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<120> Single Immunoglobulin Interleukin-1 Receptor Related (SIGIRR)
Variants And Uses Thereof

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<151> 2017-09-06

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aggcctgcct tgggcagctc agtggctctg aactgcacgg cttgggtagt ctctgggccc	120
cactgctccc tgccttcagt ccagtggctg aaagacgggc ttccattggg aattgggggc	180
cactacagcc tccacgagta ctctgggtc aaggccaacc tgtcagaggt gcttgtgtcc	240
agtgtcctgg gggatcaacgt gaccagcact gaagtctatg gggccttcac ctgctccatc	300
cagaacatca gcttctcctc cttcactctt cagagagctg gccctacaag ccacgtggct	360
gcggtgctgg cctccctcct ggtcctgctg gccctgctgc tggccgccct gctctatgtc	420
aagtgccgtc tcaacgtgct gctctggtag caggacgcgt atggggaggt ggagataaac	480
gacgggaagc tctacgacgc ctacgtctcc tacagcgact gccccgagga ccgcaagtcc	540
gtgaacttca tcctaaagcc gcagctggag cggcgctggg gctacaagct cttcctggac	600
gaccgcgacc tcctgccgcg cgctgagccc tccgccgacc tcttggtgaa cctgagccgc	660
tgccgacgcc tcatcgtggt gctttcggac gccttcctga gccgggcctg gtgcagccac	720

341832_1.txt

agcttccggg agggcctgtg ccggctgctg gagctcacc gcagacccat cttcatcacc	780
ttcgagggcc agaggcgca ccccgcgac ccggcgctcc gcctgctgcg ccagcaccgc	840
cacctggtga ccttgctgct ctggaggccc ggctccgtga ctccttcctc cgatttttgg	900
aaagaagtgc agctggcgct gccgcggaag gtgcagtaca ggcctgtgga aggagacccc	960
cagacgcagc tgcaggacga caaggacccc atgctgattc ttcgaggccg agtccttgag	1020
ggccggggccc tggactcaga ggtggacccg gaccctgagg gcgacctggg tgtccggggg	1080
cctgtctttg gagagccatc agctccaccg cacaccagtg gggctctgct gggagagagc	1140
cggagcagcg aagtggacgt ctcggatctc ggctcgcgaa actacagtgc ccgcacagac	1200
ttctactgcc tgggtgtcaa ggatgatatg tag	1233

<210> 6
 <211> 648
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> variant (c.557delA) SIGIRR cDNA

<400> 6	
atgccaggtg tctgtgatag ggcccctgac ttctctctcc cgtctgaaga ccaggtgctg	60
aggcctgcct tgggcagctc agtggctctg aactgcacgg cttgggtagt ctctggggccc	120
cactgctccc tgccttcagt ccagtggctg aaagacgggc ttccattggg aattgggggc	180
cactacagcc tccacagata ctcttggtc aaggccaacc tgtcagaggt gcttgtgtcc	240
agtgtcctgg gggatcaact gaccagcact gaagtctatg gggccttcac ctgctccatc	300
cagaacatca gcttctcctc cttcactctt cagagagctg gccctacaag ccacgtggct	360
gcggtgctgg cctccctcct ggtcctgctg gccctgctgc tggccgccct gctctatgtc	420
aagtgccgtc tcaacgtgct gctctggtac caggacgcgt atggggaggt ggagataaac	480
gacgggaagc tctacgacgc ctacgtctcc tacagcgact gccccgagga ccgcaagtcc	540
gtgaacttca tcctaagccg cagctggagc ggcgtcgggg ctacaagctc ttcttgagac	600
accgcgacct cctgccgcgc gctgagccct ccgccgacct cttggtga	648

341832_1.txt

<210> 7
 <211> 410
 <212> PRT
 <213> Homo sapien

<220>
 <223> wild type SIGIRR protein

<400> 7

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Met Pro Gly Val Cys Asp Arg Ala Pro Asp Phe Leu Ser Pro Ser Glu
1          5          10          15

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

Thr Ala Trp Val Val Ser Gly Pro His Cys Ser Leu Pro Ser Val Gln
          35          40          45

Trp Leu Lys Asp Gly Leu Pro Leu Gly Ile Gly Gly His Tyr Ser Leu
          50          55          60

His Glu Tyr Ser Trp Val Lys Ala Asn Leu Ser Glu Val Leu Val Ser
65          70          75          80

Ser Val Leu Gly Val Asn Val Thr Ser Thr Glu Val Tyr Gly Ala Phe
          85          90          95

Thr Cys Ser Ile Gln Asn Ile Ser Phe Ser Ser Phe Thr Leu Gln Arg
          100          105          110

Ala Gly Pro Thr Ser His Val Ala Ala Val Leu Ala Ser Leu Leu Val
          115          120          125

Leu Leu Ala Leu Leu Leu Ala Ala Leu Leu Tyr Val Lys Cys Arg Leu
          130          135          140

Asn Val Leu Leu Trp Tyr Gln Asp Ala Tyr Gly Glu Val Glu Ile Asn
145          150          155          160

Asp Gly Lys Leu Tyr Asp Ala Tyr Val Ser Tyr Ser Asp Cys Pro Glu
          165          170          175

Asp Arg Lys Phe Val Asn Phe Ile Leu Lys Pro Gln Leu Glu Arg Arg
          180          185          190

Arg Gly Tyr Lys Leu Phe Leu Asp Asp Arg Asp Leu Leu Pro Arg Ala
          195          200          205

Glu Pro Ser Ala Asp Leu Leu Val Asn Leu Ser Arg Cys Arg Arg Leu
          210          215          220
  
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341832_1.txt

Ile Val Val Leu Ser Asp Ala Phe Leu Ser Arg Ala Trp Cys Ser His
 225 230 235 240

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

Ile Phe Ile Thr Phe Glu Gly Gln Arg Arg Asp Pro Ala His Pro Ala
 260 265 270

Leu Arg Leu Leu Arg Gln His Arg His Leu Val Thr Leu Leu Leu Trp
 275 280 285

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

Leu Ala Leu Pro Arg Lys Val Gln Tyr Arg Pro Val Glu Gly Asp Pro
 305 310 315 320

Gln Thr Gln Leu Gln Asp Asp Lys Asp Pro Met Leu Ile Leu Arg Gly
 325 330 335

Arg Val Pro Glu Gly Arg Ala Leu Asp Ser Glu Val Asp Pro Asp Pro
 340 345 350

Glu Gly Asp Leu Gly Val Arg Gly Pro Val Phe Gly Glu Pro Ser Ala
 355 360 365

Pro Pro His Thr Ser Gly Val Ser Leu Gly Glu Ser Arg Ser Ser Glu
 370 375 380

Val Asp Val Ser Asp Leu Gly Ser Arg Asn Tyr Ser Ala Arg Thr Asp
 385 390 395 400

Phe Tyr Cys Leu Val Ser Lys Asp Asp Met
 405 410

<210> 8
 <211> 504
 <212> PRT
 <213> Homo sapien

<220>
 <223> wild type SIGIRR isoform protein

<400> 8

Met Pro Gly Val Cys Asp Arg Ala Pro Asp Phe Leu Ser Pro Ser Glu
 1 5 10 15

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

341832_1.txt

Thr Ala Trp Val Val Ser Gly Pro His Cys Ser Leu Pro Ser Val Gln
 35 40 45
 Trp Leu Lys Asp Gly Leu Pro Leu Gly Ile Gly Gly His Tyr Ser Leu
 50 55 60
 His Glu Tyr Ser Trp Val Lys Ala Asn Leu Ser Glu Val Leu Val Ser
 65 70 75 80
 Ser Val Leu Gly Val Asn Val Thr Ser Thr Glu Val Tyr Gly Ala Phe
 85 90 95
 Thr Cys Ser Ile Gln Asn Ile Ser Phe Ser Ser Phe Thr Leu Gln Arg
 100 105 110
 Ala Gly Pro Thr Ser His Val Ala Ala Val Leu Ala Ser Leu Leu Val
 115 120 125
 Leu Leu Ala Leu Leu Leu Ala Ala Leu Leu Tyr Val Lys Cys Arg Leu
 130 135 140
 Asn Val Leu Leu Trp Tyr Gln Asp Ala Tyr Gly Glu Val Glu Ile Asn
 145 150 155 160
 Asp Gly Lys Leu Tyr Asp Ala Tyr Val Ser Tyr Ser Asp Cys Pro Glu
 165 170 175
 Asp Arg Lys Phe Val Asn Phe Ile Leu Lys Pro Gln Leu Glu Arg Arg
 180 185 190
 Arg Gly Tyr Lys Leu Phe Leu Asp Asp Arg Asp Leu Leu Pro Arg Ala
 195 200 205
 Glu Pro Ser Ala Asp Leu Leu Val Asn Leu Ser Arg Cys Arg Arg Leu
 210 215 220
 Ile Val Val Leu Ser Asp Ala Phe Leu Ser Arg Ala Trp Cys Ser His
 225 230 235 240
 Ser Phe Arg Glu Gly Leu Cys Arg Leu Leu Glu Leu Thr Arg Arg Pro
 245 250 255
 Ile Phe Ile Thr Phe Glu Gly Gln Arg Arg Asp Pro Ala His Pro Ala
 260 265 270
 Leu Arg Leu Leu Arg Gln His Arg His Leu Val Thr Leu Leu Leu Trp
 275 280 285
 Arg Pro Gly Ser Val Thr Pro Ser Ser Asp Phe Trp Lys Glu Val Gln
 290 295 300

341832_1.txt

Leu Ala Leu Pro Arg Lys Val Gln Tyr Arg Pro Val Glu Gly Asp Pro
305 310 315 320

Gln Thr Gln Leu Gln Asp Asp Lys Asp Pro Met Leu Ile Leu Arg Gly
325 330 335

Arg Val Pro Glu Gly Arg Ala Leu Asp Ser Glu Val Asp Pro Asp Pro
340 345 350

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

Ala Gln His Arg Ala Glu Trp Gly Gln Ala Gln Gly Thr Gly Pro Gly
370 375 380

Gly Ala Leu Gly Val Glu Asp Ser Ser Arg His Arg Glu Pro Leu His
385 390 395 400

Gly Leu Cys Pro Gly Gly Ala Arg Pro Ser Val Cys Leu Gly Thr Ser
405 410 415

Trp Ala Ser Gln Ala Ile Thr Ala Gly Gly Glu Gln Gly Gln Pro Leu
420 425 430

Ala Val Gly Leu Gly Gln Gly Cys Gly Trp Pro Pro Gln Ala Ser Arg
435 440 445

Ser Pro His Pro Arg Cys Pro Gly Ala Cys Phe Trp Arg Ala Ile Ser
450 455 460

Ser Thr Ala His Gln Trp Gly Leu Ala Gly Arg Glu Pro Glu Gln Arg
465 470 475 480

Ser Gly Arg Leu Gly Ser Arg Leu Ala Lys Leu Gln Cys Pro His Arg
485 490 495

Leu Leu Leu Pro Gly Val Gln Gly
500

<210> 9

<211> 215

<212> PRT

<213> Homo sapien

<220>

<223> Variant SIGIRR (c.557delA)

<400> 9

Met Pro Gly Val Cys Asp Arg Ala Pro Asp Phe Leu Ser Pro Ser Glu
1 5 10 15

341832_1.txt

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

Thr Ala Trp Val Val Ser Gly Pro His Cys Ser Leu Pro Ser Val Gln
35 40 45

Trp Leu Lys Asp Gly Leu Pro Leu Gly Ile Gly Gly His Tyr Ser Leu
50 55 60

His Glu Tyr Ser Trp Val Lys Ala Asn Leu Ser Glu Val Leu Val Ser
65 70 75 80

Ser Val Leu Gly Val Asn Val Thr Ser Thr Glu Val Tyr Gly Ala Phe
85 90 95

Thr Cys Ser Ile Gln Asn Ile Ser Phe Ser Ser Phe Thr Leu Gln Arg
100 105 110

Ala Gly Pro Thr Ser His Val Ala Ala Val Leu Ala Ser Leu Leu Val
115 120 125

Leu Leu Ala Leu Leu Leu Ala Ala Leu Leu Tyr Val Lys Cys Arg Leu
130 135 140

Asn Val Leu Leu Trp Tyr Gln Asp Ala Tyr Gly Glu Val Glu Ile Asn
145 150 155 160

Asp Gly Lys Leu Tyr Asp Ala Tyr Val Ser Tyr Ser Asp Cys Pro Glu
165 170 175

Asp Arg Lys Phe Val Asn Phe Ile Leu Ser Arg Ser Trp Ser Gly Val
180 185 190

Gly Ala Thr Ser Ser Ser Trp Thr Thr Ala Thr Ser Cys Arg Ala Leu
195 200 205

Ser Pro Pro Pro Thr Ser Trp
210 215

<210> 10

<211> 30

<212> PRT

<213> Homo sapien

<220>

<223> Wild type SIGIRR amio acids 186 to 215

<400> 10

Lys Pro Gln Leu Glu Arg Arg Arg Gly Tyr Lys Leu Phe Leu Asp Asp

341832_1.txt

1 **5** **10** **15**

Arg Asp Leu Leu Pro Arg Ala Glu Pro Ser Ala Asp Leu Leu
20 25 30

<210>	11
<211>	30
<212>	PRT
<213>	Homo sapien

<220>
<223> Variant SIGIRR amio acids 186 to 215

<400> 11

Ser Arg Ser Trp Ser Gly Val Gly Ala Thr Ser Ser Ser Trp Thr Thr
1 5 10 15

Ala Thr Ser Cys Arg Ala Leu Ser Pro Pro Pro Thr Ser Trp
20 25 30

$\langle 210 \rangle$	12
$\langle 211 \rangle$	20
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> forward PCR primer for SIGIRR

```
<400> 12
tcagtggctc tgaactgcac                20
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$\langle 210 \rangle$	13
$\langle 211 \rangle$	20
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> reverse PCR primer for SIGIRR

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<400> 13
ggtcctgttg agcagaggag 20
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$\langle 210 \rangle$	14
$\langle 211 \rangle$	910
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>

<223> rilonacept fusion protein

<400> 14

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

Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
          20          25          30

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

Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
          50          55          60

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
65          70          75          80

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
          85          90          95

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

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
          115         120         125

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

Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
145          150         155         160

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

Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
          180         185         190

Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
          195         200         205

Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
          210         215         220

Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
225          230         235         240

Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
          245         250         255

```

341832_1.txt

Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
 260 265 270
 Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
 275 280 285
 Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
 290 295 300
 Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
 305 310 315 320
 Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
 325 330 335
 Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
 340 345 350
 Ala Pro Arg Tyr Thr Val Ser Gly Gly Ala Pro Met Leu Ser Glu Ala
 355 360 365
 Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu Val Ser Ser Ala
 370 375 380
 Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn Glu His Lys
 385 390 395 400
 Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro Val Ser Thr
 405 410 415
 Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys Leu Trp Phe Val
 420 425 430
 Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val Val Arg Asn
 435 440 445
 Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe Val Glu Asn
 450 455 460
 Glu Pro Asn Leu Cys Tyr Asn Ala Gln Ala Ile Phe Lys Gln Lys Leu
 465 470 475 480
 Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr Met Glu Phe Phe
 485 490 495
 Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp Tyr Lys Asp Cys
 500 505 510
 Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly Val Lys Asp Arg
 515 520 525

341832_1.txt

Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly Asn Tyr Thr Cys
 530 535 540
 His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro Ile Thr Arg Val
 545 550 555 560
 Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr Arg Pro Val Ile
 565 570 575
 Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu Gly Ser Gln Ile
 580 585 590
 Gln Leu Ile Cys Asn Val Thr Gly Gln Leu Ser Asp Ile Ala Tyr Trp
 595 600 605
 Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro Val Leu Gly Glu
 610 615 620
 Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg Arg Ser Thr Leu
 625 630 635 640
 Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg Phe Tyr Lys His
 645 650 655
 Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile Asp Ala Ala Tyr
 660 665 670
 Ile Gln Leu Ile Tyr Pro Val Thr Asn Ser Gly Asp Lys Thr His Thr
 675 680 685
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 690 695 700
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 705 710 715 720
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 725 730 735
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 740 745 750
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 755 760 765
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 770 775 780
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 785 790 795 800
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

341832_1.txt

805

810

815

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 820 825 830

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 835 840 845

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 850 855 860

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 865 870 875 880

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 885 890 895

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 900 905 910

<210> 15

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain variable region of antibody directed to IL-6R

<400> 15

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

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

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

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

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

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

Ala Lys Gly Arg Asp Ser Phe Asp Ile Trp Gly Gln Gly Thr Met Val
 100 105 110

Thr Val Ser Ser
115

<210> 16
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain variable region of antibody directed to IL-6R

<400> 16

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

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

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

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

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

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

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