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SEQUENCE LISTING

<110> SANABIO, LLC

<120> SOLUBLE INTERFERON RECEPTORS AND USES THEREOF

<130> SBN-001PC

<140> PCT/US2018/047614

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<151> 2017-08-22

<160> 155

<170> PatentIn version 3.5

<210> 1

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: RSLV-601 Leader-IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc (aa216-447)with mutations C220S, P238S, P331S,T350V, T366L, K392L, T394W

<400> 1

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
420 425 430

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
435 440 445

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
450 455 460

Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro
465 470 475 480

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
485 490 495

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
500 505 510

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
515 520 525

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
530 535 540

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
545 550 555 560

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
565 570 575

Arg Glu Pro Gln Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Leu Thr
580 585 590

Lys Asn Gln Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser
595 600 605

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
610 615 620

Leu Thr Trp Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
625 630 635 640

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
645 650 655

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
660 665 670

Ser Leu Ser Leu Ser Pro Gly Lys
675 680

<210> 2

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: RSLV-602 Leader-IFNAR2 (aa27-243) (Gly4Ser)4- IgG1 Fc (aa 216-447)with mutations C220S, P238S, P331S,T350V, T366L, K392L, T394W

<400> 2

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys 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 Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
260 265 270

Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro
275 280 285

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
290 295 300

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
305 310 315 320

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
325 330 335

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
340 345 350

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
355 360 365

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
370 375 380

Arg Glu Pro Gln Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Leu Thr
385 390 395 400

Lys Asn Gln Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser
405 410 415

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
420 425 430

Leu Thr Trp Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
435 440 445

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
450 455 460

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
465 470 475 480

Ser Leu Ser Leu Ser Pro Gly Lys
485

<210> 3

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: RSLV-603 Leader-IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc
(aa 216-447)with mutations C220S, P238S, P331S, T350V, L351Y,
F405A, Y407V

<400> 3

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
420 425 430

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
435 440 445

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
450 455 460

Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro
465 470 475 480

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
485 490 495

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
500 505 510

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
515 520 525

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
530 535 540

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
545 550 555 560

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
565 570 575

Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp Glu Leu Thr
580 585 590

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
595 600 605

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
610 615 620

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Val
625 630 635 640

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
645 650 655

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
660 665 670

Ser Leu Ser Leu Ser Pro Gly Lys
675 680

<210> 4
 <211> 488
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: RSLV-604 Leader-IFNAR2 (aa27-243)- (Gly4Ser)4- IgG1 Fc
 (aa 216-447) with mutations C220S, P238S, P331S, and ZW1 Chain A
 mutations T350V, L351Y, F405A, Y407V

<400> 4

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
 20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
 35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
 65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
 85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
 100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
 115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
 130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
 145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys 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 Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
260 265 270

Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro
275 280 285

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
290 295 300

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
305 310 315 320

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
325 330 335

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
340 345 350

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
355 360 365

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
370 375 380

Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp Glu Leu Thr
385 390 395 400

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
420 425 430

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Val
435 440 445

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
450 455 460

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
465 470 475 480

Ser Leu Ser Leu Ser Pro Gly Lys
485

<210> 5
<211> 557
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> IFNAR1

<400> 5

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val
1 5 10 15

Ala Pro Trp Val Leu Ser Ala Ala Ala Gly Gly Lys Asn Leu Lys Ser
20 25 30

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg
35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp
50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln
65 70 75 80

Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val
85 90 95

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

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile
115 120 125

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

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly
145 150 155 160

Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys Asn Ser Ser Gly Val
165 170 175

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu
180 185 190

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr
195 200 205

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr
210 215 220

Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile Glu Val Ser Val Gln
225 230 235 240

Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr
245 250 255

Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn
260 265 270

His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr
275 280 285

Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu
290 295 300

Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu
305 310 315 320

Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val
325 330 335

Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala
340 345 350

Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile
355 360 365

Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile
370 375 380

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

Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn
405 410 415

Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly
420 425 430

Asn Thr Ser Lys Ile Trp Leu Ile Val Gly Ile Cys Ile Ala Leu Phe
435 440 445

Ala Leu Pro Phe Val Ile Tyr Ala Ala Lys Val Phe Leu Arg Cys Ile
450 455 460

Asn Tyr Val Phe Phe Pro Ser Leu Lys Pro Ser Ser Ser Ile Asp Glu
465 470 475 480

Tyr Phe Ser Glu Gln Pro Leu Lys Asn Leu Leu Leu Ser Thr Ser Glu
485 490 495

Glu Gln Ile Glu Lys Cys Phe Ile Ile Glu Asn Ile Ser Thr Ile Ala
500 505 510

Thr Val Glu Glu Thr Asn Gln Thr Asp Glu Asp His Lys Lys Tyr Ser
515 520 525

Ser Gln Thr Ser Gln Asp Ser Gly Asn Tyr Ser Asn Glu Asp Glu Ser
530 535 540

Glu Ser Lys Thr Ser Glu Glu Leu Gln Gln Asp Phe Val
545 550 555

<210> 6
<211> 515
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> IFNAR2

<400> 6

Met Leu Leu Ser Gln Asn Ala Phe Ile Phe Arg Ser Leu Asn Leu Val
1 5 10 15

Leu Met Val Tyr Ile Ser Leu Val Phe Gly Ile Ser Tyr Asp Ser Pro
20 25 30

Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys Ile Ser Leu Arg Asn Phe
35 40 45

Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn His Ser Ile Val Pro Thr
50 55 60

His Tyr Thr Leu Leu Tyr Thr Ile Met Ser Lys Pro Glu Asp Leu Lys
65 70 75 80

Val Val Lys Asn Cys Ala Asn Thr Thr Arg Ser Phe Cys Asp Leu Thr
85 90 95

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

Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys Ser His Asn Phe Trp Leu
115 120 125

Ala Ile Asp Met Ser Phe Glu Pro Pro Glu Phe Glu Ile Val Gly Phe
130 135 140

Thr Asn His Ile Asn Val Met Val Lys Phe Pro Ser Ile Val Glu Glu
145 150 155 160

Glu Leu Gln Phe Asp Leu Ser Leu Val Ile Glu Glu Gln Ser Glu Gly
165 170 175

Ile Val Lys Lys His Lys Pro Glu Ile Lys Gly Asn Met Ser Gly Asn
180 185 190

Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro Asn Thr Asn Tyr Cys Val
195 200 205

Ser Val Tyr Leu Glu His Ser Asp Glu Gln Ala Val Ile Lys Ser Pro
210 215 220

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

Ser Ala Lys Ile Gly Gly Ile Ile Thr Val Phe Leu Ile Ala Leu Val
245 250 255

Leu Thr Ser Thr Ile Val Thr Leu Lys Trp Ile Gly Tyr Ile Cys Leu
260 265 270

Arg Asn Ser Leu Pro Lys Val Leu Asn Phe His Asn Phe Leu Ala Trp
275 280 285

Pro Phe Pro Asn Leu Pro Pro Leu Glu Ala Met Asp Met Val Glu Val
290 295 300

Ile Tyr Ile Asn Arg Lys Lys Lys Val Trp Asp Tyr Asn Tyr Asp Asp
305 310 315 320

Glu Ser Asp Ser Asp Thr Glu Ala Ala Pro Arg Thr Ser Gly Gly Gly
325 330 335

Tyr Thr Met His Gly Leu Thr Val Arg Pro Leu Gly Gln Ala Ser Ala
340 345 350

Thr Ser Thr Glu Ser Gln Leu Ile Asp Pro Glu Ser Glu Glu Glu Pro
355 360 365

Asp Leu Pro Glu Val Asp Val Glu Leu Pro Thr Met Pro Lys Asp Ser
370 375 380

Pro Gln Gln Leu Glu Leu Leu Ser Gly Pro Cys Glu Arg Arg Lys Ser
385 390 395 400

Pro Leu Gln Asp Pro Phe Pro Glu Glu Asp Tyr Ser Ser Thr Glu Gly
405 410 415

Ser Gly Gly Arg Ile Thr Phe Asn Val Asp Leu Asn Ser Val Phe Leu
420 425 430

Arg Val Leu Asp Asp Glu Asp Ser Asp Asp Leu Glu Ala Pro Leu Met
435 440 445

Leu Ser Ser His Leu Glu Glu Met Val Asp Pro Glu Asp Pro Asp Asn
450 455 460

Val Gln Ser Asn His Leu Leu Ala Ser Gly Glu Gly Thr Gln Pro Thr
465 470 475 480

Phe Pro Ser Pro Ser Ser Glu Gly Leu Trp Ser Glu Asp Ala Pro Ser
485 490 495

Asp Gln Ser Asp Thr Ser Glu Ser Asp Val Asp Leu Gly Asp Gly Tyr
500 505 510

Ile Met Arg
515

<210> 7
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR1 Extracellular domain (with signal sequence)

<400> 7

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val
1 5 10 15

Ala Pro Trp Val Leu Ser Ala Ala Ala Gly Gly Lys Asn Leu Lys Ser
20 25 30

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg
35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp
50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln
65 70 75 80

Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val
85 90 95

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

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile
 115 120 125

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

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly
 145 150 155 160

Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val
 165 170 175

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu
 180 185 190

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr
 195 200 205

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr
 210 215 220

Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile Glu Val Ser Val Gln
 225 230 235 240

Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr
 245 250 255

Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn
 260 265 270

His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr
 275 280 285

Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu
 290 295 300

Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu
305 310 315 320

Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val
325 330 335

Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala
340 345 350

Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile
355 360 365

Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile
370 375 380

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

Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn
405 410 415

Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly
420 425 430

Asn Thr Ser Lys
435

<210> 8

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 Extracellular domain (with signal sequence)

<400> 8

Met Leu Leu Ser Gln Asn Ala Phe Ile Phe Arg Ser Leu Asn Leu Val
1 5 10 15

Leu Met Val Tyr Ile Ser Leu Val Phe Gly Ile Ser Tyr Asp Ser Pro
20 25 30

Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys Ile Ser Leu Arg Asn Phe
35 40 45

Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn His Ser Ile Val Pro Thr
50 55 60

His Tyr Thr Leu Leu Tyr Thr Ile Met Ser Lys Pro Glu Asp Leu Lys
65 70 75 80

Val Val Lys Asn Cys Ala Asn Thr Thr Arg Ser Phe Cys Asp Leu Thr
85 90 95

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

Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys Ser His Asn Phe Trp Leu
115 120 125

Ala Ile Asp Met Ser Phe Glu Pro Pro Glu Phe Glu Ile Val Gly Phe
130 135 140

Thr Asn His Ile Asn Val Met Val Lys Phe Pro Ser Ile Val Glu Glu
145 150 155 160

Glu Leu Gln Phe Asp Leu Ser Leu Val Ile Glu Glu Gln Ser Glu Gly
165 170 175

Ile Val Lys Lys His Lys Pro Glu Ile Lys Gly Asn Met Ser Gly Asn
180 185 190

Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro Asn Thr Asn Tyr Cys Val
195 200 205

Ser Val Tyr Leu Glu His Ser Asp Glu Gln Ala Val Ile Lys Ser Pro
210 215 220

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

Ser Ala Lys

<210> 9

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IgG1 Fc (aa 216-447)with mutations C220S, P238S, P331S, T350V, L351Y, F405A, Y407V

<400> 9

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Val
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 10

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IgG1 Fc (aa216-447)with mutations C220S, P238S, P331S,
T350V, T366L, K392L, T394W

<400> 10

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

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

Leu Thr Trp Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 11
<211> 409
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR1 (aa28-436)

<400> 11

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
 35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
 65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
 85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
 100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
 115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
 130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
 145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
 165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
 180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
 195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
 210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
 225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
 245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
 260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
 290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
 305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
 325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
 340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
 355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
 370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
 385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys
 405

<210> 12
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: IFNAR2 (aa27-243)

<400> 12

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
 1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
 20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
 35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
 50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
 65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
 85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
 100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
 115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
 130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
 145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
 165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys
 210 215

<210> 13
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: Leader Sequence

<400> 13

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Thr His Ala

<210> 14
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: VK3LP leader sequence

<400> 14

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

Asp Thr Thr Gly
 20

<210> 15
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: linker

<400> 15

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

Gly Gly Gly Ser
 20

<210> 16
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: linker

<400> 16

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

<210> 17
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: linker

<400> 17

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser
 20 25

<210> 18
 <211> 18

<212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic: NLG linker

<400> 18

Val Asp Gly Ala Ser Ser Pro Val Asn Val Ser Ser Pro Ser Val Gln
 1 5 10 15

Asp Ile

<210> 19
 <211> 50
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: linker

<400> 19

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

Ala Lys Glu Ala Ala Ala Lys Ala Leu Glu Ala Glu Ala Ala Ala Lys
 20 25 30

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
 35 40 45

Leu Glu
 50

<210> 20
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: IgG1 Fc (SCC hinge)

<400> 20

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 21
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: IgG1 Fc domain (SSS hinge)

<400> 21

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala
 1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 22
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IgG1 Fc domain with P238S (SCC hinge)

<400> 22

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 23
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IgG1 Fc domain with P331S

<400> 23

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 24
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: IgG1 Fc domain with SSS, P238S, and P331S

<400> 24

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala
 1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 25
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IgG1 Fc domain with SCC, P238S, and P331S

<400> 25

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 26
<211> 232
<212> PRT
<213> Homo sapiens

<220>

<221> misc_feature

<223> Human IgG1 Fc domain (wild-type)

<400> 26

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 27
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: linker

<400> 27

Gly Gly Ser Gly
 1

<210> 28
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: linker

<400> 28

Gly Ser Ala Thr
 1

<210> 29
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: O-linked glycosylation consensus site

<220>

<221> misc_feature
 <222> (2)..(3)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> X = T/S

<400> 29

Cys Xaa Xaa Gly Gly Xaa Cys
 1 5

<210> 30
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: O-linked glycosylation consensus site

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> X = E/D

<400> 30

Asn Ser Thr Xaa Ala
 1 5

<210> 31
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: O-linked glycosylation consensus site

<400> 31

Asn Ile Thr Gln Ser
 1 5

<210> 32
 <211> 5
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: O-linked glycosylation consensus site

<400> 32

Gln Ser Thr Gln Ser
1 5

<210> 33

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: O-linked glycosylation consensus site

<220>

<221> misc_feature

<222> (1)..(1)

<223> X = D/E

<220>

<221> misc_feature

<222> (4)..(4)

<223> X = R/K

<400> 33

Xaa Phe Thr Xaa Val
1 5

<210> 34

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: O-linked glycosylation consensus site

<220>

<221> misc_feature

<222> (2)..(2)

<223> X = E/D

<400> 34

Cys Xaa Ser Asn

1

<210> 35

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: O-linked glycosylation consensus site

<220>

<221> misc_feature

<222> (5)..(5)

<223> X = K/R

<400> 35

Gly Gly Ser Cys Xaa

1 5

<210> 36

<211> 530

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (without signal sequence)

<400> 36

Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp

1 5 10 15

Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val

20 25 30

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys

35 40 45

Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser

50 55 60

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu

65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

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

Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr Ala Ala Lys Val
420 425 430

Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser Leu Lys Pro Ser
435 440 445

Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu Lys Asn Leu Leu
450 455 460

Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe Ile Ile Glu Asn
465 470 475 480

Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln Thr Asp Glu Asp
485 490 495

His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser Gly Asn Tyr Ser
500 505 510

Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu Leu Gln Gln Asp
515 520 525

Phe Val
530

<210> 37
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR2 (without signal sequence)

<400> 37

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
 115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
 130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
 145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
 165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Ile Gly Gly Ile Ile Thr Val
 210 215 220

Phe Leu Ile Ala Leu Val Leu Thr Ser Thr Ile Val Thr Leu Lys Trp
 225 230 235 240

Ile Gly Tyr Ile Cys Leu Arg Asn Ser Leu Pro Lys Val Leu Asn Phe
 245 250 255

His Asn Phe Leu Ala Trp Pro Phe Pro Asn Leu Pro Pro Leu Glu Ala
 260 265 270

Met Asp Met Val Glu Val Ile Tyr Ile Asn Arg Lys Lys Lys Val Trp
 275 280 285

Asp Tyr Asn Tyr Asp Asp Glu Ser Asp Ser Asp Thr Glu Ala Ala Pro
 290 295 300

Arg Thr Ser Gly Gly Gly Tyr Thr Met His Gly Leu Thr Val Arg Pro
 305 310 315 320

Leu Gly Gln Ala Ser Ala Thr Ser Thr Glu Ser Gln Leu Ile Asp Pro
325 330 335

Glu Ser Glu Glu Glu Pro Asp Leu Pro Glu Val Asp Val Glu Leu Pro
340 345 350

Thr Met Pro Lys Asp Ser Pro Gln Gln Leu Glu Leu Leu Ser Gly Pro
355 360 365

Cys Glu Arg Arg Lys Ser Pro Leu Gln Asp Pro Phe Pro Glu Glu Asp
370 375 380

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

Leu Asn Ser Val Phe Leu Arg Val Leu Asp Asp Glu Asp Ser Asp Asp
405 410 415

Leu Glu Ala Pro Leu Met Leu Ser Ser His Leu Glu Glu Met Val Asp
420 425 430

Pro Glu Asp Pro Asp Asn Val Gln Ser Asn His Leu Leu Ala Ser Gly
435 440 445

Glu Gly Thr Gln Pro Thr Phe Pro Ser Pro Ser Ser Glu Gly Leu Trp
450 455 460

Ser Glu Asp Ala Pro Ser Asp Gln Ser Asp Thr Ser Glu Ser Asp Val
465 470 475 480

Asp Leu Gly Asp Gly Tyr Ile Met Arg
485

<210> 38
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: linker

<400> 38

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

<210> 39

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: linker

<400> 39

Gly Gly Gly Gly Ser
1 5

<210> 40

<211> 661

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: RSLV-601 Without a leader sequence

<400> 40

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
420 425 430

Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
435 440 445

Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
450 455 460

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
465 470 475 480

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
485 490 495

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
500 505 510

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
515 520 525

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
530 535 540

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
545 550 555 560

Gln Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
565 570 575

Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
580 585 590

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp
595 600 605

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
610 615 620

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
625 630 635 640

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
645 650 655

Leu Ser Pro Gly Lys
660

<210> 41

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: RSLV-602 Without a leader sequence

<400> 41

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
 1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
 20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
 35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
 50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
 65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
 85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
 100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
 115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
 130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
 145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
 165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
225 230 235 240

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

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

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

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

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

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

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

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

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

Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

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

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

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

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

Leu Ser Pro Gly Lys
465

<210> 42
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: RSLV-603 Without a leader sequence

<400> 42

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
420 425 430

Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
435 440 445

Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
450 455 460

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
465 470 475 480

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
485 490 495

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
500 505 510

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
515 520 525

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
530 535 540

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
545 550 555 560

Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
565 570 575

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
580 585 590

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
595 600 605

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Val Ser Lys Leu
610 615 620

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
625 630 635 640

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
645 650 655

Leu Ser Pro Gly Lys
660

<210> 43

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: RSLV-604 without a leader sequence

<400> 43

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
 20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
 35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
 50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
 65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
 85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
 100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
 115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
 130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
 145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
 165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
 210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
225 230 235 240

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

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

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

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

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

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

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

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

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Val Ser Lys Leu
420 425 430

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

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

Leu Ser Pro Gly Lys
465

<210> 44
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Leader-IFNAR2 (aa27-243) (Gly4Ser)2- IgG1 Fc (aa
216-447)with mutations C220S, P238S, P331S,T350V, T366L, K392L,
T394W

<400> 44

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
 115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
 130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
 145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
 165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
 180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
 195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
 210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly
 225 230 235 240

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

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

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

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 290 295 300

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

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

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

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Leu Pro Pro
370 375 380

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Leu Cys Leu Val
385 390 395 400

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

Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu Asp Ser Asp
420 425 430

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 45

<211> 459

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243) (Gly4Ser)2- IgG1 Fc (aa
216-447)with mutations C220S, P238S, P331S,T350V, T366L, K392L,
T394W, without a leader sequence

<400> 45

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
 210 215 220

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
 225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro
 245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 290 295 300

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

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 325 330 335

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Leu Pro Pro Ser Arg Asp
 355 360 365

Glu Leu Thr Lys Asn Gln Val Ser Leu Leu Cys Leu Val Lys Gly Phe
 370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 385 390 395 400

Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 405 410 415

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 46

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader-IFNAR2 (aa27-243) IgG1 Fc (aa 216-447)with
mutations C220S, P238S, P331S,T350V, T366L, K392L, T394W

<400> 46

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu

115

120

125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
 130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
 145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
 165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
 180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
 195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
 210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser
 225 230 235 240

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

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

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

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

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

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

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

Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro
 405 410 415

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

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

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

Ser Pro Gly Lys
 465

<210> 47
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: IFNAR2 (aa27-243) IgG1 Fc (aa 216-447)with mutations
 C220S, P238S, P331S,T350V, T366L, K392L, T394W, without a leader
 sequence

<400> 47

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

1

5

10

15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
 20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
 35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
 50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
 65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
 85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
 100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
 115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
 130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
 145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
 165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser Ser Asp Lys

210

215

220

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

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

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

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

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

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

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

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

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

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu
 385 390 395 400

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

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

Lys

<210> 48
<211> 670
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Leader- IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc (aa
216-447)with mutations C220S, P238S, P331S, T350V, L351Y, F405A,
Y407V

<400> 48

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu

115

120

125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
 145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
 165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
 180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
 195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
 210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
 225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
 245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
 260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
 275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
 290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
 305 310 315 320

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

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
420 425 430

Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr
435 440 445

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe
450 455 460

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
465 470 475 480

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
485 490 495

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
500 505 510

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
515 520 525

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

530

535

540

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
 545 550 555 560

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro
 565 570 575

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 580 585 590

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 595 600 605

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 610 615 620

Gly Ser Phe Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 625 630 635 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 645 650 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 660 665 670

<210> 49

<211> 651

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc (aa
 216-447)with mutations C220S, P238S, P331S, T350V, L351Y, F405A,
 Y407V, without a leader sequence

<400> 49

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

Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys

225 230 — 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
420 425 430

Cys Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro

435

440

445

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 450 455 460

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 465 470 475 480

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 485 490 495

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 500 505 510

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 515 520 525

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 530 535 540

Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp
 545 550 555 560

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 565 570 575

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 580 585 590

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 595 600 605

Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 610 615 620

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 625 630 635 640

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

<210> 50
<211> 660
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Leader- IFNAR1 (aa28-436)- IgG1 Fc (aa 216-447)with
mutations C220S, P238S, P331S, T350V, L351Y, F405A, Y407V

<400> 50

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser
420 425 430

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
435 440 445

Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
450 455 460

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
465 470 475 480

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
485 490 495

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
500 505 510

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
530 535 540

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
545 550 555 560

Val Tyr Val Tyr Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
565 570 575

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
580 585 590

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
595 600 605

Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Val Ser Lys Leu Thr
610 615 620

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
625 630 635 640

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
645 650 655

Ser Pro Gly Lys
660

<210> 51

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (aa28-436)- IgG1 Fc (aa 216-447)with mutations
C220S, P238S, P331S, T350V, L351Y, F405A, Y407V, without a leader
sequence

<400> 51

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser Ser Asp Lys
405 410 415

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Ser
420 425 430

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
435 440 445

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
450 455 460

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
465 470 475 480

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
485 490 495

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
500 505 510

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
515 520 525

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val
530 535 540

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
565 570 575

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
580 585 590

Asp Ser Asp Gly Ser Phe Ala Leu Val Ser Lys Leu Thr Val Asp Lys
595 600 605

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
610 615 620

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
625 630 635 640

Lys

<210> 52

<211> 670

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: RSLV-606 Leader- IFNAR1 (aa28-436)- (Gly4Ser)2- Fc (aa216-447)with mutations C220S, P238S, P331S, T350V, T366L, K392L, T394W

<400> 52

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
420 425 430

Ser Gly Gly Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr
435 440 445

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe
450 455 460

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
465 470 475 480

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
485 490 495

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
500 505 510

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
515 520 525

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
530 535 540

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
545 550 555 560

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Leu Cys Leu Val
580 585 590

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
595 600 605

Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu Asp Ser Asp
610 615 620

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
625 630 635 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
645 650 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665 670

<210> 53
<211> 651
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: RSLV-606 Without a leader sequence

<400> 53

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
 100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
 115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
 130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
 145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
 165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
 180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
 195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
 210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
 225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
 245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
 260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
 290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
420 425 430

Cys Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro
435 440 445

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
450 455 460

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
465 470 475 480

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
485 490 495

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
500 505 510

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
515 520 525

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
530 535 540

Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Leu Pro Pro Ser Arg Asp
545 550 555 560

Glu Leu Thr Lys Asn Gln Val Ser Leu Leu Cys Leu Val Lys Gly Phe
565 570 575

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
580 585 590

Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
595 600 605

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
610 615 620

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
625 630 635 640

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650

<210> 54
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: RSLV-611 Leader- IFNAR2 (aa27-243)- (Gly4Ser)2- Fc (aa
216-447) with mutations C220S, P238S, P331S, T350V, L351Y, F405A,
Y407V

<400> 54

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
 20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
 35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
 65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
 85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
 100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
 115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
 130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
 145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
 165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
 180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
 195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
 210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly
 225 230 235 240

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

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

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

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 290 295 300

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

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 325 330 335

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

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro
 370 375 380

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 385 390 395 400

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 420 425 430

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475

<210> 55
 <211> 459
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: RSLV-611 Without a leader sequence

<400> 55

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
 1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
 20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
 35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
 50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
 65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
 85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
 100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
 115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
290 295 300

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

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
325 330 335

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp
355 360 365

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
385 390 395 400

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

Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 56

<211> 660

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: RSLV-608 Leader- IFNAR1 (aa28-436)- Fc (aa216-447)with
mutations C220S, P238S, P331S, T350V, T366L, K392L, T394W

<400> 56

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser
420 425 430

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
435 440 445

Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
450 455 460

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
465 470 475 480

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
485 490 495

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
500 505 510

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
530 535 540

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
545 550 555 560

Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
565 570 575

Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
580 585 590

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro
595 600 605

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
610 615 620

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
625 630 635 640

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
645 650 655

Ser Pro Gly Lys
660

<210> 57
<211> 641
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: RSLV-608 Without a leader sequence

<400> 57

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His

145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn

355

360

365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
 370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
 385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser Ser Asp Lys
 405 410 415

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Ser
 420 425 430

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 435 440 445

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 450 455 460

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 465 470 475 480

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 485 490 495

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 500 505 510

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
 515 520 525

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val
 530 535 540

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Leu
 545 550 555 560

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu
580 585 590

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
595 600 605

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
610 615 620

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
625 630 635 640

Lys

<210> 58
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: RSLV-613 Leader- IFNAR2 (aa27-243)- Fc (aa 216-447)
with mutations C220S, P238S, P331S, T350V, L351Y, F405A, Y407V

<400> 58

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

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

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

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

Ser Pro Gly Lys
465

<210> 59
<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: RSLV-613 Without a leader sequence

<400> 59

Ile	Ser	Tyr	Asp	Ser	Pro	Asp	Tyr	Thr	Asp	Glu	Ser	Cys	Thr	Phe	Lys
1				5					10					15	

Ile	Ser	Leu	Arg	Asn	Phe	Arg	Ser	Ile	Leu	Ser	Trp	Glu	Leu	Lys	Asn
		20					25						30		

His	Ser	Ile	Val	Pro	Thr	His	Tyr	Thr	Leu	Leu	Tyr	Thr	Ile	Met	Ser
		35					40					45			

Lys	Pro	Glu	Asp	Leu	Lys	Val	Val	Lys	Asn	Cys	Ala	Asn	Thr	Thr	Arg
	50					55					60				

Ser	Phe	Cys	Asp	Leu	Thr	Asp	Glu	Trp	Arg	Ser	Thr	His	Glu	Ala	Tyr
65					70				75						80

Val	Thr	Val	Leu	Glu	Gly	Phe	Ser	Gly	Asn	Thr	Thr	Leu	Phe	Ser	Cys
			85						90					95	

Ser	His	Asn	Phe	Trp	Leu	Ala	Ile	Asp	Met	Ser	Phe	Glu	Pro	Pro	Glu
			100					105					110		

Phe	Glu	Ile	Val	Gly	Phe	Thr	Asn	His	Ile	Asn	Val	Met	Val	Lys	Phe
		115					120					125			

Pro	Ser	Ile	Val	Glu	Glu	Glu	Leu	Gln	Phe	Asp	Leu	Ser	Leu	Val	Ile
	130					135					140				

Glu	Glu	Gln	Ser	Glu	Gly	Ile	Val	Lys	Lys	His	Lys	Pro	Glu	Ile	Lys
145					150					155					160

Gly	Asn	Met	Ser	Gly	Asn	Phe	Thr	Tyr	Ile	Ile	Asp	Lys	Leu	Ile	Pro
				165					170					175	

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser Ser Asp Lys
 210 215 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 60

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc domain
with T366Y mutation

<400> 60

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly

290

295

300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
 305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
 325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
 340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
 355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
 370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
 385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
 405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
 420 425 430

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 435 440 445

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 450 455 460

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 465 470 475 480

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 485 490 495

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
515 520 525

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
530 535 540

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
545 550 555 560

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
565 570 575

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
580 585 590

Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser
595 600 605

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
610 615 620

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
625 630 635 640

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
645 650 655

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
660 665 670

Ser Leu Ser Leu Ser Pro Gly Lys
675 680

<210> 61
<211> 661
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc domain with
T366Y mutation without a leader sequence

<400> 61

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
420 425 430

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
435 440 445

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
450 455 460

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
465 470 475 480

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
485 490 495

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
500 505 510

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
515 520 525

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
530 535 540

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
545 550 555 560

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
565 570 575

Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
580 585 590

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
595 600 605

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
610 615 620

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
625 630 635 640

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
645 650 655

Leu Ser Pro Gly Lys
660

<210> 62
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Leader- IFNAR2 (aa27-243) (Gly4Ser)4- IgG1 Fc domain
with T366Y mutation

<400> 62

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys 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 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
260 265 270

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
275 280 285

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
290 295 300

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
305 310 315 320

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
325 330 335

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
340 345 350

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
355 360 365

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
370 375 380

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
385 390 395 400

Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser
405 410 415

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
420 425 430

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
435 440 445

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
450 455 460

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
465 470 475 480

Ser Leu Ser Leu Ser Pro Gly Lys
485

<210> 63
<211> 469
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243) (Gly4Ser)4- IgG1 Fc domain with T366Y mutation without a leader sequence

<400> 63

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
 210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
 225 230 235 240

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

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

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

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

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

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

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

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

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

Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

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

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

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

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

Leu Ser Pro Gly Lys
465

<210> 64

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc domain
with Y407T mutation

<400> 64

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn

65

70

75

80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
 85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
 100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
 115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
 145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
 165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
 180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
 195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
 210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
 225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
 245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
 260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn

275

280

285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
 290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
 305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
 325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
 340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
 355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
 370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
 385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
 405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
 420 425 430

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 435 440 445

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 450 455 460

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 465 470 475 480

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
500 505 510

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
515 520 525

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
530 535 540

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
545 550 555 560

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
565 570 575

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
580 585 590

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
595 600 605

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
610 615 620

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr
625 630 635 640

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
645 650 655

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
660 665 670

Ser Leu Ser Leu Ser Pro Gly Lys
675 680

<210> 65

<211> 661

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc domain with Y407T mutation without a leader sequence

<400> 65

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
420 425 430

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
435 440 445

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
450 455 460

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
465 470 475 480

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
485 490 495

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
500 505 510

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
515 520 525

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
530 535 540

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
545 550 555 560

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
565 570 575

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
580 585 590

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
595 600 605

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu
610 615 620

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
625 630 635 640

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
645 650 655

Leu Ser Pro Gly Lys
660

<210> 66

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243)- (Gly4Ser)4- IgG1 Fc domain
with Y407T mutation

<400> 66

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys 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 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
260 265 270

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
275 280 285

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
290 295 300

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
305 310 315 320

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
325 330 335

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
340 345 350

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
355 360 365

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
370 375 380

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
385 390 395 400

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
420 425 430

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr
435 440 445

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
450 455 460

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
465 470 475 480

Ser Leu Ser Leu Ser Pro Gly Lys
485

<210> 67

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243)- (Gly4Ser)4- IgG1 Fc domain with Y407T mutation without a leader sequence

<400> 67

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
 165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
 210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
 225 230 235 240

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

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

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

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

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

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

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

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

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

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

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

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

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

Leu Ser Pro Gly Lys
465

<210> 68

<211> 670

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc domain
with T366Y mutation

<400> 68

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn

50

55

60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
 65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
 85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
 100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
 115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
 145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
 165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
 180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
 195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
 210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
 225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
 245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
420 425 430

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
450 455 460

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro

465 470 — 475 480

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
485 490 495

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
500 505 510

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
515 520 525

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
530 535 540

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
545 550 555 560

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
565 570 575

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val
580 585 590

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
595 600 605

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
610 615 620

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
625 630 635 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
645 650 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665 670

<210> 69

<211> 651

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc domain with T366Y mutation without a leader sequence

<400> 69

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
420 425 430

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
435 440 445

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
450 455 460

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
465 470 475 480

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
485 490 495

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
500 505 510

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
515 520 525

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
530 535 540

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
545 550 555 560

Glu Leu Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe
565 570 575

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
580 585 590

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
595 600 605

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
610 615 620

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
625 630 635 640

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650

<210> 70

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243)- (Gly4Ser)2- IgG1 Fc domain
with T366Y mutation

<400> 70

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly
225 230 235 240

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

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

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

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

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

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

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

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

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val
385 390 395 400

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
420 425 430

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 71

<211> 459

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243)- (Gly4Ser)2- IgG1 Fc domain with

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T366Y mutation without a leader sequence

<400> 71

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
 210 215 220

Gly Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 290 295 300

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

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 355 360 365

Glu Leu Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe
 370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 385 390 395 400

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 72

<211> 670

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc domain
with Y407T mutation

<400> 72

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile

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

515

520

525

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 530 535 540

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 545 550 555 560

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 565 570 575

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 580 585 590

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 595 600 605

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 610 615 620

Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 625 630 635 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 645 650 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 660 665 670

<210> 73

<211> 651

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc domain with
 Y407T mutation without a leader sequence

<400> 73

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
420 425 430

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
435 440 445

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
450 455 460

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
465 470 475 480

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
485 490 495

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
500 505 510

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
515 520 525

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
530 535 540

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
545 550 555 560

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
565 570 575

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
580 585 590

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
595 600 605

Phe Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
610 615 620

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
625 630 635 640

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650

<210> 74

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243)- (Gly4Ser)2- IgG1 Fc domain
with Y407T mutation

<400> 74

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly
225 230 235 240

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

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

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

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

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

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

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

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

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 385 390 395 400

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 420 425 430

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475

<210> 75
 <211> 459
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: IFNAR2 (aa27-243)- (Gly4Ser)2- IgG1 Fc domain with
 Y407T mutation without a leader sequence

<400> 75

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
 1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
 20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
 35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
 50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
 65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
 85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
 100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
 115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
 130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
 145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
 165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
 195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
 210 215 220

Gly Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 290 295 300

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

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 355 360 365

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 385 390 395 400

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

Phe Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 76
<211> 660
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Leader- IFNAR1 (aa28-436)- IgG1 Fc domain with T366Y mutation

<400> 76

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

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

145 150 155 160
 Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
 165 170 175
 Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
 180 185 190
 Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
 195 200 205
 Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
 210 215 220
 Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
 225 230 235 240
 Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
 245 250 255
 Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
 260 265 270
 Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
 275 280 285
 Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
 290 295 300
 Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
 305 310 315 320
 Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
 325 330 335
 Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
 340 345 350
 Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn

355

360

365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
 370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
 385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
 405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser
 420 425 430

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 435 440 445

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 450 455 460

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 465 470 475 480

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 485 490 495

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 500 505 510

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 530 535 540

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 545 550 555 560

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
580 585 590

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
595 600 605

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
610 615 620

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
625 630 635 640

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
645 650 655

Ser Pro Gly Lys
660

<210> 77

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (aa28-436)- IgG1 Fc domain with T366Y mutation
without a leader sequence

<400> 77

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser Cys Asp Lys
405 410 415

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
420 425 430

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
435 440 445

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
450 455 460

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
465 470 475 480

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
485 490 495

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
500 505 510

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
515 520 525

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
530 535 540

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
565 570 575

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
580 585 590

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
595 600 605

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
610 615 620

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
625 630 635 640

Lys

<210> 78

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243)- IgG1 Fc domain with T366Y mutation

<400> 78

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser
225 230 235 240

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245 250 255

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

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

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

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

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

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

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

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

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

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

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

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

Ser Pro Gly Lys
465

<210> 79

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243)- IgG1 Fc domain with T366Y mutation
without a leader sequence

<400> 79

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser Cys Asp Lys
210 215 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 80

<211> 660

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- IgG1 Fc domain with Y407T mutation

<400> 80

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
 20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
 35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
 50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
 65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
 85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
 100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
 115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
 145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
 165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
 180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser

195

200

205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
 210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
 225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
 245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
 260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
 275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
 290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
 305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
 325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
 340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
 355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
 370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
 385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser
420 425 430

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
435 440 445

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
450 455 460

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
465 470 475 480

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
485 490 495

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
500 505 510

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
530 535 540

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
545 550 555 560

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
565 570 575

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
580 585 590

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
595 600 605

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr

610

615

620

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 625 630 635 640

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 645 650 655

Ser Pro Gly Lys
 660

<210> 81

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (aa28-436)- IgG1 Fc domain with Y407T mutation
 without a leader sequence

<400> 81

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
 35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
 65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
 85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
 100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser Cys Asp Lys
405 410 415

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
420 425 430

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
435 440 445

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
450 455 460

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
465 470 475 480

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
485 490 495

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
500 505 510

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
515 520 525

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
530 535 540

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
545 550 555 560

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
565 570 575

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
580 585 590

Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val Asp Lys
595 600 605

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
610 615 620

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
625 630 635 640

Lys

<210> 82

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243)- IgG1 Fc domain with Y407T mutation
without a leader sequence

<400> 82

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser Cys Asp Lys
210 215 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 83

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc domain
with T366W mutation

<400> 83

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
 355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
 370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
 385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
 405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
 420 425 430

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 435 440 445

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 450 455 460

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 465 470 475 480

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 485 490 495

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 500 505 510

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 515 520 525

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 530 535 540

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 545 550 555 560

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
565 570 575

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
580 585 590

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
595 600 605

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
610 615 620

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
625 630 635 640

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
645 650 655

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
660 665 670

Ser Leu Ser Leu Ser Pro Gly Lys
675 680

<210> 84
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc domain with
T366W mutation without a leader sequence

<400> 84

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys

35

40

45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
 65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
 85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
 100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
 115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
 130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
 145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
 165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
 180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
 195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
 210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
 225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
420 425 430

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
435 440 445

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

450

455

460

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 465 470 475 480

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 485 490 495

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 500 505 510

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 515 520 525

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 530 535 540

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 545 550 555 560

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 565 570 575

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 580 585 590

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 595 600 605

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 610 615 620

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 625 630 635 640

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 645 650 655

Leu Ser Pro Gly Lys

<210> 85
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR2 (aa27-243) (Gly4Ser)4- IgG1 Fc domain with
T366W mutation without a leader sequence

<400> 85

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
225 230 235 240

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

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

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

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

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

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

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

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

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

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

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

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

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

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

Leu Ser Pro Gly Lys
465

<210> 86

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc domain
with T366S, L368A, and Y407V mutations

<400> 86

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
420 425 430

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
435 440 445

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
450 455 460

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
465 470 475 480

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
485 490 495

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
500 505 510

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
515 520 525

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
530 535 540

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
545 550 555 560

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
565 570 575

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
580 585 590

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
595 600 605

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
610 615 620

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
625 630 635 640

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
645 650 655

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
660 665 670

Ser Leu Ser Leu Ser Pro Gly Lys
675 680

<210> 87
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR1 (aa28-436)- (Gly4Ser)4- IgG1 Fc domain with
T366S, L368A, and Y407V mutations without a leader sequence

<400> 87

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
 145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
 165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
 180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
 195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
 210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
 225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
 245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
 260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
 290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
 305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
 325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
 340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
 355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
 370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
 385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
 405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
 420 425 430

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 435 440 445

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 450 455 460

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 465 470 475 480

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 485 490 495

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 500 505 510

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 515 520 525

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 530 535 540

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 545 550 555 560

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
565 570 575

Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
580 585 590

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
595 600 605

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu
610 615 620

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
625 630 635 640

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
645 650 655

Leu Ser Pro Gly Lys
660

<210> 88

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243)- (Gly4Ser)4- IgG1 Fc domain
with T366S, L368A, and Y407V mutations

<400> 88

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

Leu Lys Asn His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr

50

55

60

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys 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 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
275 280 285

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
290 295 300

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
305 310 315 320

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
325 330 335

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
340 345 350

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
355 360 365

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
370 375 380

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
385 390 395 400

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
420 425 430

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
435 440 445

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
450 455 460

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

465 470 475 480

Ser Leu Ser Leu Ser Pro Gly Lys
485

<210> 89

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243)- (Gly4Ser)4- IgG1 Fc domain with
T366S, L368A, and Y407V mutations without a leader sequence

<400> 89

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Pro Lys
225 230 235 240

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

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

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

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

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

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

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

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

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

Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu
420 425 430

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

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

Leu Ser Pro Gly Lys
465

<210> 90

<211> 670

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc domain
with T366W mutation

<400> 90

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
420 425 430

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
450 455 460

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
465 470 475 480

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
485 490 495

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
500 505 510

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
515 520 525

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
530 535 540

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
545 550 555 560

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
565 570 575

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
580 585 590

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
595 600 605

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
610 615 620

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
625 630 635 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
645 650 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665 670

<210> 91
<211> 651
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc domain with
T366W mutation without a leader sequence

<400> 91

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
 145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
 165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
 180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
 195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
 210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
 225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
 245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
 260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
 290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
 305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
 325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
 340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
 355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
 370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
 385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
 405 410 415

Gly Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 420 425 430

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 435 440 445

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 450 455 460

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 465 470 475 480

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 485 490 495

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 500 505 510

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 515 520 525

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 530 535 540

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 545 550 555 560

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
565 570 575

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
580 585 590

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
595 600 605

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
610 615 620

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
625 630 635 640

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650

<210> 92

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243)- (Gly4Ser)2- IgG1 Fc domain
with T366W mutation

<400> 92

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn

65

70

75

80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
 85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
 100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
 115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
 130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
 145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
 165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
 180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
 195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
 210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly
 225 230 235 240

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

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

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro

275

280

285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 290 295 300

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

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 325 330 335

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

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

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 385 390 395 400

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 420 425 430

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475

<210> 93

<211> 459

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243)- (Gly4Ser)2- IgG1 Fc domain with T366W mutation without a leader sequence

<400> 93

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
290 295 300

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

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
355 360 365

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
385 390 395 400

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 94

<211> 670

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc domain
with T366S, L368A, and Y407V mutations

<400> 94

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly
420 425 430

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
450 455 460

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
465 470 475 480

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
485 490 495

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
500 505 510

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
515 520 525

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
530 535 540

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
545 550 555 560

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
565 570 575

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

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
595 600 605

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
610 615 620

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
625 630 635 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
645 650 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665 670

<210> 95

<211> 651

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR1 (aa28-436)- (Gly4Ser)2- IgG1 Fc domain with

<400> 95

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
 195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
 210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
 225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
 245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
 260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
 290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
 305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
 325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
 340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
 355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
 370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
 385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly
 405 410 415

Gly Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 420 425 430

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 435 440 445

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 450 455 460

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 465 470 475 480

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 485 490 495

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 500 505 510

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 515 520 525

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 530 535 540

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 545 550 555 560

Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
 565 570 575

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 580 585 590

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 595 600 605

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
610 615 620

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
625 630 635 640

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
645 650

<210> 96

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243)- (Gly4Ser)2- IgG1 Fc domain
with T366S, L368A, and Y407V mutations

<400> 96

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu

115

120

125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
 130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
 145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
 165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
 180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
 195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
 210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly
 225 230 235 240

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

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

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

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 290 295 300

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

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val

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

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

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
385 390 395 400

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
420 425 430

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 97

<211> 459

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243)- (Gly4Ser)2- IgG1 Fc domain with
T366S, L368A, and Y407V mutations without a leader sequence

<400> 97

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
290 295 300

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

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
355 360 365

Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
385 390 395 400

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

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 98

<211> 660

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- IgG1 Fc domain with T366W mutation

<400> 98

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
 20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
 35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
 50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
 65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
 85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
 100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
 115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser
420 425 430

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
435 440 445

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
450 455 460

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
465 470 475 480

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
485 490 495

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
500 505 510

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
530 535 540

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
545 550 555 560

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
565 570 575

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
580 585 590

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
595 600 605

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
610 615 620

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
625 630 635 640

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
645 650 655

Ser Pro Gly Lys
660

<210> 99
<211> 641
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR1 (aa28-436)- IgG1 Fc domain with T366W mutation
without a leader sequence

<400> 99

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
 35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
 65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
 85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
 100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
 115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
 130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
 145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
 165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
 180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
 195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
 210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
 225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
 245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
 260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
 290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
 305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
 325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
 340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
 355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
 370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
 385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser Cys Asp Lys
 405 410 415

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 420 425 430

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 435 440 445

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 450 455 460

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 465 470 475 480

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 485 490 495

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 500 505 510

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 515 520 525

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 530 535 540

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
 545 550 555 560

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 565 570 575

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 580 585 590

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 595 600 605

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 610 615 620

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 625 630 635 640

Lys

<210> 100

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243)- IgG1 Fc domain with T366W mutation

<400> 100

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser
225 230 235 240

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245 250 255

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

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

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

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

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

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

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

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val

370

375

380

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415

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

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

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

Ser Pro Gly Lys
 465

<210> 101

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IFNAR2 (aa27-243)- IgG1 Fc domain with T366W mutation
 without a leader sequence

<400> 101

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
 1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
 20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
 35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
 50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser Cys Asp Lys
210 215 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 102

<211> 660

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR1 (aa28-436)- IgG1 Fc domain with T366S, L368A, and Y407V mutations

<400> 102

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile
20 25 30

Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val
35 40 45

Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn
50 55 60

Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn
65 70 75 80

Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile
85 90 95

Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe
100 105 110

Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu
115 120 125

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

Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val
145 150 155 160

Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr
165 170 175

Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu
180 185 190

Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser
195 200 205

Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro
210 215 220

Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp
225 230 235 240

Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala
245 250 255

Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile
260 265 270

Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn
275 280 285

Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly
290 295 300

Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile
305 310 315 320

Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp
325 330 335

Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro
340 345 350

Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn
355 360 365

Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr
370 375 380

Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala
385 390 395 400

His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala
405 410 415

Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser
420 425 430

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
435 440 445

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
450 455 460

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
465 470 475 480

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
485 490 495

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
500 505 510

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
530 535 540

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
545 550 555 560

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
565 570 575

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
580 585 590

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
595 600 605

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
610 615 620

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
625 630 635 640

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
645 650 655

Ser Pro Gly Lys
660

<210> 103
<211> 641
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR1 (aa28-436)- IgG1 Fc domain with T366S, L368A,
and Y407V mutations without a leader sequence

<400> 103

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

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

Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
35 40 45

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

Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65 70 75 80

Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
85 90 95

Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
100 105 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
115 120 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
130 135 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145 150 155 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
165 170 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
180 185 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
195 200 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
210 215 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225 230 235 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
245 250 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
260 265 270

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

Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
290 295 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305 310 315 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
325 330 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
340 345 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
355 360 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
370 375 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385 390 395 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Glu Pro Lys Ser Cys Asp Lys
405 410 415

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
420 425 430

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
435 440 445

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
450 455 460

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
465 470 475 480

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
485 490 495

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
500 505 510

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
515 520 525

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
530 535 540

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser
545 550 555 560

Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
565 570 575

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
580 585 590

Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys
595 600 605

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
610 615 620

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
625 630 635 640

Lys

<210> 104

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243)- IgG1 Fc domain with T366S,
L368A, and Y407V mutations

<400> 104

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly

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1           5           10           15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
      20                25                30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
      35                40                45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65          70                75                80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
      85                90                95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
      100               105               110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
      115               120               125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
      130               135               140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145          150               155               160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
      165               170               175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
      180               185               190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
      195               200               205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro

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210

215

220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser
 225 230 235 240

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255

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

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

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

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

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

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

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

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

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr

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

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

Ser Pro Gly Lys
465

<210> 105
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IFNAR2 (aa27-243)- IgG1 Fc domain with T366S, L368A,
and Y407V mutations without a leader sequence

<400> 105

Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
130 135 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145 150 155 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
165 170 175

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

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
195 200 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser Cys Asp Lys
210 215 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 106

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IgG1 Fc domain with T366Y mutation (knob hole 1)

<400> 106

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

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

Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 107
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: IgG1 Fc domain with Y407T mutation (knob hole 1)

<400> 107

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 108

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IgG1 Fc domain with T366W mutation (knob hole 2)

<400> 108

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 109

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: IgG1 Fc domain with T366S, L368A, and Y407V mutations
(knob hole 2)

<400> 109

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

1 5 10 15

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

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

 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

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

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

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

 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
 180 185 190

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

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

210

215

220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 110
 <211> 327
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Human IgG4

<400> 110

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

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

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

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

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

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

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

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

130

135

140

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
 325

<210> 111

<211> 218
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Human IgG4 Fc domain

<400> 111

Pro Ala Pro Glu Phe 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 Gln Glu Asp Pro Glu Val Gln 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 Phe 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 Gly Leu Pro Ser Ser 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 Gln 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

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu 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 Leu Gly Lys
210 215

<210> 112
<211> 229
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human IgG4 Hinge + Fc domain

<400> 112

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 113
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Representative Fc domain sourced from Dulaglutide
(S228P, F234A, L235A, L445P (EU) and K478del (Kabat)

<400> 113

Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
1 5 10 15

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
35 40 45

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
50 55 60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
65 70 75 80

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
85 90 95

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
100 105 110

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
115 120 125

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
130 135 140

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
145 150 155 160

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
165 170 175

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
180 185 190

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
195 200 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
210 215 220

Ser Leu Ser Leu Gly
225

<210> 114
 <211> 327
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic: Human IgG4 with mutations K196Q, S228P, F296Y, E356K, R409K, and H435R mutations from emicizumab

<400> 114

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
325

<210> 115

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Human IgG4 with mutations K196Q, S228P, F296Y, R409K,

2018-11-02 SBN-001PC_ST25 - 4828-4044-0698 v 1.TXT
and K439E mutations from emicizumab

<400> 115

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
325

<210> 116
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Human IgG4 Fc domain with mutations F296Y, E356K,
R409K, and H435R mutations from emicizumab

<400> 116

Pro Ala Pro Glu Phe 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

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln 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 Gly Leu Pro Ser Ser 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 Gln Lys 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 Glu Gly Asn
180 185 190

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Tyr Thr
195 200 205

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
210 215

<210> 117

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Human IgG4 Fc domain with mutations F296Y, R409K, and K439E mutations from emicizumab

<400> 117

Pro Ala Pro Glu Phe 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 Gln Glu Asp Pro Glu Val Gln 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 Gly Leu Pro Ser Ser 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 Gln 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 Glu 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 Glu Ser Leu Ser Leu Ser Leu Gly Lys
210 215

<210> 118

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Human IgG4 Hinge + Fc domain with mutations S228P, F296Y, E356K, R409K, H435R, L445P, G446del (EU) and K478del(Kabat) mutations from emicizumab

<400> 118

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Lys Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn Arg Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Pro
225

<210> 119
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Human IgG4 Hinge + Fc domain with mutations S228P,
F296Y, R409K, K439E, L445P, G446del (EU)and K478del(Kabat)
mutations from emicizumab

<400> 119

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser
210 215 220

Leu Ser Pro
225

<210> 120
 <211> 229
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: Human IgG4 Hinge + Fc domain with mutations T350V,
 T366L, K392L, T394W (zymeworks)

<400> 120

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
 1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 115 120 125

Gln Val Tyr Val Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 130 135 140

Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 145 150 155 160

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 121
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Human IgG4 Hinge + Fc domain with mutations T350V,
L351Y, F405A, Y407V (zymeworks)

<400> 121

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Val Tyr Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Val Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 122
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Human IgG4 Hinge + Fc domain with mutation T366Y (knob
hole 1)

<400> 122

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe

1 5 10 15

 Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45

 Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 50 55 60

 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 65 70 75 80

 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 85 90 95

 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 100 105 110

 Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 115 120 125

 Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 130 135 140

 Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 145 150 155 160

 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 165 170 175

 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
 180 185 190

 Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
 195 200 205

 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

210

215

220

Leu Ser Leu Gly Lys
225

<210> 123

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Human IgG4 Hinge + Fc domain with mutation Y407T (knob hole 1)

<400> 123

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 124

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Human IgG4 Hinge + Fc domain with mutation T336W (knob
hole 2)

<400> 124

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 125
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Human IgG4 Hinge + Fc domain with mutations T366S,

<400> 125

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 126
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Human IgG4 Hinge + Fc domain with mutation S228P
(stability: reduced Fab arm exchange)

<400> 126

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

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

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 128

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Human IgG4 Hinge + Fc domain with mutation F234A, L235A (decrease FcR binding) Xu et al Cell Immunol 2000 200(1):16-26)

<400> 128

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Ala
1 5 10 15

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 129
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Human IgG4 Hinge + Fc domain with mutation S228P,
L235E (decrease FcR binding) Reddy et al., J Immunol 2000
164(4):1925-33)

<400> 129

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 130

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Human IgG4 Hinge + Fc domain with mutation N297A
(affects glycosylation, thus FcR binding) Borrok et al ACS Chem
Biol 2012 7(9):1596-1602

<400> 130

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 131
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: linker

<220>
<221> misc_feature
<222> (1)..(50)
<223> "Gly Gly Gly Gly Ser" is present at least once, and may repeat up to 10 times

<400> 131

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser
50

<210> 132
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: linker

<220>
<221> misc_feature
<223> "Gly Gly Gly Gly Ser" is present at least once, and may repeat up to 5 times

<400> 132

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 133

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: linker

<220>

<221> misc_feature

<222> (2)..(26)

<223> "Glu Ala Ala Ala Lys" repeats at least twice and up to 5 times

<400> 133

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

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
20 25

<210> 134

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: linker

<220>

<221> misc_feature

<222> (1)..(20)

<223> "Gly Gly Ser Gly" is present at least once and may repeat up to 5 times

<400> 134

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

Gly Gly Ser Gly
20

<210> 135
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: linker

<220>
<221> misc_feature
<222> (1)..(30)
<223> "Gly Gly Ser Gly Gly Ser" is present at least once and may repeat
up to 5 times

<400> 135

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

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

<210> 136
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: TFRC Probe

<220>
<221> misc_feature
<223> 56-FAM at 5' end, ZEN modification mid-sequence, 3IABkFQ at 3'
end

<400> 136
ccattgtcat atacccggtt cagcct

26

<210> 137

<211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic: TFRC Primer 1
 <400> 137
 atctacagca agtttcatct cca 23

<210> 138
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic: TFRC Primer 2
 <400> 138
 tcaagctaga tcagcattct ctaac 25

<210> 139
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic: HPRT1 Probe
 <220>
 <221> misc_feature
 <223> 56-FAM at 5' end, ZEN modification mid-sequence, 3IABkFQ at 3' end
 <400> 139
 tccattccta tgactgtaga ttttatcaga ctgaaga 37

<210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic: HPRT1 Primer 1
 <400> 140
 ccaattactt ttatgtcccc tggt 24

<210> 141
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic: HPRT1 Primer 2

 <400> 141
 catcaaagca ctgaatagaa atagtga 27

 <210> 142
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic: GUSB Probe

 <220>
 <221> misc_feature
 <223> 56-FAM at 5' end, ZEN modification mid-sequence, 3IABkFQ at 3'
 end

 <400> 142
 tgcagggttt caccaggatc cac 23

 <210> 143
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic: GUSB Primer 1

 <400> 143
 gtttttgatc cagacccaga tg 22

 <210> 144
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic: GUSB Primer 2

 <400> 144

gccccattatt cagagcgagt a 21

<210> 145
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic: CMPK2 Probe

<220>
 <221> misc_feature
 <223> 56-FAM at 5' end, ZEN modification mid-sequence, 3IABkFQ at 3' end

<400> 145
 atgccacggg taaaaccacg gt 22

<210> 146
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic: CMPK2 Primer 1

<400> 146
 aggacagcct taagtgaatc tg 22

<210> 147
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic: CMPK2 Primer 2

<400> 147
 gcccaaaaca gatccagaaa g 21

<210> 148
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic: HERC5 Probe

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<220>
<221> misc_feature
<223> 56-FAM at 5' end, ZEN modification mid-sequence, 3IABkFQ at 3'
      end

<400> 148
atacccaaca agctcagcca cca                                     23

<210> 149
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: HERC5 Primer 1

<400> 149
cccaaatacag aaacataggc aag                                     23

<210> 150
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: HERC5 Primer 2

<400> 150
tcaacacaga atgagctaag acc                                     23

<210> 151
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: EPSTI1 Probe

<220>
<221> misc_feature
<223> 56-FAM at 5' end, ZEN modification mid-sequence, 3IABkFQ at 3'
      end

<400> 151
agagccaaaa tccaccagac tgaaca                                   26

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<210> 152
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic: EPSTI1Primer 1

<400> 152
 tccaacagcc tccagattg 19

<210> 153
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic: EPSTI1 Primer 2

<400> 153
 gtgaattact ggaactgaaa cgg 23

<210> 154
 <211> 468
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic: Leader- IFNAR2 (aa27-243)- IgG1 Fc domain with Y407T mutation

<400> 154

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
 20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
 35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro
165 170 175

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Glu Pro Lys Ser
225 230 235 240

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245 250 255

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

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

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

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

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

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

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

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

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

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

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

Ser Pro Gly Lys
465

<210> 155

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Leader- IFNAR2 (aa27-243) (Gly4Ser)4- IgG1 Fc domain
with T366W mutation

<400> 155

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys
20 25 30

Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu
35 40 45

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

Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn
65 70 75 80

Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His
85 90 95

Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu
100 105 110

Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu
115 120 125

Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met
130 135 140

Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser
145 150 155 160

Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro

Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys
180 185 190

Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser
195 200 205

Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro
210 215 220

Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys 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 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
260 265 270

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
275 280 285

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
290 295 300

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
305 310 315 320

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
325 330 335

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
340 345 350

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
355 360 365

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

370

375

380

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 385 390 395 400

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
 405 410 415

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 420 425 430

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 435 440 445

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 450 455 460

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 465 470 475 480

Ser Leu Ser Leu Ser Pro Gly Lys
 485