ala His Pro Pro Glu Leu Leu Phe Ser Ala Ser Leu Pro Ala
1055 1060 1065

Leu Gly Phe Ser Thr Tyr Ser Val Ala Gln Val Pro Arg Trp Lys
1070 1075 1080

Pro Gln Ala Arg Ala Pro Gln Pro Ile Pro Arg Arg Ser Trp Ser
1085 1090 1095

Pro Ala Leu Thr Ile Glu Asn Glu His Ile Arg Ala Thr Phe Asp
1100 1105 1110

Pro Asp Thr Gly Leu Leu Met Glu Ile Met Asn Met Asn Gln Gln
1115 1120 1125

Leu Leu Leu Pro Val Arg Gln Thr Phe Phe Trp Tyr Asn Ala Ser
1130 1135 1140

Ile Gly Asp Asn Glu Ser Asp Gln Ala Ser Gly Ala Tyr Ile Phe
1145 1150 1155

Arg Pro Asn Gln Gln Lys Pro Leu Pro Val Ser Arg Trp Ala Gln
1160 1165 1170

Ile His Leu Val Lys Thr Pro Leu Val Gln Glu Val His Gln Asn
1175 1180 1185

Phe Ser Ala Trp Cys Ser Gln Val Val Arg Leu Tyr Pro Gly Gln
1190 1195 1200

Arg His Leu Glu Leu Glu Trp Ser Val Gly Pro Ile Pro Val Gly
1205 1210 1215

Asp Thr Trp Gly Lys Glu Val Ile Ser Arg Phe Asp Thr Pro Leu
1220 1225 1230

Glu Thr Lys Gly Arg Phe Tyr Thr Asp Ser Asn Gly Arg Glu Ile
1235 1240 1245

Leu Glu Arg Arg Arg Asp Tyr Arg Pro Thr Trp Lys Leu Asn Gln
1250 1255 1260

Thr Glu Pro Val Ala Gly Asn Tyr Tyr Pro Val Asn Thr Arg Ile
1265 1270 1275

Tyr Ile Thr Asp Gly Asn Met Gln Leu Thr Val Leu Thr Asp Arg
1280 1285 1290

Ser Gln Gly Gly Ser Ser Leu Arg Asp Gly Ser Leu Glu Leu Met
1295 1300 1305

Val His Arg Arg Leu Leu Lys Asp Asp Gly Arg Gly Val Ser Glu
1310 1315 1320

Pro Leu Met Glu Asn Gly Ser Gly Ala Trp Val Arg Gly Arg His

1325		1330		1335
Leu Val 1340	Leu Leu Asp Thr	Ala 1345	Gln Ala Ala Ala Ala	Gly His Arg 1350
Leu Leu 1355	Ala Glu Gln Glu	Val 1360	Leu Ala Pro Gln	Val Val Leu Ala 1365
Pro Gly 1370	Gly Gly Ala Ala	Tyr 1375	Asn Leu Gly Ala	Pro Pro Arg Thr 1380
Gln Phe 1385	Ser Gly Leu Arg	Arg 1390	Asp Leu Pro Pro	Ser Val His Leu 1395
Leu Thr 1400	Leu Ala Ser Trp	Gly 1405	Pro Glu Met Val	Leu Leu Arg Leu 1410
Glu His 1415	Gln Phe Ala Val	Gly 1420	Glu Asp Ser Gly	Arg Asn Leu Ser 1425
Ala Pro 1430	Val Thr Leu Asn	Leu 1435	Arg Asp Leu Phe	Ser Thr Phe Thr 1440
Ile Thr 1445	Arg Leu Gln Glu	Thr 1450	Thr Leu Val Ala	Asn Gln Leu Arg 1455
Glu Ala 1460	Ala Ser Arg Leu	Lys 1465	Trp Thr Thr Asn	Thr Gly Pro Thr 1470
Pro His 1475	Gln Thr Pro Tyr	Gln 1480	Leu Asp Pro Ala	Asn Ile Thr Leu 1485
Glu Pro 1490	Met Glu Ile Arg	Thr 1495	Phe Leu Ala Ser	Val Gln Trp Lys 1500
Glu Val 1505	Asp Gly			

<210> 186
<211> 1203
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino LAMANid sequence of fusion protein of the Fab heavy chain
of humanized anti-hTfR antibody No. 3N and hLAMAN, Fab
HC-GS3-LAMAN

<400> 186

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Tyr Glu Thr Cys Pro Thr Val Gln Pro Asn Met Leu Asn
245 250 255

Val His Leu Leu Pro His Thr His Asp Asp Val Gly Trp Leu Lys Thr
260 265 270

Val Asp Gln Tyr Phe Tyr Gly Ile Lys Asn Asp Ile Gln His Ala Gly
275 280 285

Val Gln Tyr Ile Leu Asp Ser Val Ile Ser Ala Leu Leu Ala Asp Pro
290 295 300

Thr Arg Arg Phe Ile Tyr Val Glu Ile Ala Phe Phe Ser Arg Trp Trp
305 310 315 320

His Gln Gln Thr Asn Ala Thr Gln Glu Val Val Arg Asp Leu Val Arg
325 330 335

Gln Gly Arg Leu Glu Phe Ala Asn Gly Gly Trp Val Met Asn Asp Glu
340 345 350

Ala Ala Thr His Tyr Gly Ala Ile Val Asp Gln Met Thr Leu Gly Leu
355 360 365

Arg Phe Leu Glu Asp Thr Phe Gly Asn Asp Gly Arg Pro Arg Val Ala
370 375 380

Trp His Ile Asp Pro Phe Gly His Ser Arg Glu Gln Ala Ser Leu Phe
385 390 395 400

Ala Gln Met Gly Phe Asp Gly Phe Phe Phe Gly Arg Leu Asp Tyr Gln
405 410 415

Asp Lys Trp Val Arg Met Gln Lys Leu Glu Met Glu Gln Val Trp Arg
420 425 430

Ala Ser Thr Ser Leu Lys Pro Pro Thr Ala Asp Leu Phe Thr Gly Val
435 440 445

Leu Pro Asn Gly Tyr Asn Pro Pro Arg Asn Leu Cys Trp Asp Val Leu
450 455 460

Cys Val Asp Gln Pro Leu Val Glu Asp Pro Arg Ser Pro Glu Tyr Asn
465 470 475 480

Ala Lys Glu Leu Val Asp Tyr Phe Leu Asn Val Ala Thr Ala Gln Gly
485 490 495

Arg Tyr Tyr Arg Thr Asn His Thr Val Met Thr Met Gly Ser Asp Phe
500 505 510

Gln Tyr Glu Asn Ala Asn Met Trp Phe Lys Asn Leu Asp Lys Leu Ile
515 520 525

Arg Leu Val Asn Ala Gln Gln Ala Lys Gly Ser Ser Val His Val Leu

530

535

540

Tyr Ser Thr Pro Ala Cys Tyr Leu Trp Glu Leu Asn Lys Ala Asn Leu
 545 550 555 560

Thr Trp Ser Val Lys His Asp Asp Phe Phe Pro Tyr Ala Asp Gly Pro
 565 570 575

His Gln Phe Trp Thr Gly Tyr Phe Ser Ser Arg Pro Ala Leu Lys Arg
 580 585 590

Tyr Glu Arg Leu Ser Tyr Asn Phe Leu Gln Val Cys Asn Gln Leu Glu
 595 600 605

Ala Leu Val Gly Leu Ala Ala Asn Val Gly Pro Tyr Gly Ser Gly Asp
 610 615 620

Ser Ala Pro Leu Asn Glu Ala Met Ala Val Leu Gln His His Asp Ala
 625 630 635 640

Val Ser Gly Thr Ser Arg Gln His Val Ala Asn Asp Tyr Ala Arg Gln
 645 650 655

Leu Ala Ala Gly Trp Gly Pro Cys Glu Val Leu Leu Ser Asn Ala Leu
 660 665 670

Ala Arg Leu Arg Gly Phe Lys Asp His Phe Thr Phe Cys Gln Gln Leu
 675 680 685

Asn Ile Ser Ile Cys Pro Leu Ser Gln Thr Ala Ala Arg Phe Gln Val
 690 695 700

Ile Val Tyr Asn Pro Leu Gly Arg Lys Val Asn Trp Met Val Arg Leu
 705 710 715 720

Pro Val Ser Glu Gly Val Phe Val Val Lys Asp Pro Asn Gly Arg Thr
 725 730 735

Val Pro Ser Asp Val Val Ile Phe Pro Ser Ser Asp Ser Gln Ala His
740 745 750

Pro Pro Glu Leu Leu Phe Ser Ala Ser Leu Pro Ala Leu Gly Phe Ser
755 760 765

Thr Tyr Ser Val Ala Gln Val Pro Arg Trp Lys Pro Gln Ala Arg Ala
770 775 780

Pro Gln Pro Ile Pro Arg Arg Ser Trp Ser Pro Ala Leu Thr Ile Glu
785 790 795 800

Asn Glu His Ile Arg Ala Thr Phe Asp Pro Asp Thr Gly Leu Leu Met
805 810 815

Glu Ile Met Asn Met Asn Gln Gln Leu Leu Pro Val Arg Gln Thr
820 825 830

Phe Phe Trp Tyr Asn Ala Ser Ile Gly Asp Asn Glu Ser Asp Gln Ala
835 840 845

Ser Gly Ala Tyr Ile Phe Arg Pro Asn Gln Gln Lys Pro Leu Pro Val
850 855 860

Ser Arg Trp Ala Gln Ile His Leu Val Lys Thr Pro Leu Val Gln Glu
865 870 875 880

Val His Gln Asn Phe Ser Ala Trp Cys Ser Gln Val Val Arg Leu Tyr
885 890 895

Pro Gly Gln Arg His Leu Glu Leu Glu Trp Ser Val Gly Pro Ile Pro
900 905 910

Val Gly Asp Thr Trp Gly Lys Glu Val Ile Ser Arg Phe Asp Thr Pro
915 920 925

Leu Glu Thr Lys Gly Arg Phe Tyr Thr Asp Ser Asn Gly Arg Glu Ile
930 935 940

Leu Glu Arg Arg Arg Asp Tyr Arg Pro Thr Trp Lys Leu Asn Gln Thr
945 950 955 960

Glu Pro Val Ala Gly Asn Tyr Tyr Pro Val Asn Thr Arg Ile Tyr Ile
965 970 975

Thr Asp Gly Asn Met Gln Leu Thr Val Leu Thr Asp Arg Ser Gln Gly
980 985 990

Gly Ser Ser Leu Arg Asp Gly Ser Leu Glu Leu Met Val His Arg Arg
995 1000 1005

Leu Leu Lys Asp Asp Gly Arg Gly Val Ser Glu Pro Leu Met Glu
1010 1015 1020

Asn Gly Ser Gly Ala Trp Val Arg Gly Arg His Leu Val Leu Leu
1025 1030 1035

Asp Thr Ala Gln Ala Ala Ala Ala Gly His Arg Leu Leu Ala Glu
1040 1045 1050

Gln Glu Val Leu Ala Pro Gln Val Val Leu Ala Pro Gly Gly Gly
1055 1060 1065

Ala Ala Tyr Asn Leu Gly Ala Pro Pro Arg Thr Gln Phe Ser Gly
1070 1075 1080

Leu Arg Arg Asp Leu Pro Pro Ser Val His Leu Leu Thr Leu Ala
1085 1090 1095

Ser Trp Gly Pro Glu Met Val Leu Leu Arg Leu Glu His Gln Phe
1100 1105 1110

Ala Val Gly Glu Asp Ser Gly Arg Asn Leu Ser Ala Pro Val Thr
1115 1120 1125

Leu Asn Leu Arg Asp Leu Phe Ser Thr Phe Thr Ile Thr Arg Leu
1130 1135 1140

Gln Glu Thr Thr Leu Val Ala Asn Gln Leu Arg Glu Ala Ala Ser
1145 1150 1155

Arg Leu Lys Trp Thr Thr Asn Thr Gly Pro Thr Pro His Gln Thr
1160 1165 1170

Pro Tyr Gln Leu Asp Pro Ala Asn Ile Thr Leu Glu Pro Met Glu
1175 1180 1185

Ile Arg Thr Phe Leu Ala Ser Val Gln Trp Lys Glu Val Asp Gly
1190 1195 1200

<210> 187

<211> 1213

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino LAMANid sequence of fusion protein of the Fab heavy chain
of humanized anti-hTfR antibody No. 3N and hLAMAN, Fab
HC-GS5-LAMAN

<400> 187

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe

50

55

60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Tyr Glu Thr
245 250 255

Cys Pro Thr Val Gln Pro Asn Met Leu Asn Val His Leu Leu Pro His
260 265 270

Thr His Asp Asp Val Gly Trp Leu Lys Thr Val Asp Gln Tyr Phe Tyr
275 280 285

Gly Ile Lys Asn Asp Ile Gln His Ala Gly Val Gln Tyr Ile Leu Asp
290 295 300

Ser Val Ile Ser Ala Leu Leu Ala Asp Pro Thr Arg Arg Phe Ile Tyr
305 310 315 320

Val Glu Ile Ala Phe Phe Ser Arg Trp Trp His Gln Gln Thr Asn Ala
325 330 335

Thr Gln Glu Val Val Arg Asp Leu Val Arg Gln Gly Arg Leu Glu Phe
340 345 350

Ala Asn Gly Gly Trp Val Met Asn Asp Glu Ala Ala Thr His Tyr Gly
355 360 365

Ala Ile Val Asp Gln Met Thr Leu Gly Leu Arg Phe Leu Glu Asp Thr
370 375 380

Phe Gly Asn Asp Gly Arg Pro Arg Val Ala Trp His Ile Asp Pro Phe
385 390 395 400

Gly His Ser Arg Glu Gln Ala Ser Leu Phe Ala Gln Met Gly Phe Asp
405 410 415

Gly Phe Phe Phe Gly Arg Leu Asp Tyr Gln Asp Lys Trp Val Arg Met
420 425 430

Gln Lys Leu Glu Met Glu Gln Val Trp Arg Ala Ser Thr Ser Leu Lys
435 440 445

Pro Pro Thr Ala Asp Leu Phe Thr Gly Val Leu Pro Asn Gly Tyr Asn
450 455 460

Pro Pro Arg Asn Leu Cys Trp Asp Val Leu Cys Val Asp Gln Pro Leu
465 470 475 480

Val Glu Asp Pro Arg Ser Pro Glu Tyr Asn Ala Lys Glu Leu Val Asp
485 490 495

Tyr Phe Leu Asn Val Ala Thr Ala Gln Gly Arg Tyr Tyr Arg Thr Asn
500 505 510

His Thr Val Met Thr Met Gly Ser Asp Phe Gln Tyr Glu Asn Ala Asn
515 520 525

Met Trp Phe Lys Asn Leu Asp Lys Leu Ile Arg Leu Val Asn Ala Gln
530 535 540

Gln Ala Lys Gly Ser Ser Val His Val Leu Tyr Ser Thr Pro Ala Cys
545 550 555 560

Tyr Leu Trp Glu Leu Asn Lys Ala Asn Leu Thr Trp Ser Val Lys His
565 570 575

Asp Asp Phe Phe Pro Tyr Ala Asp Gly Pro His Gln Phe Trp Thr Gly
580 585 590

Tyr Phe Ser Ser Arg Pro Ala Leu Lys Arg Tyr Glu Arg Leu Ser Tyr
595 600 605

Asn Phe Leu Gln Val Cys Asn Gln Leu Glu Ala Leu Val Gly Leu Ala
610 615 620

Ala Asn Val Gly Pro Tyr Gly Ser Gly Asp Ser Ala Pro Leu Asn Glu
625 630 635 640

Ala Met Ala Val Leu Gln His His Asp Ala Val Ser Gly Thr Ser Arg
645 650 655

Gln His Val Ala Asn Asp Tyr Ala Arg Gln Leu Ala Ala Gly Trp Gly
660 665 670

Pro Cys Glu Val Leu Leu Ser Asn Ala Leu Ala Arg Leu Arg Gly Phe
675 680 685

Lys Asp His Phe Thr Phe Cys Gln Gln Leu Asn Ile Ser Ile Cys Pro
690 695 700

Leu Ser Gln Thr Ala Ala Arg Phe Gln Val Ile Val Tyr Asn Pro Leu
705 710 715 720

Gly Arg Lys Val Asn Trp Met Val Arg Leu Pro Val Ser Glu Gly Val
725 730 735

Phe Val Val Lys Asp Pro Asn Gly Arg Thr Val Pro Ser Asp Val Val
740 745 750

Ile Phe Pro Ser Ser Asp Ser Gln Ala His Pro Pro Glu Leu Leu Phe
755 760 765

Ser Ala Ser Leu Pro Ala Leu Gly Phe Ser Thr Tyr Ser Val Ala Gln
770 775 780

Val Pro Arg Trp Lys Pro Gln Ala Arg Ala Pro Gln Pro Ile Pro Arg
785 790 795 800

Arg Ser Trp Ser Pro Ala Leu Thr Ile Glu Asn Glu His Ile Arg Ala
805 810 815

Thr Phe Asp Pro Asp Thr Gly Leu Leu Met Glu Ile Met Asn Met Asn
820 825 830

Gln Gln Leu Leu Leu Pro Val Arg Gln Thr Phe Phe Trp Tyr Asn Ala

835

840

845

Ser Ile Gly Asp Asn Glu Ser Asp Gln Ala Ser Gly Ala Tyr Ile Phe
 850 855 860

Arg Pro Asn Gln Gln Lys Pro Leu Pro Val Ser Arg Trp Ala Gln Ile
 865 870 875 880

His Leu Val Lys Thr Pro Leu Val Gln Glu Val His Gln Asn Phe Ser
 885 890 895

Ala Trp Cys Ser Gln Val Val Arg Leu Tyr Pro Gly Gln Arg His Leu
 900 905 910

Glu Leu Glu Trp Ser Val Gly Pro Ile Pro Val Gly Asp Thr Trp Gly
 915 920 925

Lys Glu Val Ile Ser Arg Phe Asp Thr Pro Leu Glu Thr Lys Gly Arg
 930 935 940

Phe Tyr Thr Asp Ser Asn Gly Arg Glu Ile Leu Glu Arg Arg Arg Asp
 945 950 955 960

Tyr Arg Pro Thr Trp Lys Leu Asn Gln Thr Glu Pro Val Ala Gly Asn
 965 970 975

Tyr Tyr Pro Val Asn Thr Arg Ile Tyr Ile Thr Asp Gly Asn Met Gln
 980 985 990

Leu Thr Val Leu Thr Asp Arg Ser Gln Gly Gly Ser Ser Leu Arg Asp
 995 1000 1005

Gly Ser Leu Glu Leu Met Val His Arg Arg Leu Leu Lys Asp Asp
 1010 1015 1020

Gly Arg Gly Val Ser Glu Pro Leu Met Glu Asn Gly Ser Gly Ala
 1025 1030 1035

Trp	Val	Arg	Gly	Arg	His	Leu	Val	Leu	Leu	Asp	Thr	Ala	Gln	Ala
1040						1045					1050			
Ala	Ala	Ala	Gly	His	Arg	Leu	Leu	Ala	Glu	Gln	Glu	Val	Leu	Ala
1055						1060					1065			
Pro	Gln	Val	Val	Leu	Ala	Pro	Gly	Gly	Gly	Ala	Ala	Tyr	Asn	Leu
1070						1075					1080			
Gly	Ala	Pro	Pro	Arg	Thr	Gln	Phe	Ser	Gly	Leu	Arg	Arg	Asp	Leu
1085						1090					1095			
Pro	Pro	Ser	Val	His	Leu	Leu	Thr	Leu	Ala	Ser	Trp	Gly	Pro	Glu
1100						1105					1110			
Met	Val	Leu	Leu	Arg	Leu	Glu	His	Gln	Phe	Ala	Val	Gly	Glu	Asp
1115						1120					1125			
Ser	Gly	Arg	Asn	Leu	Ser	Ala	Pro	Val	Thr	Leu	Asn	Leu	Arg	Asp
1130						1135					1140			
Leu	Phe	Ser	Thr	Phe	Thr	Ile	Thr	Arg	Leu	Gln	Glu	Thr	Thr	Leu
1145						1150					1155			
Val	Ala	Asn	Gln	Leu	Arg	Glu	Ala	Ala	Ser	Arg	Leu	Lys	Trp	Thr
1160						1165					1170			
Thr	Asn	Thr	Gly	Pro	Thr	Pro	His	Gln	Thr	Pro	Tyr	Gln	Leu	Asp
1175						1180					1185			
Pro	Ala	Asn	Ile	Thr	Leu	Glu	Pro	Met	Glu	Ile	Arg	Thr	Phe	Leu
1190						1195					1200			
Ala	Ser	Val	Gln	Trp	Lys	Glu	Val	Asp	Gly					
1205						1210								

<210> 188
 <211> 1238
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Amino LAMANid sequence of fusion protein of the Fab heavy chain
 of humanized anti-hTfR antibody No. 3N and hLAMAN, Fab
 HC-GS10-LAMAN

<400> 188

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
 20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
 50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Tyr Glu Thr Cys Pro Thr Val Gln Pro Asn
275 280 285

Met Leu Asn Val His Leu Leu Pro His Thr His Asp Asp Val Gly Trp
290 295 300

Leu Lys Thr Val Asp Gln Tyr Phe Tyr Gly Ile Lys Asn Asp Ile Gln
305 310 315 320

His Ala Gly Val Gln Tyr Ile Leu Asp Ser Val Ile Ser Ala Leu Leu
325 330 335

Ala Asp Pro Thr Arg Arg Phe Ile Tyr Val Glu Ile Ala Phe Phe Ser

340

345

350

Arg Trp Trp His Gln Gln Thr Asn Ala Thr Gln Glu Val Val Arg Asp
 355 360 365

Leu Val Arg Gln Gly Arg Leu Glu Phe Ala Asn Gly Gly Trp Val Met
 370 375 380

Asn Asp Glu Ala Ala Thr His Tyr Gly Ala Ile Val Asp Gln Met Thr
 385 390 395 400

Leu Gly Leu Arg Phe Leu Glu Asp Thr Phe Gly Asn Asp Gly Arg Pro
 405 410 415

Arg Val Ala Trp His Ile Asp Pro Phe Gly His Ser Arg Glu Gln Ala
 420 425 430

Ser Leu Phe Ala Gln Met Gly Phe Asp Gly Phe Phe Phe Gly Arg Leu
 435 440 445

Asp Tyr Gln Asp Lys Trp Val Arg Met Gln Lys Leu Glu Met Glu Gln
 450 455 460

Val Trp Arg Ala Ser Thr Ser Leu Lys Pro Pro Thr Ala Asp Leu Phe
 465 470 475 480

Thr Gly Val Leu Pro Asn Gly Tyr Asn Pro Pro Arg Asn Leu Cys Trp
 485 490 495

Asp Val Leu Cys Val Asp Gln Pro Leu Val Glu Asp Pro Arg Ser Pro
 500 505 510

Glu Tyr Asn Ala Lys Glu Leu Val Asp Tyr Phe Leu Asn Val Ala Thr
 515 520 525

Ala Gln Gly Arg Tyr Tyr Arg Thr Asn His Thr Val Met Thr Met Gly
 530 535 540

Ser Asp Phe Gln Tyr Glu Asn Ala Asn Met Trp Phe Lys Asn Leu Asp
545 550 555 560

Lys Leu Ile Arg Leu Val Asn Ala Gln Gln Ala Lys Gly Ser Ser Val
565 570 575

His Val Leu Tyr Ser Thr Pro Ala Cys Tyr Leu Trp Glu Leu Asn Lys
580 585 590

Ala Asn Leu Thr Trp Ser Val Lys His Asp Asp Phe Phe Pro Tyr Ala
595 600 605

Asp Gly Pro His Gln Phe Trp Thr Gly Tyr Phe Ser Ser Arg Pro Ala
610 615 620

Leu Lys Arg Tyr Glu Arg Leu Ser Tyr Asn Phe Leu Gln Val Cys Asn
625 630 635 640

Gln Leu Glu Ala Leu Val Gly Leu Ala Ala Asn Val Gly Pro Tyr Gly
645 650 655

Ser Gly Asp Ser Ala Pro Leu Asn Glu Ala Met Ala Val Leu Gln His
660 665 670

His Asp Ala Val Ser Gly Thr Ser Arg Gln His Val Ala Asn Asp Tyr
675 680 685

Ala Arg Gln Leu Ala Ala Gly Trp Gly Pro Cys Glu Val Leu Leu Ser
690 695 700

Asn Ala Leu Ala Arg Leu Arg Gly Phe Lys Asp His Phe Thr Phe Cys
705 710 715 720

Gln Gln Leu Asn Ile Ser Ile Cys Pro Leu Ser Gln Thr Ala Ala Arg
725 730 735

Phe Gln Val Ile Val Tyr Asn Pro Leu Gly Arg Lys Val Asn Trp Met
740 745 750

Val Arg Leu Pro Val Ser Glu Gly Val Phe Val Val Lys Asp Pro Asn
755 760 765

Gly Arg Thr Val Pro Ser Asp Val Val Ile Phe Pro Ser Ser Asp Ser
770 775 780

Gln Ala His Pro Pro Glu Leu Leu Phe Ser Ala Ser Leu Pro Ala Leu
785 790 795 800

Gly Phe Ser Thr Tyr Ser Val Ala Gln Val Pro Arg Trp Lys Pro Gln
805 810 815

Ala Arg Ala Pro Gln Pro Ile Pro Arg Arg Ser Trp Ser Pro Ala Leu
820 825 830

Thr Ile Glu Asn Glu His Ile Arg Ala Thr Phe Asp Pro Asp Thr Gly
835 840 845

Leu Leu Met Glu Ile Met Asn Met Asn Gln Gln Leu Leu Leu Pro Val
850 855 860

Arg Gln Thr Phe Phe Trp Tyr Asn Ala Ser Ile Gly Asp Asn Glu Ser
865 870 875 880

Asp Gln Ala Ser Gly Ala Tyr Ile Phe Arg Pro Asn Gln Gln Lys Pro
885 890 895

Leu Pro Val Ser Arg Trp Ala Gln Ile His Leu Val Lys Thr Pro Leu
900 905 910

Val Gln Glu Val His Gln Asn Phe Ser Ala Trp Cys Ser Gln Val Val
915 920 925

Arg Leu Tyr Pro Gly Gln Arg His Leu Glu Leu Glu Trp Ser Val Gly
930 935 940

Pro Ile Pro Val Gly Asp Thr Trp Gly Lys Glu Val Ile Ser Arg Phe
945 950 955 960

Asp Thr Pro Leu Glu Thr Lys Gly Arg Phe Tyr Thr Asp Ser Asn Gly
965 970 975

Arg Glu Ile Leu Glu Arg Arg Arg Asp Tyr Arg Pro Thr Trp Lys Leu
980 985 990

Asn Gln Thr Glu Pro Val Ala Gly Asn Tyr Tyr Pro Val Asn Thr Arg
995 1000 1005

Ile Tyr Ile Thr Asp Gly Asn Met Gln Leu Thr Val Leu Thr Asp
1010 1015 1020

Arg Ser Gln Gly Gly Ser Ser Leu Arg Asp Gly Ser Leu Glu Leu
1025 1030 1035

Met Val His Arg Arg Leu Leu Lys Asp Asp Gly Arg Gly Val Ser
1040 1045 1050

Glu Pro Leu Met Glu Asn Gly Ser Gly Ala Trp Val Arg Gly Arg
1055 1060 1065

His Leu Val Leu Leu Asp Thr Ala Gln Ala Ala Ala Ala Gly His
1070 1075 1080

Arg Leu Leu Ala Glu Gln Glu Val Leu Ala Pro Gln Val Val Leu
1085 1090 1095

Ala Pro Gly Gly Gly Ala Ala Tyr Asn Leu Gly Ala Pro Pro Arg
1100 1105 1110

Thr Gln Phe Ser Gly Leu Arg Arg Asp Leu Pro Pro Ser Val His

1115

1120

1125

Leu Leu Thr Leu Ala Ser Trp Gly Pro Glu Met Val Leu Leu Arg
 1130 1135 1140

Leu Glu His Gln Phe Ala Val Gly Glu Asp Ser Gly Arg Asn Leu
 1145 1150 1155

Ser Ala Pro Val Thr Leu Asn Leu Arg Asp Leu Phe Ser Thr Phe
 1160 1165 1170

Thr Ile Thr Arg Leu Gln Glu Thr Thr Leu Val Ala Asn Gln Leu
 1175 1180 1185

Arg Glu Ala Ala Ser Arg Leu Lys Trp Thr Thr Asn Thr Gly Pro
 1190 1195 1200

Thr Pro His Gln Thr Pro Tyr Gln Leu Asp Pro Ala Asn Ile Thr
 1205 1210 1215

Leu Glu Pro Met Glu Ile Arg Thr Phe Leu Ala Ser Val Gln Trp
 1220 1225 1230

Lys Glu Val Asp Gly
 1235

<210> 189

<211> 1288

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino LAMANid sequence of fusion protein of the Fab heavy chain
 of humanized anti-hTfR antibody No. 3N and hLAMAN, Fab
 HC-GS20-LAMAN

<400> 189

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
290 295 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305 310 315 320

Ser Gly Gly Gly Gly Ser Gly Gly Tyr Glu Thr Cys Pro Thr Val Gln
325 330 335

Pro Asn Met Leu Asn Val His Leu Leu Pro His Thr His Asp Asp Val
340 345 350

Gly Trp Leu Lys Thr Val Asp Gln Tyr Phe Tyr Gly Ile Lys Asn Asp
355 360 365

Ile Gln His Ala Gly Val Gln Tyr Ile Leu Asp Ser Val Ile Ser Ala
370 375 380

Leu Leu Ala Asp Pro Thr Arg Arg Phe Ile Tyr Val Glu Ile Ala Phe
385 390 395 400

Phe Ser Arg Trp Trp His Gln Gln Thr Asn Ala Thr Gln Glu Val Val
405 410 415

Arg Asp Leu Val Arg Gln Gly Arg Leu Glu Phe Ala Asn Gly Gly Trp
420 425 430

Val Met Asn Asp Glu Ala Ala Thr His Tyr Gly Ala Ile Val Asp Gln
435 440 445

Met Thr Leu Gly Leu Arg Phe Leu Glu Asp Thr Phe Gly Asn Asp Gly
450 455 460

Arg Pro Arg Val Ala Trp His Ile Asp Pro Phe Gly His Ser Arg Glu
465 470 475 480

Gln Ala Ser Leu Phe Ala Gln Met Gly Phe Asp Gly Phe Phe Phe Gly
485 490 495

Arg Leu Asp Tyr Gln Asp Lys Trp Val Arg Met Gln Lys Leu Glu Met
500 505 510

Glu Gln Val Trp Arg Ala Ser Thr Ser Leu Lys Pro Pro Thr Ala Asp
515 520 525

Leu Phe Thr Gly Val Leu Pro Asn Gly Tyr Asn Pro Pro Arg Asn Leu
530 535 540

Cys Trp Asp Val Leu Cys Val Asp Gln Pro Leu Val Glu Asp Pro Arg
545 550 555 560

Ser Pro Glu Tyr Asn Ala Lys Glu Leu Val Asp Tyr Phe Leu Asn Val
565 570 575

Ala Thr Ala Gln Gly Arg Tyr Tyr Arg Thr Asn His Thr Val Met Thr
580 585 590

Met Gly Ser Asp Phe Gln Tyr Glu Asn Ala Asn Met Trp Phe Lys Asn

595

600

605

Leu Asp Lys Leu Ile Arg Leu Val Asn Ala Gln Gln Ala Lys Gly Ser
 610 615 620

Ser Val His Val Leu Tyr Ser Thr Pro Ala Cys Tyr Leu Trp Glu Leu
 625 630 635 640

Asn Lys Ala Asn Leu Thr Trp Ser Val Lys His Asp Asp Phe Phe Pro
 645 650 655

Tyr Ala Asp Gly Pro His Gln Phe Trp Thr Gly Tyr Phe Ser Ser Arg
 660 665 670

Pro Ala Leu Lys Arg Tyr Glu Arg Leu Ser Tyr Asn Phe Leu Gln Val
 675 680 685

Cys Asn Gln Leu Glu Ala Leu Val Gly Leu Ala Ala Asn Val Gly Pro
 690 695 700

Tyr Gly Ser Gly Asp Ser Ala Pro Leu Asn Glu Ala Met Ala Val Leu
 705 710 715 720

Gln His His Asp Ala Val Ser Gly Thr Ser Arg Gln His Val Ala Asn
 725 730 735

Asp Tyr Ala Arg Gln Leu Ala Ala Gly Trp Gly Pro Cys Glu Val Leu
 740 745 750

Leu Ser Asn Ala Leu Ala Arg Leu Arg Gly Phe Lys Asp His Phe Thr
 755 760 765

Phe Cys Gln Gln Leu Asn Ile Ser Ile Cys Pro Leu Ser Gln Thr Ala
 770 775 780

Ala Arg Phe Gln Val Ile Val Tyr Asn Pro Leu Gly Arg Lys Val Asn
 785 790 795 800

Trp Met Val Arg Leu Pro Val Ser Glu Gly Val Phe Val Val Lys Asp
805 810 815

Pro Asn Gly Arg Thr Val Pro Ser Asp Val Val Ile Phe Pro Ser Ser
820 825 830

Asp Ser Gln Ala His Pro Pro Glu Leu Leu Phe Ser Ala Ser Leu Pro
835 840 845

Ala Leu Gly Phe Ser Thr Tyr Ser Val Ala Gln Val Pro Arg Trp Lys
850 855 860

Pro Gln Ala Arg Ala Pro Gln Pro Ile Pro Arg Arg Ser Trp Ser Pro
865 870 875 880

Ala Leu Thr Ile Glu Asn Glu His Ile Arg Ala Thr Phe Asp Pro Asp
885 890 895

Thr Gly Leu Leu Met Glu Ile Met Asn Met Asn Gln Gln Leu Leu Leu
900 905 910

Pro Val Arg Gln Thr Phe Phe Trp Tyr Asn Ala Ser Ile Gly Asp Asn
915 920 925

Glu Ser Asp Gln Ala Ser Gly Ala Tyr Ile Phe Arg Pro Asn Gln Gln
930 935 940

Lys Pro Leu Pro Val Ser Arg Trp Ala Gln Ile His Leu Val Lys Thr
945 950 955 960

Pro Leu Val Gln Glu Val His Gln Asn Phe Ser Ala Trp Cys Ser Gln
965 970 975

Val Val Arg Leu Tyr Pro Gly Gln Arg His Leu Glu Leu Glu Trp Ser
980 985 990

Val Gly Pro Ile Pro Val Gly Asp Thr Trp Gly Lys Glu Val Ile Ser
 995 1000 1005

Arg Phe Asp Thr Pro Leu Glu Thr Lys Gly Arg Phe Tyr Thr Asp
 1010 1015 1020

Ser Asn Gly Arg Glu Ile Leu Glu Arg Arg Arg Asp Tyr Arg Pro
 1025 1030 1035

Thr Trp Lys Leu Asn Gln Thr Glu Pro Val Ala Gly Asn Tyr Tyr
 1040 1045 1050

Pro Val Asn Thr Arg Ile Tyr Ile Thr Asp Gly Asn Met Gln Leu
 1055 1060 1065

Thr Val Leu Thr Asp Arg Ser Gln Gly Gly Ser Ser Leu Arg Asp
 1070 1075 1080

Gly Ser Leu Glu Leu Met Val His Arg Arg Leu Leu Lys Asp Asp
 1085 1090 1095

Gly Arg Gly Val Ser Glu Pro Leu Met Glu Asn Gly Ser Gly Ala
 1100 1105 1110

Trp Val Arg Gly Arg His Leu Val Leu Leu Asp Thr Ala Gln Ala
 1115 1120 1125

Ala Ala Ala Gly His Arg Leu Leu Ala Glu Gln Glu Val Leu Ala
 1130 1135 1140

Pro Gln Val Val Leu Ala Pro Gly Gly Gly Ala Ala Tyr Asn Leu
 1145 1150 1155

Gly Ala Pro Pro Arg Thr Gln Phe Ser Gly Leu Arg Arg Asp Leu
 1160 1165 1170

Pro Pro Ser Val His Leu Leu Thr Leu Ala Ser Trp Gly Pro Glu
1175 1180 1185

Met Val Leu Leu Arg Leu Glu His Gln Phe Ala Val Gly Glu Asp
1190 1195 1200

Ser Gly Arg Asn Leu Ser Ala Pro Val Thr Leu Asn Leu Arg Asp
1205 1210 1215

Leu Phe Ser Thr Phe Thr Ile Thr Arg Leu Gln Glu Thr Thr Leu
1220 1225 1230

Val Ala Asn Gln Leu Arg Glu Ala Ala Ser Arg Leu Lys Trp Thr
1235 1240 1245

Thr Asn Thr Gly Pro Thr Pro His Gln Thr Pro Tyr Gln Leu Asp
1250 1255 1260

Pro Ala Asn Ile Thr Leu Glu Pro Met Glu Ile Arg Thr Phe Leu
1265 1270 1275

Ala Ser Val Gln Trp Lys Glu Val Asp Gly
1280 1285