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<110> FRED HUTCHINSON CANCER RESEARCH CENTER
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 <211> 2335
 <212> ADN
 45 <213> Homo sapiens
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 tcgttagaaa caggagcaga tgtacagggt ttgcctgact cacactcaag gttgcataag 180

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 tacctctaga tctgtttggt tcagttgctg agaagcctga cataccagga ctgcctgaga 420
 10 caagccacaa gctgaacaga gaaagtggat tgaacaagga cgcatttccc cagtacatcc 480
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 5 cactcaatct ctgattctgt caatgtcttg aaatcaaggg ccagctggag gtgaagaaga 1920
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 10 aggagggaga catgagcatg gctgagcctg gacaaagaca aaggtgagca aagggtcac 2040
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 15 tccgatgatt ctctttgca taagtcatg acatatttt gctttattac agtttatcta 2220
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 20 ttctaggcc acatcccct gtctaaaaat tcagaaaatt ttgtttata aaaga 2335

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 25 <212> ADN
 <213> Homo sapiens

 <400> 13
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 30 gagcaagcct ggcattgcct cacagacctt cctcagagcc gcttcagaa aagcaagctg 120
 ctctgggtg ggcccagacc tgcctgagg agcctgtaga gttaaaaaat gaacccacg 180
 35 gatatagcag acaccacct cgatgaaagc atatacagca attactatct gtatgaaagt 240
 atccccaagc ctgcaacca agaaggcatc aaggcattg gggagctctt cctgccccca 300
 ctgtattcct tggttttgt atttggctg ctggaaatt ctgtggtggt tctggtcctg 360
 40 ttcaaataca agcgggtcag gtccatgact gatgtgtacc tgctaacct tgccatctcg 420
 gatctgctct tctgttttc cctccctttt tggggctact atgcagcaga ccagtgggtt 480
 45 ttgggctag gtctgtgcaa gatgattcc tggatgtact tgggtggctt ttacagtggc 540
 atattcttg tcatgtcat gagcattgat agatactgg caattgtga cgcggtgtt 600
 tcttgaggg caaggacctt gacttatggg gtcatcacca gtttggtac atggtcagt 660
 50 gctgtgttcg cctcccttc tggcttctg ttcagcactt gttatactga gcgcaacct 720

acctactgca aaaccaagta ctctctcaac tccacgacgt ggaaggttct cagctccctg 780
 gaaatcaaca ttctgggatt ggtgatcccc ttagggatca tgctgttttg ctactccatg 840
 5 atcatcagga ccttgcagca ttgtaaaaat gagaagaaga acaaggcggt gaagatgatc 900
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 25 acctgggctg aggcatcctt cctcacacca ggcttgctg caggcatgag tcagtctgat 1500
 gagaactctg agcagtgtt gaatgaagtt gtaggtaata ttgcaaggca aagactattc 1560
 ccttctaacc tgaactgatg ggtttctcca gaggggaattg cagagtactg gctgatggag 1620
 30 taaatcgcta ccttttgctg tggcaaattg gcctct 1657

 <210> 14
 35 <211> 750
 <212> PRT
 <213> Homo sapiens

 <400> 14
 40 Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
 1 5 10 15

 45 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
 20 25 30

 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
 50 35 40 45

Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
 50 55 60

5 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
 65 70 75 80

10 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
 85 90 95

15 Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
 100 105 110

Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
 115 120 125

20 Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
 130 135 140

25 Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
 145 150 155 160

30 Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
 165 170 175

35 Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
 180 185 190

Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
 195 200 205

40 Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
 210 215 220

45 Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
 225 230 235 240

50 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
 245 250 255

Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
 260 265 270

5 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
 275 280 285

10 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
 290 295 300

15 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
 305 310 315 320

Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
 325 330 335

20 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
 340 345 350

25 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
 355 360 365

30 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
 370 375 380

35 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
 385 390 395 400

Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
 405 410 415

40 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
 420 425 430

45 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
 435 440 445

50 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
 450 455 460

Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
 465 470 475 480

5 Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
 485 490 495

10 Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
 500 505 510

15 Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
 515 520 525

20 Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
 530 535 540

Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
 545 550 555 560

25 Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
 565 570 575

30 Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
 580 585 590

35 Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
 595 600 605

Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
 610 615 620

40 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
 625 630 635 640

45 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
 645 650 655

50 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
 660 665 670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
 675 680 685

5 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
 690 695 700

10 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
 705 710 715 720

15 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
 725 730 735

Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
 740 745 750

<210> 15
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 15

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
 1 5 10 15

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

35 Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
 35 40 45

40 Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
 50 55 60

45 Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
 65 70 75 80

Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
 85 90 95

Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala

100 105 110

5 Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
 115 120

<210> 16
 <211> 622
 10 <212> PRT
 <213> Homo sapiens

<400> 16

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

20 Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
 20 25 30

25 Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
 35 40 45

30 Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
 50 55 60

Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
 65 70 75 80

35 Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
 85 90 95

40 Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
 100 105 110

Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
 115 120 125

45 Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr His Phe Phe Ser Arg Ile
 130 135 140

50 Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
 145 150 155 160

Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
 165 170 175
 5

Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
 180 185 190

10

Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
 195 200 205

15

Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
 210 215 220

20

Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
 225 230 235 240

Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
 245 250 255

25

Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
 260 265 270

30

Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile
 275 280 285

35

Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser
 290 295 300

40

Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys
 305 310 315 320

Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met
 325 330 335

45

Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu
 340 345 350

50

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

Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile
 370 375 380
 5

Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu
 385 390 395 400

10

Val Asn Lys Gly His Glu Met Ser Pro Gln Val Ala Thr Leu Ile Asp
 405 410 415

15

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

20

Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys Ser Leu Ser Pro Glu Glu
 435 440 445

25

Leu Ser Ser Val Pro Pro Ser Ser Ile Trp Ala Val Arg Pro Gln Asp
 450 455 460

30

Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys Ala
 465 470 475 480

35

Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys Ile
 485 490 495

40

Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu Ser
 500 505 510

45

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

Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu Gly
 530 535 540

50

Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val Arg
 545 550 555 560

Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly Leu
 565 570 575

Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu Ser
 580 585 590
 5

Val Gln Glu Ala Leu Ser Gly Thr Pro Cys Leu Leu Gly Pro Gly Pro
 595 600 605
 10

Val Leu Thr Val Leu Ala Leu Leu Ala Ser Thr Leu Ala
 610 615 620
 15

<210> 17
 <211> 556
 <212> PRT
 <213> Homo sapiens
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Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met
 1 5 10 15
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Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp
 20 25 30
 30

Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln
 35 40 45
 35

Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu
 50 55 60
 40

Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ser
 65 70 75 80
 45

Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu
 85 90 95
 50

Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr
 100 105 110
 55

Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp
 115 120 125
 60

Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro
 130 135 140

5

Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala
 145 150 155 160

10

Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Val Pro Pro
 165 170 175

15

Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro
 180 185 190

20

Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser
 195 200 205

25

Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser
 210 215 220

30

Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp
 225 230 235 240

35

Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala
 245 250 255

40

Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu
 260 265 270

45

Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly
 275 280 285

50

Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr Leu Ile Phe Cys Leu
 290 295 300

55

Cys Ser Leu Val Gly Ile Leu His Leu Gln Arg Ala Leu Val Leu Arg
 305 310 315 320

60

Arg Lys Arg Lys Arg Met Thr Asp Pro Thr Arg Arg Phe Phe Lys Val
 325 330 335

Thr Pro Pro Pro Gly Ser Gly Pro Gln Asn Gln Tyr Gly Asn Val Leu
 340 345 350

5

Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala
 355 360 365

10

Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp
 370 375 380

15

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

20

Pro Glu Glu Glu Glu Gly Glu Gly Tyr Glu Glu Pro Asp Ser Glu Glu
 405 410 415

25

Asp Ser Glu Phe Tyr Glu Asn Asp Ser Asn Leu Gly Gln Asp Gln Leu
 420 425 430

30

Ser Gln Asp Gly Ser Gly Tyr Glu Asn Pro Glu Asp Glu Pro Leu Gly
 435 440 445

35

Pro Glu Asp Glu Asp Ser Phe Ser Asn Ala Glu Ser Tyr Glu Asn Glu
 450 455 460

40

Asp Glu Glu Leu Thr Gln Pro Val Ala Arg Thr Met Asp Phe Leu Ser
 465 470 475 480

45

Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly
 485 490 495

50

Ser Gln Ser Tyr Glu Asp Met Arg Gly Ile Leu Tyr Ala Ala Pro Gln
 500 505 510

55

Leu Arg Ser Ile Arg Gly Gln Pro Gly Pro Asn His Glu Glu Asp Ala
 515 520 525

60

Asp Ser Tyr Glu Asn Met Asp Asn Pro Asp Gly Pro Asp Pro Ala Trp
 530 535 540

Gly Gly Gly Gly Arg Met Gly Thr Trp Ser Thr Arg
 545 550 555

5

<210> 18
 <211> 297
 <212> PRT
 <213> Homo sapiens

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<400> 18

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
 1 5 10 15

15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
 20 25 30

20

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

25

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
 50 55 60

30

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
 65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
 85 90 95

35

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
 100 105 110

40

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
 115 120 125

45

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
 130 135 140

50

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
 145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
 165 170 175

5 Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
 180 185 190

10 Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
 195 200 205

15 Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
 210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
 225 230 235 240

20 Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
 245 250 255

25 Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu
 260 265 270

30 Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
 275 280 285

35 Ser Pro Ile Glu Asn Asp Ser Ser Pro
 290 295

<210> 19
 <211> 937
 <212> PRT
 40 <213> Homo sapiens

<400> 19

45 Met His Arg Pro Arg Arg Arg Gly Thr Arg Pro Pro Leu Leu Ala Leu
 1 5 10 15

50 Leu Ala Ala Leu Leu Leu Ala Ala Arg Gly Ala Ala Ala Gln Glu Thr
 20 25 30

Glu Leu Ser Val Ser Ala Glu Leu Val Pro Thr Ser Ser Trp Asn Ile

35

40

45

5 Ser Ser Glu Leu Asn Lys Asp Ser Tyr Leu Thr Leu Asp Glu Pro Met
50 55 60

10 Asn Asn Ile Thr Thr Ser Leu Gly Gln Thr Ala Glu Leu His Cys Lys
65 70 75 80

15 Val Ser Gly Asn Pro Pro Pro Thr Ile Arg Trp Phe Lys Asn Asp Ala
85 90 95

Pro Val Val Gln Glu Pro Arg Arg Leu Ser Phe Arg Ser Thr Ile Tyr
100 105 110

20 Gly Ser Arg Leu Arg Ile Arg Asn Leu Asp Thr Thr Asp Thr Gly Tyr
115 120 125

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

30 Val Leu Phe Val Lys Phe Gly Pro Pro Pro Thr Ala Ser Pro Gly Tyr
145 150 155 160

Ser Asp Glu Tyr Glu Glu Asp Gly Phe Cys Gln Pro Tyr Arg Gly Ile
165 170 175

35 Ala Cys Ala Arg Phe Ile Gly Asn Arg Thr Val Tyr Met Glu Ser Leu
180 185 190

40 His Met Gln Gly Glu Ile Glu Asn Gln Ile Thr Ala Ala Phe Thr Met
195 200 205

45 Ile Gly Thr Ser Ser His Leu Ser Asp Lys Cys Ser Gln Phe Ala Ile
210 215 220

50 Pro Ser Leu Cys His Tyr Ala Phe Pro Tyr Cys Asp Glu Thr Ser Ser
225 230 235 240

Val Pro Lys Pro Arg Asp Leu Cys Arg Asp Glu Cys Glu Ile Leu Glu

245

250

255

5 Asn Val Leu Cys Gln Thr Glu Tyr Ile Phe Ala Arg Ser Asn Pro Met
260 265 270

10 Ile Leu Met Arg Leu Lys Leu Pro Asn Cys Glu Asp Leu Pro Gln Pro
275 280 285

15 Glu Ser Pro Glu Ala Ala Asn Cys Ile Arg Ile Gly Ile Pro Met Ala
290 295 300

Asp Pro Ile Asn Lys Asn His Lys Cys Tyr Asn Ser Thr Gly Val Asp
305 310 315 320

20 Tyr Arg Gly Thr Val Ser Val Thr Lys Ser Gly Arg Gln Cys Gln Pro
325 330 335

25 Trp Asn Ser Gln Tyr Pro His Thr His Thr Phe Thr Ala Leu Arg Phe
340 345 350

30 Pro Glu Leu Asn Gly Gly His Ser Tyr Cys Arg Asn Pro Gly Asn Gln
355 360 365

Lys Glu Ala Pro Trp Cys Phe Thr Leu Asp Glu Asn Phe Lys Ser Asp
370 375 380

35 Leu Cys Asp Ile Pro Ala Cys Asp Ser Lys Asp Ser Lys Glu Lys Asn
385 390 395 400

40 Lys Met Glu Ile Leu Tyr Ile Leu Val Pro Ser Val Ala Ile Pro Leu
405 410 415

45 Ala Ile Ala Leu Leu Phe Phe Phe Ile Cys Val Cys Arg Asn Asn Gln
420 425 430

50 Lys Ser Ser Ser Ala Pro Val Gln Arg Gln Pro Lys His Val Arg Gly
435 440 445

Gln Asn Val Glu Met Ser Met Leu Asn Ala Tyr Lys Pro Lys Ser Lys

450

455

460

5 Ala Lys Glu Leu Pro Leu Ser Ala Val Arg Phe Met Glu Glu Leu Gly
465 470 475 480

10 Glu Cys Ala Phe Gly Lys Ile Tyr Lys Gly His Leu Tyr Leu Pro Gly
485 490 495

15 Met Asp His Ala Gln Leu Val Ala Ile Lys Thr Leu Lys Asp Tyr Asn
500 505 510

20 Asn Pro Gln Gln Trp Thr Glu Phe Gln Gln Glu Ala Ser Leu Met Ala
515 520 525

25 Glu Leu His His Pro Asn Ile Val Cys Leu Leu Gly Ala Val Thr Gln
530 535 540

30 Glu Gln Pro Val Cys Met Leu Phe Glu Tyr Ile Asn Gln Gly Asp Leu
545 550 555 560

35 His Glu Phe Leu Ile Met Arg Ser Pro His Ser Asp Val Gly Cys Ser
565 570 575

40 Ser Asp Glu Asp Gly Thr Val Lys Ser Ser Leu Asp His Gly Asp Phe
580 585 590

45 Leu His Ile Ala Ile Gln Ile Ala Ala Gly Met Glu Tyr Leu Ser Ser
595 600 605

50 His Phe Phe Val His Lys Asp Leu Ala Ala Arg Asn Ile Leu Ile Gly
610 615 620

55 Glu Gln Leu His Val Lys Ile Ser Asp Leu Gly Leu Ser Arg Glu Ile
625 630 635 640

60 Tyr Ser Ala Asp Tyr Tyr Arg Val Gln Ser Lys Ser Leu Leu Pro Ile
645 650 655

Arg Trp Met Pro Pro Glu Ala Ile Met Tyr Gly Lys Phe Ser Ser Asp

	660	665	670	
5	Ser Asp Ile Trp Ser Phe Gly Val Val Leu Trp Glu Ile Phe Ser Phe	675	680	685
10	Gly Leu Gln Pro Tyr Tyr Gly Phe Ser Asn Gln Glu Val Ile Glu Met	690	695	700
15	Val Arg Lys Arg Gln Leu Leu Pro Cys Ser Glu Asp Cys Pro Pro Arg	705	710	715
			720	
20	Met Tyr Ser Leu Met Thr Glu Cys Trp Asn Glu Ile Pro Ser Arg Arg	725	730	735
25	Pro Arg Phe Lys Asp Ile His Val Arg Leu Arg Ser Trp Glu Gly Leu	740	745	750
30	Ser Ser His Thr Ser Ser Thr Thr Pro Ser Gly Gly Asn Ala Thr Thr	755	760	765
35	Gln Thr Thr Ser Leu Ser Ala Ser Pro Val Ser Asn Leu Ser Asn Pro	770	775	780
40	Arg Tyr Pro Asn Tyr Met Phe Pro Ser Gln Gly Ile Thr Pro Gln Gly	785	790	795
			800	
45	Gln Ile Ala Gly Phe Ile Gly Pro Pro Ile Pro Gln Asn Gln Arg Phe	805	810	815
50	Ile Pro Ile Asn Gly Tyr Pro Ile Pro Pro Gly Tyr Ala Ala Phe Pro	820	825	830
	Ala Ala His Tyr Gln Pro Thr Gly Pro Pro Arg Val Ile Gln His Cys	835	840	845
	Pro Pro Pro Lys Ser Arg Ser Pro Ser Ser Ala Ser Gly Ser Thr Ser	850	855	860
	Thr Gly His Val Thr Ser Leu Pro Ser Ser Gly Ser Asn Gln Glu Ala			

865 870 875 880

5 Asn Ile Pro Leu Leu Pro His Met Ser Ile Pro Asn His Pro Gly Gly
 885 890 895

10 Met Gly Ile Thr Val Phe Gly Asn Lys Ser Gln Lys Pro Tyr Lys Ile
 900 905 910

15 Asp Ser Lys Gln Ala Ser Leu Leu Gly Asp Ala Asn Ile His Gly His
 915 920 925

20 Thr Glu Ser Met Ile Ser Ala Glu Leu
 930 935

25 <210> 20
 <211> 168
 <212> PRT
 <213> Homo sapiens

30 <400> 20
 Met Gly His His His His His His His His His His Ser Ser Gly His
 1 5 10 15

35 Ile Glu Gly Arg His Met Arg Arg Val Pro Gly Val Ala Pro Thr Leu
 20 25 30

40 Val Arg Ser Ala Ser Glu Thr Ser Glu Lys Arg Pro Phe Met Cys Ala
 35 40 45

45 Tyr Pro Gly Cys Asn Lys Arg Tyr Phe Lys Leu Ser His Leu Gln Met
 50 55 60

50 His Ser Arg Lys His Thr Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys
 65 70 75 80

55 Asp Cys Glu Arg Arg Phe Phe Arg Ser Asp Gln Leu Lys Arg His Gln
 85 90 95

60 Arg Arg His Thr Gly Val Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg
 100 105 110

5 Lys Phe Ser Arg Ser Asp His Leu Lys Thr His Thr Arg Thr His Thr
 115 120 125

10 Gly Glu Lys Pro Phe Ser Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe
 130 135 140

15 Ala Arg Ser Asp Glu Leu Val Arg His His Asn Met His Gln Arg Asn
 145 150 155 160

20 Met Thr Lys Leu Gln Leu Ala Leu
 165

25 <210> 21
 <211> 347
 <212> PRT
 <213> Homo sapiens
 <400> 21

30 Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu
 1 5 10 15

35 Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
 20 25 30

40 Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
 35 40 45

45 Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu
 50 55 60

50 Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro Ser
 65 70 75 80

55 Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
 85 90 95

60 Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
 100 105 110

	Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
	115 120 125
5	Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
	130 135 140
10	Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
	145 150 155 160
15	Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
	165 170 175
20	Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
	180 185 190
	Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
	195 200 205
25	Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
	210 215 220
30	Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly Val
	225 230 235 240
35	Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu Ala Leu
	245 250 255
40	Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg Lys Ala
	260 265 270
	Ala Arg Thr Ala Val Gly Arg Asn Asp Thr His Pro Thr Thr Gly Ser
	275 280 285
45	Ala Ser Pro Lys His Gln Lys Lys Ser Lys Leu His Gly Pro Thr Glu
	290 295 300
50	Thr Ser Ser Cys Ser Gly Ala Ala Pro Thr Val Glu Met Asp Glu Glu
	305 310 315 320

Leu His Tyr Ala Ser Leu Asn Phe His Gly Met Asn Pro Ser Lys Asp
 325 330 335

5

Thr Ser Thr Glu Tyr Ser Glu Val Arg Thr Gln
 340 345

10

<210> 22
 <211> 11
 <212> PRT
 <213> Secuencia artificial

15

<220>
 <223> scFV anti-CD19 CDRL1

 <400> 22

20

Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn
 1 5 10

25

<210> 23
 <211> 7
 <212> PRT
 <213> Secuencia artificial

30

<220>
 <223> scFV anti-CD19 CDRL2

 <400> 23

35

Ser Arg Leu His Ser Gly Val
 1 5

40

<210> 24
 <211> 9
 <212> PRT
 <213> Secuencia artificial

45

<220>
 <223> scFV anti-CD19 CDRL3

 <400> 24

50

Gly Asn Thr Leu Pro Tyr Thr Phe Gly
 1 5

<210> 25

<211> 5
 <212> PRT
 <213> Secuencia artificial

 5 <220>
 <223> scFV anti-CD19 CDRH1

 <400> 25

 10 Asp Tyr Gly Val Ser
 1 5

 <210> 26
 15 <211> 16
 <212> PRT
 <213> Secuencia artificial

 <220>
 20 <223> scFV anti-CD19 CDRH2

 <400> 26

 Val Thr Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
 25 1 5 10 15

 <210> 27
 <211> 7
 30 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> scFV anti-CD19 CDRH3
 35 <400> 27

 Tyr Ala Met Asp Tyr Trp Gly
 1 5
 40

 <210> 28
 <211> 734
 <212> ADN
 45 <213> Secuencia artificial

 <220>
 <223> scFv anti-CD19 (VH-VL) FMC63

 50 <400> 28
 cacatccaga tgaccagac cacctccagc ctgagcgcca gcctgggcga ccgggtgacc 60

atcagctgcc gggccagcca ggacatcagc aagtacctga actggtatca gcagaagccc 120
 gacggcaccg tcaagctgct gatctaccac accagccggc tgcacagcgg cgtgcccagc 180
 5 cggtttagcg gcagcggctc cggcaccgac tacagcctga ccatctcaa cctggaacag 240
 gaagatatcg ccacctactt ttgccagcag ggcaacacac tgccttacac ctttggcggc 300
 ggaacaaagc tggaatcac cggcagcacc tccggcagcg gcaagcctgg cagcggcgag 360
 10 ggcagcacca agggcgaggt gaagctgcag gaaagcggcc ctggcctggt ggcccccagc 420
 cagagcctga gcgtgacctg caccgtgagc ggcgtagacc tgcccgacta cggcgtagc 480
 15 tggatccggc agccccccag gaagggcctg gaatggctgg gcgtgatctg gggcagcgag 540
 accacctact acaacagcgc cctgaagagc cggctgacca tcatcaagga caacagcaag 600
 agccaggtgt tctgaagat gaacagcctg cagaccgacg acaccgcat ctactactgc 660
 20 gccaagcact actactacgg cggcagctac gccatggact actggggcca gggcaccagc 720
 gtgaccgtga gcag 734
 25
 <210> 29
 <211> 245
 <212> PRT
 <213> Secuencia artificial
 30
 <220>
 <223> scFv anti-CD19 (VH-VL) FMC63
 <400> 29
 35 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 40 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 45 35 40 45
 Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 50 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln

	65	70	75	80	
5	Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr				
	85	90	95		
10	Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly				
	100	105	110		
15	Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys				
	115	120	125		
20	Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser				
	130	135	140		
25	Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser				
	145	150	155	160	
30	Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile				
	165	170	175		
35	Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu				
	180	185	190		
40	Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn				
	195	200	205		
45	Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr				
	210	215	220		
50	Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser				
	225	230	235	240	
	Val Thr Val Ser Ser				
	245				
	<210> 30				
	<211> 11				
	<212> PRT				
	<213> Secuencia artificial				

<220>

<223> scFV anti-ROR1 CDRL1

<400> 30

5

Ala Ser Gly Phe Asp Phe Ser Ala Tyr Tyr Met

1 5 10

10 <210> 31

<211> 7

<212> PRT

<213> Secuencia artificial

15 <220>

<223> scFV anti-ROR1 CDRL2

<400> 31

20 Thr Ile Tyr Pro Ser Ser Gly

1 5

25 <210> 32

<211> 9

<212> PRT

<213> Secuencia artificial

30 <220>

<223> scFV anti-ROR1 CDRL3

<400> 32

35 Ala Asp Arg Ala Thr Tyr Phe Cys Ala

1 5

40 <210> 33

<211> 6

<212> PRT

<213> Secuencia artificial

45 <220>

<223> scFV anti-ROR1 CDRH1

<400> 33

50 Asp Thr Ile Asp Trp Tyr

1 5

<210> 34

<211> 16
 <212> PRT
 <213> Secuencia artificial

5 <220>
 <223> scFV anti-ROR1 CDRH2
 <400> 34

10 Val Gln Ser Asp Gly Ser Tyr Thr Lys Arg Pro Gly Val Pro Asp Arg
 1 5 10 15

15 <210> 35
 <211> 8
 <212> PRT
 <213> Secuencia artificial

20 <220>
 <223> scFV anti-ROR1 CDRH3
 <400> 35

25 Tyr Ile Gly Gly Tyr Val Phe Gly
 1 5

30 <210> 36
 <211> 123
 <212> ADN
 <213> Homo sapiens

35 <400> 36
 cggagcaagc ggagcagagg cggccacagc gactacatga acatgacccc cagacggcct 60
 ggccccaccc ggaagcacta ccagccctac gccccaccca gggactttgc cgcctacaga 120
 agc 123

40 <210> 37
 <211> 1476
 <212> ADN
 <213> Secuencia artificial

45 <220>
 <223> P28z CAR

50 <400> 37
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 atcctgggga gtggagaagc tgagggtcag ctgcagcagt caggacctga actggtgaag 120

cctgggactt cagtgaggat atcctgcaag acttctggat acacattcac tgaatatacc 180
 atacactggg tgaagcagag ccatggaaag agccttgagt ggattggaaa catcaatcct 240
 5 aacaatgggtg gtaccaccta caatcagaag ttcgaggaca aggccacatt gactgtagac 300
 aagtcctcca gtacagccta catggagctc cgcagcctaa catctgagga ttctgcagtc 360
 10 tattattgtg cagctggtg gaacttgac tactggggcc aagggaccac ggtcacctgc 420
 tcctcaggtg gaggtggatc aggtggaggt ggatctggtg gaggtggatc tgacattgtg 480
 atgaccacgt ctacaaaatt catgtccaca tcagtaggag acagggtcag catcatctgt 540
 15 aaggccagtc aagatgtggg tactgctgta gactggatc aacagaaacc aggacaatct 600
 cctaaactac tgatttattg ggcatccact cggcacactg gagtccctga tcgcttcaca 660
 20 ggacgtggat ctgggacaga cttactctc accattacta atgttcagtc tgaagacttg 720
 gcagattatt tctgtcagca atataacagc tatcccctca cgttcgggtc tgggaccatg 780
 ctggacctga aacgggcggc cgcacttact actaccaagc cagtgtctgc aactccctca 840
 25 cctgtgcacc ctaccgggac atctcagccc cagagaccag aagattgtcg gccccgtggc 900
 tcagtgaagg ggaccggatt ggactcgc tgtgatattt acatctgggc acccttgccc 960
 30 ggaatctgcg tggcccttct gctgtccttg atcatcactc tcactgtcta caatagtaga 1020
 aggaacagac tccttcaaag tgactacatg aacatgactc cccggaggcc tgggctcact 1080
 cgaaagcctt accagcccta cgcccctgcc agagactttg cagcgtaccg ccccagagca 1140
 35 aaattcagca ggagtgcaga gactgtgcc aacctgcagg accccaacca gctctacaat 1200
 gagctcaatc tagggcgaag agaggaatat gacgtcttgg agaagaagcg ggctcgggat 1260
 40 ccagagatgg gaggcaaaca gcagaggagg aggaaccccc aggaaggcgt atacaatgca 1320
 ctgcagaaag acaagatggc agaagcctac agtgagatcg gcacaaaagg cgagaggcgg 1380
 agaggcaagg ggcacgatgg cctttaccag ggtctcagca ctgccaccaa ggacacctat 1440
 45 gatgcctgc atatgcagac cctggcccct cgctaa 1476

50 <210> 38
 <211> 15
 <212> PRT
 <213> Secuencia artificial

<220>

<223> Enlazador

5 <400> 38

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

10

<210> 39

<211> 327

<212> PRT

<213> Secuencia artificial

15

<220>

<223> IgG4-Fc

<400> 39

20

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

25

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

30

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

35

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

40

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

45

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

50

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
5	Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
	145 150 155 160
10	Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
	165 170 175
15	Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
	180 185 190
20	Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
	195 200 205
25	Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
	210 215 220
30	Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
	225 230 235 240
35	Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
	245 250 255
40	Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
	260 265 270
45	Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
	275 280 285
50	Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
	290 295 300
55	Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
	305 310 315 320
60	Leu Ser Leu Ser Leu Gly Lys
	325

<210> 40
 <211> 229
 <212> PRT
 <213> Secuencia artificial

5

<220>
 <223> Bisagra-CH2-CH3

<400> 40
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Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
 1 5 10 15

15 Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

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

25 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

30 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 85 90 95

35 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 100 105 110

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

45 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

50 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 165 170 175

5 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
 180 185 190

10 Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
 195 200 205

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

20 Leu Ser Leu Gly Lys
 225

25 <210> 41
 <211> 119
 <212> PRT
 <213> Secuencia artificial

30 <220>
 <223> Bisagra-CH3
 <400> 41

35 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Gly Gln Pro Arg
 1 5 10 15

40 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 20 25 30

45 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 35 40 45

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

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

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 100 105 110

5 Leu Ser Leu Ser Leu Gly Lys
 115

10 <210> 42
 <211> 12
 <212> PRT
 <213> Secuencia artificial

15 <220>
 <223> Bisagra sola

<400> 42

20 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 1 5 10

25 <210> 43
 <211> 28
 <212> PRT
 <213> Homo sapiens
 <400> 43

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

35 Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
 20 25

40 <210> 44
 <211> 41
 <212> PRT
 <213> Secuencia artificial

45 <220>
 <223> dominio citoplásmico de CD28 con sustitución de LL a GG
 <400> 44

50 Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
 1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro

20 25 30

5 Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 45
<211> 42
10 <212> PRT
<213> Homo sapiens

<400> 45

15 Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

20 Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

25 Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 46
<211> 112
30 <212> PRT
<213> Homo sapiens

<400> 46

35 Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

40 Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

45 Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

50 Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
 85 90 95

5

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 100 105 110

10

<210> 47
 <211> 24
 <212> PRT
 <213> Secuencia artificial

15

<220>
 <223> elemento de omisión ribosomal T2A

 <400> 47

20

Leu Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
 1 5 10 15

25

Val Glu Glu Asn Pro Gly Pro Arg
 20

30

<210> 48
 <211> 356
 <212> PRT
 <213> Secuencia artificial

35

<220>
 <223> tEGFR

 <400> 48

40

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 1 5 10 15

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
 20 25 30

45

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
 35 40 45

50

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
 50 55 60

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
 65 70 75 80

5

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
 85 90 95

10

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
 100 105 110

15

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

20

Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile
 130 135 140

25

Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala
 145 150 155 160

30

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

35

Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln
 180 185 190

40

Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
 195 200 205

45

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
 210 215 220

50

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
 225 230 235 240

55

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
 245 250 255

60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
 260 265 270

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
 275 280 285

5

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

10

Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly
 305 310 315 320

15

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

20

Gly Met Val Gly Ala Leu Leu Leu Leu Val Val Ala Leu Gly Ile
 340 345 350

Gly Leu Phe Met
 355

25

<210> 49
 <211> 8
 <212> PRT
 <213> Secuencia artificial

30

<220>
 <223> STREP TAG II

35

<400> 49
 Trp Ser His Pro Gln Phe Glu Lys
 1 5

40

<210> 50
 <211> 10
 <212> PRT
 <213> Secuencia artificial

45

<220>
 <223> Etiqueta Myc

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