

Sequencing Listing

<110> SHANGHAI JIAO TONG UNIVERSITY SCHOOL OF MEDICINE

<120> ANTIBODY FC REGION HAVING ENHANCED binding affinity to FcγRIIB

<130> P2020-2571

<150> CN201911223227.1

<151> 2019-12-03

<160> 23

<170> PatentIn version 3.5

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<213> Artificial sequence

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gacactgcaa cctattactg tcagcagagt tggaatgata cgtggacgtt cggaggaggc	360
accaagctgg aattgaaacg aactgtggct gcaccatctg tcttcattctt cccgccatct	420
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc	480
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ggaccc	66

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aaa	1383

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acaggtggaa aaggagggga ctatgctctg gctccaggct ccagacctc tgatctgtct	180
ctcccagatt gtaaagtgat gggtcatgac cctcattctc tagcgtga	228

<210> 13

<211> 791
<212> PRT
<213> Artificial sequence

<400> 13

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1 5 10 15

Gly Ser Thr Gly Asp Thr Val Leu Thr Gln Ser Pro Ala Leu Ala Val
20 25 30

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

Ser Thr Leu Met His Trp Tyr Gln Gln Lys Pro Gly Gln Gln Pro Lys
50 55 60

Leu Leu Ile Tyr Leu Ala Ser His Leu Glu Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asp Pro
85 90 95

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

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

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

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Ser Gly Ala Thr Asn Phe
225 230 235 240

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met
245 250 255

Asp Ile Arg Leu Ser Leu Val Phe Leu Val Leu Phe Ile Lys Gly Val
260 265 270

Gln Cys Glu Val Gln Leu Val Glu Ser Asp Gly Gly Leu Val Gln Pro
275 280 285

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

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

Trp Val Ala Ser Ile Ser Tyr Asp Gly Ser Ser Thr Tyr Tyr Arg Asp
325 330 335

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Thr
340 345 350

Leu Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr
355 360 365

Tyr Cys Gly Arg His Ser Ser Tyr Phe Asp Tyr Trp Gly Gln Gly Val
370 375 380

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 385 390 395 400

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 420 425 430

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 435 440 445

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 450 455 460

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 465 470 475 480

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
 485 490 495

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
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Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 515 520 525

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
 530 535 540

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 545 550 555 560

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
 565 570 575

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
580 585 590

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
595 600 605

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
610 615 620

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
625 630 635 640

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
645 650 655

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
660 665 670

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
675 680 685

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
690 695 700

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Glu Pro Pro
705 710 715 720

Pro Ser Thr Val Ser Asn Met Ala Thr Val Ala Val Leu Val Val Leu
725 730 735

Gly Ala Ala Ile Val Thr Gly Ala Val Val Ala Phe Val Met Lys Met
740 745 750

Arg Arg Arg Asn Thr Gly Gly Lys Gly Gly Asp Tyr Ala Leu Ala Pro
755 760 765

Gly Ser Gln Thr Ser Asp Leu Ser Leu Pro Asp Cys Lys Val Met Val
770 775 780

His Asp Pro His Ser Leu Ala
785 790

<210> 14
<211> 216
<212> PRT
<213> Artificial sequence

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Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
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Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
35 40 45

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50 55 60

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65 70 75 80

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
85 90 95

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
100 105 110

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
115 120 125

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

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

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
100 105

<210> 16
<211> 708
<212> DNA
<213> Artificial sequence

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cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcaccgct cactttcggc 360
ggagggacca aggtggagat caaacgaact gtggctgcac catctgtctt catcttcccg 420
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540
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acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 660
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtggtga 708

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<212> DNA
<213> Artificial sequence

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tgcgctgtct ctggtggctc catcagcagt agtatctggt ggagctgggt ccgccagccc 180
ccagggaagg ggctggaatg gattggggaa atccatcata gtgggaacac caactgcaat 240
ccgtccctca agagtcgagt caccatatca atagacaagt ccaagaacca gttctcctg 300

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aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga     1080
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gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc     1260
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<210> 18
<211> 235
<212> PRT
<213> Artificial sequence

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
20 25 30

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

Val Ser Gly Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Leu Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ile Arg Ala Thr Gly Ile Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Lys Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

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

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

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

210

215

220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 19

<211> 463

<212> PRT

<213> Artificial sequence

<400> 19

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
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Pro Ser Gly Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile
 35 40 45

Ser Ser Ser Ile Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Ile Gly Glu Ile His His Ser Gly Asn Thr Asn Cys Asn
 65 70 75 80

Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Lys Ser Lys Asn
 85 90 95

Gln Phe Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Ala Gly Thr Gly Thr Thr Leu Asp Tyr Trp Gly
 115 120 125

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 195 200 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
 225 230 235 240

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

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

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 275 280 285

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

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
 305 310 315 320

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

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

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

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

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 20
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<212> PRT
<213> Artificial sequence

<400> 20

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
1 5 10 15

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
20 25 30

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
35 40 45

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn

50

55

60

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
 65 70 75 80

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 85 90 95

Ala Pro Ile

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 <222> (19)..(20)
 <223> n is a, c, g, or t

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<210> 22
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 <212> DNA
 <213> Artificial sequence

<400> 22
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<210> 23
 <211> 54
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (20)..(20)
 <223> n is a, c, g, or t

<400> 23

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54