

SEQUENCE LISTING

<110> FIVE PRIME THERAPEUTICS, INC.

<120> FGFR2 INHIBITORS ALONE OR IN COMBINATION WITH IMMUNE STIMULATING AGENTS IN CANCER TREATMENT

<130> 01134-0046-00PCT

<150> US 62/258,731

<151> 2015-11-23

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<160> 46

<170> PatentIn version 3.5

<210> 1

<211> 801

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Mature human FGFR2-IIb

<400> 1

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
245 250 255

3

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
260 265 270

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

Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser Asn Ala Glu Val Leu
290 295 300

Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly Glu Tyr Ile Cys Lys
305 310 315 320

Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser Ala Trp Leu Thr Val
325 330 335

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

Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile
355 360 365

Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr
370 375 380

Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys
385 390 395 400

Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser
405 410 415

Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser
420 425 430

Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu
435 440 445

Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly

450

455

460

Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala
 465 470 475 480

Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val
 485 490 495

Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val
 500 505 510

Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile
 515 520 525

Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val
 530 535 540

Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg
 545 550 555 560

Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu
 565 570 575

Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg
 580 585 590

Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala
 595 600 605

Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp
 610 615 620

Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr
 625 630 635 640

Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe
 645 650 655

Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu
 660 665 670

Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro
 675 680 685

Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys
 690 695 700

Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp
 705 710 715 720

His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp
 725 730 735

Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu
 740 745 750

Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser
 755 760 765

Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro
 770 775 780

Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys
 785 790 795 800

Thr

<210> 2

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FGFR2b heavy chain

<220>

<221> MISC_FEATURE

<222> (294)..(294)

<223> Asn297

<400> 2

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

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

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

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

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

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

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

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

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

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

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

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

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

Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 210 215 220

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

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

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

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

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

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

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

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

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

355

360

365

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

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

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

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

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

<210> 3

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FGFR2b light chain

<400> 3

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Ser Thr Thr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 4
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-FGFR2b heavy chain variable region

10

<400> 4

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

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

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

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

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

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

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

Ser Ser

<210> 5

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FGFR2b light chain variable region

<400> 5

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Ser Thr Thr Pro Tyr
 85 90 95

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

<210> 6
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-FGFR2b heavy chain (HC) HVR1
 <400> 6

Thr Tyr Asn Val His
 1 5

<210> 7
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-FGFR2b HC HVR2

<400> 7

Ser Ile Tyr Pro Asp Asn Gly Asp Thr Ser Tyr Asn Gln Asn Phe Lys
 1 5 10 15

Gly

<210> 8

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FGFR2b HC HVR3

<400> 8

Gly Asp Phe Ala Tyr
 1 5

<210> 9

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FGFR2b light chain (LC) HVR1

<400> 9

Lys Ala Ser Gln Gly Val Ser Asn Asp Val Ala
 1 5 10

<210> 10

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FGFR2b LC HVR2

<400> 10

Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 11

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FGFR2b LC HVR3

<400> 11

Gln Gln His Ser Thr Thr Pro Tyr Thr
1 5

<210> 12

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FGFR2b N297Q heavy chain

<220>

<221> MISC_FEATURE

<222> (294)..(294)

<223> N297Q

<400> 12

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

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

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

Gly Ser Ile Tyr Pro Asp Asn Gly Asp Thr Ser Tyr Asn Gln Asn Phe
50 55 60 14

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

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

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

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

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

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

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

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

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

Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
210 215 220

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

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

245

250

255

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

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

Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300

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

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

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

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

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

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

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

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

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

<210> 13
 <211> 800
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Mature human FGFR2-IIIC

<400> 13

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
 100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

18

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

Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala
355 360 365

Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys
370 375 380

Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg
385 390 395 400

Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser
405 410 415

Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser
420 425 430

Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro
435 440 445

Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys
450 455 460

Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val
465 470 475 480

Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys
485 490 495

Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser
500 505 510

Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn
515 520 525

Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu

530

535

540

Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro
 545 550 555 560

Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln
 565 570 575

Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly
 580 585 590

Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala
 595 600 605

Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe
 610 615 620

Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr
 625 630 635 640

Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp
 645 650 655

Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met
 660 665 670

Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val
 675 680 685

Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro
 690 695 700

Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His
 705 710 715 720

Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu
 725 730 735

Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu Ser
 740 745 750

Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser Ser
 755 760 765

Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro Tyr
 770 775 780

Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys Thr
 785 790 795 800

<210> 14
 <211> 356
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> FGFR2 ECD

<400> 14

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
 100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu
275 280 285 22

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
325 330 335

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

Asp Tyr Leu Glu
355

<210> 15
<211> 353
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> FGFR2 ECD delta-3

<400> 15

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
20 25 30

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

Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn Asn Arg Thr

50					55					23		60				
Val 65	Leu	Ile	Gly	Glu	Tyr 70	Leu	Gln	Ile	Lys	Gly 75	Ala	Thr	Pro	Arg	Asp 80	
Ser	Gly	Leu	Tyr	Ala 85	Cys	Thr	Ala	Ser	Arg 90	Thr	Val	Asp	Ser	Glu 95	Thr	
Trp	Tyr	Phe	Met 100	Val	Asn	Val	Thr	Asp 105	Ala	Ile	Ser	Ser	Gly 110	Asp	Asp	
Glu	Asp	Asp 115	Thr	Asp	Gly	Ala	Glu 120	Asp	Phe	Val	Ser	Glu 125	Asn	Ser	Asn	
Asn	Lys 130	Arg	Ala	Pro	Tyr	Trp 135	Thr	Asn	Thr	Glu	Lys 140	Met	Glu	Lys	Arg	
Leu 145	His	Ala	Val	Pro	Ala 150	Ala	Asn	Thr	Val	Lys 155	Phe	Arg	Cys	Pro	Ala 160	
Gly	Gly	Asn	Pro	Met 165	Pro	Thr	Met	Arg	Trp 170	Leu	Lys	Asn	Gly	Lys 175	Glu	
Phe	Lys	Gln	Glu 180	His	Arg	Ile	Gly	Gly 185	Tyr	Lys	Val	Arg	Asn 190	Gln	His	
Trp	Ser	Leu 195	Ile	Met	Glu	Ser	Val 200	Val	Pro	Ser	Asp	Lys 205	Gly	Asn	Tyr	
Thr	Cys 210	Val	Val	Glu	Asn	Glu 215	Tyr	Gly	Ser	Ile	Asn 220	His	Thr	Tyr	His	
Leu 225	Asp	Val	Val	Glu	Arg 230	Ser	Pro	His	Arg	Pro 235	Ile	Leu	Gln	Ala	Gly 240	
Leu	Pro	Ala	Asn	Ala 245	Ser	Thr	Val	Val	Gly 250	Gly	Asp	Val	Glu	Phe 255	Val	

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

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

Asp

<210> 16
 <211> 352
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> FGFR2 ECD delta-4

<400> 16

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
 100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
225 230 235 240 26

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
325 330 335

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

<210> 17
<211> 351
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> FGFR2 ECD delta-5

<400> 17

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala

[illegible]

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

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

<210> 18
 <211> 348
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> FGFR2 ECD delta-8

<400> 18

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
 100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 30 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile
 340 345

<210> 19
 <211> 347
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> FGFR2 ECD delta-9

<400> 19

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu

1	5	10	31	15											
Pro	Pro	Thr	Lys	Tyr	Gln	Ile	Ser	Gln	Pro	Glu	Val	Tyr	Val	Ala	Ala
			20					25					30		
Pro	Gly	Glu	Ser	Leu	Glu	Val	Arg	Cys	Leu	Leu	Lys	Asp	Ala	Ala	Val
		35					40					45			
Ile	Ser	Trp	Thr	Lys	Asp	Gly	Val	His	Leu	Gly	Pro	Asn	Asn	Arg	Thr
	50					55					60				
Val	Leu	Ile	Gly	Glu	Tyr	Leu	Gln	Ile	Lys	Gly	Ala	Thr	Pro	Arg	Asp
65					70					75					80
Ser	Gly	Leu	Tyr	Ala	Cys	Thr	Ala	Ser	Arg	Thr	Val	Asp	Ser	Glu	Thr
				85					90					95	
Trp	Tyr	Phe	Met	Val	Asn	Val	Thr	Asp	Ala	Ile	Ser	Ser	Gly	Asp	Asp
			100					105					110		
Glu	Asp	Asp	Thr	Asp	Gly	Ala	Glu	Asp	Phe	Val	Ser	Glu	Asn	Ser	Asn
		115					120					125			
Asn	Lys	Arg	Ala	Pro	Tyr	Trp	Thr	Asn	Thr	Glu	Lys	Met	Glu	Lys	Arg
	130					135					140				
Leu	His	Ala	Val	Pro	Ala	Ala	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala
145					150					155					160
Gly	Gly	Asn	Pro	Met	Pro	Thr	Met	Arg	Trp	Leu	Lys	Asn	Gly	Lys	Glu
				165					170					175	
Phe	Lys	Gln	Glu	His	Arg	Ile	Gly	Gly	Tyr	Lys	Val	Arg	Asn	Gln	His
			180					185					190		
Trp	Ser	Leu	Ile	Met	Glu	Ser	Val	Val	Pro	Ser	Asp	Lys	Gly	Asn	Tyr
		195					200					205			

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu
 340 345

<210> 20
 <211> 346
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> FGFR2 ECD delta-10

<400> 20

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205 34

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

Thr Val Leu Pro Ala Pro Gly Arg Glu Lys
 340 345

<210> 21
 <211> 342
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> FGFR2 ECD delta-14

<400> 21

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
 100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

Thr Val Leu Pro Ala Pro
 340

<210> 22
 <211> 341
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> FGFR2 ECD delta-15

<400> 22

Arg	Pro	Ser	Phe	Ser	Leu	Val	Glu	Asp	Thr	Thr	Leu	Glu	Pro	Glu	Glu
1				5					10					15	

Pro	Pro	Thr	Lys	Tyr	Gln	Ile	Ser	Gln	Pro	Glu	Val	Tyr	Val	Ala	Ala
			20					25					30		

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

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

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

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

Trp	Tyr	Phe	Met	Val	Asn	Val	Thr	Asp	Ala	Ile	Ser	Ser	Gly	Asp	Asp
			100					105					110		

Glu	Asp	Asp	Thr	Asp	Gly	Ala	Glu	Asp	Phe	Val	Ser	Glu	Asn	Ser	Asn
		115					120					125			

Asn	Lys	Arg	Ala	Pro	Tyr	Trp	Thr	Asn	Thr	Glu	Lys	Met	Glu	Lys	Arg
	130					135					140				

Leu	His	Ala	Val	Pro	Ala	Ala	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala
145					150					155					160

Gly	Gly	Asn	Pro	Met	Pro	Thr	Met	Arg	Trp	Leu	Lys	Asn	Gly	Lys	Glu
				165					170					175	

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

Thr Val Leu Pro Ala
 340

<210> 23
 <211> 340
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> FGFR2 ECD delta-16

<400> 23

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
 100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

Thr Val Leu Pro
 340

<210> 24
 <211> 339
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> FGFR2 ECD delta-17

<400> 24

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
165 170 175 42

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
325 330 335

Thr Val Leu

<210> 25

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

<220>
 <223> Fc C237S

<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 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 44

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> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc

<400> 26

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

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

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

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

45

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

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

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

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145 150 155 160

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

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

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

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

Ser Pro Gly Lys
225

<210> 27
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc

<400> 27

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> 28
 <211> 8
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> FGFR2(111-118)

<400> 28

Asp Asp Glu Asp Asp Thr Asp Gly
 1 5

<210> 29
 <211> 8
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> FGFR1(105-112)

<400> 29

Glu Asp Asp Asp Asp Asp Asp
 1 5

<210> 30
 <211> 356
 <212> PRT
 <213> Artificial Sequence

<220>

<223> FGFR2 ECD with R2(111-118) replaced by R1(105-112)

<400> 30

Arg	Pro	Ser	Phe	Ser	Leu	Val	Glu	Asp	Thr	Thr	Leu	Glu	Pro	Glu	Glu
1				5					10					15	

Pro	Pro	Thr	Lys	Tyr	Gln	Ile	Ser	Gln	Pro	Glu	Val	Tyr	Val	Ala	Ala
			20					25					30		

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

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

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

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

Trp	Tyr	Phe	Met	Val	Asn	Val	Thr	Asp	Ala	Ile	Ser	Ser	Gly	Glu	Asp
			100					105					110		

Asp	Asp	Asp	Asp	Asp	Asp	Ala	Glu	Asp	Phe	Val	Ser	Glu	Asn	Ser	Asn
			115				120					125			

Asn	Lys	Arg	Ala	Pro	Tyr	Trp	Thr	Asn	Thr	Glu	Lys	Met	Glu	Lys	Arg
	130					135					140				

Leu	His	Ala	Val	Pro	Ala	Ala	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala
145					150					155					160

Gly	Gly	Asn	Pro	Met	Pro	Thr	Met	Arg	Trp	Leu	Lys	Asn	Gly	Lys	Glu
				165					170					175	

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

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

Asp Tyr Leu Glu
 355

<210> 31
 <211> 588
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FGFR2 ECD with R2(111-118) replaced by R1(105-112) + Fc
 <400> 31

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Glu Asp
 100 105 110

Asp Asp Asp Asp Asp Asp Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
 260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

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

Asp Tyr Leu Glu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
355 360 52 365

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
370 375 380

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
385 390 395 400

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
405 410 415

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
420 425 430

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
435 440 445

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
450 455 460

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
465 470 475 480

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
500 505 510

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
515 520 525

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
530 535 540

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

54
Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr

305		310		55 315		320									
Cys	Leu	Ala	Gly	Asn	Ser	Ile	Gly	Ile	Ser	Phe	His	Ser	Ala	Trp	Leu
				325					330					335	
Thr	Val	Leu	Pro	Ala	Pro	Gly	Arg	Glu	Lys	Glu	Ile	Thr	Ala	Ser	Pro
			340					345					350		
Asp	Gly	Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
		355					360					365			
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
	370					375					380				
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
385					390					395					400
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
				405					410					415	
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
			420					425					430		
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
		435					440					445			
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
	450					455					460				
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
465					470					475					480
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
				485					490					495	
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
			500					505					510		

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 515 520 525

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 530 535 540

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 545 550 555 560

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 565 570 575

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 580 585

<210> 33

<211> 353

<212> PRT

<213> Artificial Sequence

<220>

<223> FGFR2 ECD delta-3 with R2(111-118) replaced by R1(105-112)

<400> 33

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

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

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

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

65										57							80
										75							
Ser	Gly	Leu	Tyr	Ala	Cys	Thr	Ala	Ser	Arg	Thr	Val	Asp	Ser	Glu	Thr		
				85					90					95			
Trp	Tyr	Phe	Met	Val	Asn	Val	Thr	Asp	Ala	Ile	Ser	Ser	Gly	Glu	Asp		
			100					105					110				
Asp	Asp	Asp	Asp	Asp	Asp	Ala	Glu	Asp	Phe	Val	Ser	Glu	Asn	Ser	Asn		
			115				120					125					
Asn	Lys	Arg	Ala	Pro	Tyr	Trp	Thr	Asn	Thr	Glu	Lys	Met	Glu	Lys	Arg		
	130					135					140						
Leu	His	Ala	Val	Pro	Ala	Ala	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala		
145					150					155					160		
Gly	Gly	Asn	Pro	Met	Pro	Thr	Met	Arg	Trp	Leu	Lys	Asn	Gly	Lys	Glu		
				165				170						175			
Phe	Lys	Gln	Glu	His	Arg	Ile	Gly	Gly	Tyr	Lys	Val	Arg	Asn	Gln	His		
			180					185					190				
Trp	Ser	Leu	Ile	Met	Glu	Ser	Val	Val	Pro	Ser	Asp	Lys	Gly	Asn	Tyr		
		195					200					205					
Thr	Cys	Val	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Ile	Asn	His	Thr	Tyr	His		
	210					215					220						
Leu	Asp	Val	Val	Glu	Arg	Ser	Pro	His	Arg	Pro	Ile	Leu	Gln	Ala	Gly		
225					230					235					240		
Leu	Pro	Ala	Asn	Ala	Ser	Thr	Val	Val	Gly	Gly	Asp	Val	Glu	Phe	Val		
			245						250					255			
Cys	Lys	Val	Tyr	Ser	Asp	Ala	Gln	Pro	His	Ile	Gln	Trp	Ile	Lys	His		
		260					265					270					

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
 290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
 325 330 335

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

Asp

<210> 34
 <211> 587
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FGFR2 ECD delta-3 with R2(111-118) replaced by R1(105-112) + GS
 linker + Fc (also called FGFR2ECD(FGFR2(111-118):FGFR1(105-112):
 delta3)-GS linker-Fc and R2(111-118):R1(105-112))

<400> 34

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1 5 10 15

Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

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

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Glu Asp
 100 105 110

Asp Asp Asp Asp Asp Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
245 250 255 60

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
260 265 270

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

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
325 330 335

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

Asp Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
355 360 365

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
370 375 380

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
385 390 395 400

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
405 410 415

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
420 425 430

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val

435 440 61 445
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 450 455 460
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 465 470 475 480
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 485 490 495
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 500 505 510
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 515 520 525
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 530 535 540
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 545 550 555 560
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 565 570 575
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 580 585

<210> 35
 <211> 288
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> human PD-1 precursor (with signal sequence)

<400> 35

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
 1 5 10 15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
 20 25 30

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

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
 50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
 65 70 75 80

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

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
 100 105 110

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

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
 130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
 145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
 165 170 175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
 180 185 190

Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro
 195 200 205

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

Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro
 225 230 235 240

Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
 245 250 255

Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
 260 265 270

Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
 275 280 285

<210> 36
 <211> 268
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> human PD-1 (mature, without signal sequence)

<400> 36

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
 1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
 20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
 35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60 64

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

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly Leu Leu Gly Ser
145 150 155 160

Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys Ser Arg Ala Ala
165 170 175

Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro Leu Lys Glu Asp
180 185 190

Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr Gly Glu Leu Asp Phe
195 200 205

Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro Cys Val Pro Glu
210 215 220

Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly Met Gly Thr Ser
225 230 235 240

Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg Ser Ala Gln Pro

245 250 65 255

Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
260 265

<210> 37
<211> 290
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> human PD-L1 precursor (with signal sequence)

<400> 37

Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
1 5 10 15

Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
20 25 30

Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
35 40 45

Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
50 55 60

Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
65 70 75 80

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

Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
100 105 110

Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
115 120 125

Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
 130 135 140

Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
 145 150 155 160

Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
 165 170 175

Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
 180 185 190

Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
 195 200 205

Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
 210 215 220

Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
 225 230 235 240

Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
 245 250 255

Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
 260 265 270

Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
 275 280 285

Glu Thr
 290

<210> 38
 <211> 272
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> human PD-L1 (mature, without signal sequence)

<400> 38

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

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

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

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 68 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His Leu Val
210 215 220

Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr Phe Ile
225 230 235 240

Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys Gly Ile
245 250 255

Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu Glu Thr
260 265 270

<210> 39
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-FGFR2 Gal-FR22 heavy chain variable region

<400> 39

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

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

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

69

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

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

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

Phe Tyr Tyr Gly Tyr Asp Asp Tyr Val Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
115

<210> 40
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-FGFR2 Gal-FR22 heavy chain CDR1

<400> 40

Ser Phe Gly Val His
1 5

<210> 41
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-FGFR2 Gal-FR22 heavy chain CDR2

<400> 41

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

<210> 42
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-FGFR2 Gal-FR22 heavy chain CDR3

<400> 42

Phe Tyr Tyr Gly Tyr Asp Asp Tyr Val Met Asp Tyr
 1 5 10

<210> 43
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-FGFR2 Gal-FR22 light chain variable region

<400> 43

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

Gly Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Asn Tyr
 20 25 30

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

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

Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn Leu Glu Pro
 65 70 75 80

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

Met Phe Gly Gly Gly Thr Lys Leu Asp Ile Lys

100

105

<210> 44
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-FGFR2 Gal-FR22 light chain CDR1

<400> 44

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

<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-FGFR2 Gal-FR22 light chain CDR2

<400> 45

Tyr Thr Ser Thr Leu Gln Pro
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-FGFR2 Gal-FR22 light chain CDR3

<400> 46

Leu Gln Tyr Asp Asp Leu Tyr Met
1 5