SEQUENCE LISTING

<110> ¿Æ¼ÃÉúÎïÒ½Ò©£¨ÉÏº££©ÓÐÏÞ¹«Ë¾
ÉÏº£ÊÐÖ×ÁöÑÐ¾¿Ëù

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<151> 2018-05-15

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<151> 2018-09-18

<150> CN201811552806.6
<151> 2018-12-19

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<151> 2019-02-28

<160> 35

<170> PatentIn version 3.5

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aaccccgccc tgcggagccg ggtgaccatc agcgtggaca ccagcaagaa ccagttcagc 240

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cccgacagcc tggccgtgag cctgggcgag cgggccacca tcaactgcaa gagcagccag 480

agcctgttca acagcggcaa ccagaagaac tacctgacct ggtaccagca gaagcccggc 540

cagcccccca agctgctgat ctactgggcc agcacccggg agagcggcgt gcccgaccgg 600

ttcagcggca gcggcagcgg caccgacttc accctgacca tcagcagcct gcaggccgag 660

gacgtggccg tgtactactg ccagaacgcc tacagcttcc cctacacctt cggcggcggc 720

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<220>
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1 5 10 15

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

Tyr Asn Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile His Tyr Thr Gly Ser Thr Asn Tyr Asn Pro Ala Leu
50 55 60

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Ile Tyr Asn Gly Asn Ser Phe Pro Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
130 135 140

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln

145 150 155 160

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

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

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
210 215 220

Tyr Tyr Cys Gln Asn Ala Tyr Ser Phe Pro Tyr Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys Arg
245

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1 5 10 15

Gly Glu Ser Ile Ile Leu Gly Ser Gly Glu Ala
            20   25

<210> 5
<211> 216
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<213> Artificial Sequence

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<400> 6

Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro Thr
1   5   10   15

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

Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
        35   40   45

Pro Leu Ala Gly Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr
    50   55   60

Leu Ile Cys Tyr His Arg Ser Arg
65   70

<210> 7

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gggctcactc gaaagcctta ccagccctac gcccctgcca gagactttgc agcgtaccgc 120

ccc 123

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<211> 41
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<220>
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<400> 8

Asn Ser Arg Arg Asn Arg Leu Leu Gln Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro
            20 25 30

Ala Arg Asp Phe Ala Ala Tyr Arg Pro
        35 40

<210> 9
<211> 321
<212> DNA
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<220>
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aatctagggc gaagagagga atatgacgtc ttggagaaga agcgggctcg ggatccagag 120

atgggaggca aacagcagag gaggaggaac ccccaggaag gcgtatacaa tgcactgcag 180

aaagacaaga tggcagaagc ctacagtgag atcggcacaa aaggcgagag gcggagaggc 240

aaggggcacg atggccttta ccagggtctc agcactgcca ccaaggacac ctatgatgcc 300

ctgcatatgc agaccctggc c 321

<210> 10
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse CD3µÄºûÄÚ¶ÎCD3¦Î°±»ùËáÐòÁÐ

<400> 10

Ser Arg Ser Ala Glu Thr Ala Ala Asn Leu Gln Asp Pro Asn Gln Leu
1 5 10 15

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Glu
20 25 30

Lys Lys Arg Ala Arg Asp Pro Glu Met Gly Gly Lys Gln Gln Arg Arg
35 40 45

Arg Asn Pro Gln Glu Gly Val Tyr Asn Ala Leu Gln Lys Asp Lys Met
50 55 60

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

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

Thr Tyr Asp Ala Leu His Met Gln Thr Leu Ala
100 105

<210> 11
<211> 66
<212> DNA
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<220>
<223> F2AºËËáÐòÁÐ

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gggccc 66

<210> 12
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> F2A°±»ùËáÐòÁÐ

<400> 12

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
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<210> 13
<211> 462
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse IL7ºËËáÐòÁÐ

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cctgtcacat catctgagtg ccacattaaa gacaaagaag gtaaagcata tgagagtgta 120

ctgatgatca gcatcgatga attggacaaa atgacaggaa ctgatagtaa ttgcccgaat 180

aatgaaccaa acttttttag aaaacatgta tgtgatgata caaaggaagc tgcttttcta 240

aatcgtgctg ctcgcaagtt gaagcaattt cttaaaatga atatcagtga agaattcaat 300

gtccacttac taacagtatc acaaggcaca caaacactgg tgaactgcac aagtaaggaa 360

gaaaaaaacg taaaggaaca gaaaaagaat gatgcatgtt tcctaaagag actactgaga 420

gaaataaaaa cttgttggaa taaaattttg aagggcagta ta 462

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<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse CCL21aºËËáÐòÁÐ

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acccaaggca gtgatggagg gggtcaggac tgctgcctta agtacagcca gaagaaaatt 120

ccctacagta ttgtccgagg ctataggaag caagaaccaa gtttaggctg tcccatcccg 180

gcaatcctgt tctcaccccg gaagcactct aagcctgagc tatgtgcaaa ccctgaggaa 240

ggctgggtgc agaacctgat gcgccgcctg gaccagcctc agccccagg gaaacaaagc 300

cccggctgca ggaagaaccg gggaacctct aagtctggaa agaaaggaaa gggctccaag 360

ggctgcaaga gaactgaaca gacacagccc tcaagagga 399

<210> 15
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse CCL21bºËËáÐòÁÐ

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acccaaggca gtgatggagg gggacaggac tgctgcctta agtacagcca gaagaaaatt 120

ccctacagta ttgtccgagg ctataggaag caagaaccaa gtttaggctg tcccatcccg 180

gcaatcctgt tcttaccccg gaagcactct aagcctgagc tatgtgcaaa ccctgaggaa 240

ggctgggtgc agaacctgat gcgccgcctg gaccagcctc agccccagg gaaacaaagc 300

cccggctgca ggaagaaccg gggaacctct aagtctggaa agaaaggaaa gggctccaag 360

ggctgcaaga gaactgaaca gacacagccc tcaagagga 399

<210> 16
<211> 57
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<220>
<223> P2AºËËáÐòÁÐ

<400> 16
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<210> 17

<211> 534
<212> DNA
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<220>
<223> ÈËIL7ºËËáÐòÁÐ

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ctaatggtca gcatcgatca attattggac agcatgaaag aaattggtag caattgcctg 180

aataatgaat ttaacttttt taaaagacat atctgtgatg ctaataagga aggtatgttt 240

ttattccgtg ctgctcgcaa gttgaggcaa tttcttaaaa tgaatagcac tggtgatttt 300

gatctccact tattaaaagt ttcagaaggc acaacaatac tgttgaactg cactggccag 360

gttaaaggaa gaaaaccagc tgccctgggt gaagcccaac caacaaagag tttggaagaa 420

aataaatctt taaaggaaca gaaaaaactg aatgacttgt gtttcctaaa gagactatta 480

caagagataa aaacttgttg gaataaaatt ttgatgggca ctaaagaaca ctga 534

<210> 18
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> ÈËIL7°±»ùËáÐòÁÐ

<400> 18

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile
1   5   10   15

Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys
            20   25   30

Asp Gly Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu
        35   40   45

Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
    50   55   60

Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe

65 70 75 80

Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
85 90 95

Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
100 105 110

Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
115 120 125

Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu
130 135 140

Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu
145 150 155 160

Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu
165 170 175

His

<210> 19
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> ÈËIL7R°±»ùËáÐòÁÐ

<400> 19

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
1 5 10 15

Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp
20 25 30

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
35 40 45

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val

```
    50                  55                  60

Asn Ile Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
65                  70                  75                  80

Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
                85                  90                  95

Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
            100                 105                 110

Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
        115                 120                 125

Pro Glu Ala Pro Phe Asp Leu Ser Val Val Tyr Arg Glu Gly Ala Asn
    130                 135                 140

Asp Phe Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val
145                 150                 155                 160

Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
                165                 170                 175

Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
            180                 185                 190

Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
        195                 200                 205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
    210                 215                 220

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro
225                 230                 235                 240

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

Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val
            260                 265                 270
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Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys
        275                 280                 285

Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu
    290                 295                 300

Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val
305                 310                 315                 320

Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu
                325                 330                 335

Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu
            340                 345                 350

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

Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser
    370                 375                 380

Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val
385                 390                 395                 400

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

Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala
            420                 425                 430

Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala
        435                 440                 445

Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
    450                 455
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<210> 20
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> ÈËCCL21ºËËáÐòÁÐ

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acccaaggca gtgatggagg ggctcaggac tgttgcctca agtacagcca aaggaagatt 120

cccgccaagg ttgtccgcag ctaccggaag caggaaccaa gcttaggctg ctccatccca 180

gctatcctgt tcttgccccg caagcgctct caggcagagc tatgtgcaga cccaaaggag 240

ctctgggtgc agcagctgat gcagcatctg gacaagacac catccccaca gaaaccagcc 300

cagggctgca ggaaggacag gggggcctcc aagactggca agaaaggaaa gggctccaaa 360

ggctgcaaga ggactgagcg gtcacagacc cctaaagggc catag   405

<210> 21
<211> 134
<212> PRT
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<220>
<223> ÈËCCL21°±»ùËáÐòÁÐ

<400> 21

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

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

Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
        35   40   45

Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
    50   55   60

Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
65   70   75   80

Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro
                85   90   95

Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr

100 105 110

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
115 120 125

Gln Thr Pro Lys Gly Pro
130

<210> 22
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Claudin18.2°±»ùËáÐòÁÐ

<400> 22

Met Ala Val Thr Ala Cys Gln Gly Leu Gly Phe Val Val Ser Leu Ile
1 5 10 15

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

Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln Gly
35 40 45

Leu Trp Arg Ser Cys Val Arg Glu Ser Ser Gly Phe Thr Glu Cys Arg
50 55 60

Gly Tyr Phe Thr Leu Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65 70 75 80

Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85 90 95

Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100 105 110

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

Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val

130 135 140

Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145 150 155 160

Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165 170 175

Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180 185 190

Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195 200 205

Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210 215 220

Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225 230 235 240

Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245 250 255

Lys His Asp Tyr Val
260

<210> 23
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Claudin18.1°±»ùËáÐòÁÐ

<400> 23

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1 5 10 15

Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20 25 30

Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly

```
        35                  40                  45

Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
    50                  55                  60

Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65                  70                  75                  80

Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
                85                  90                  95

Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
            100                 105                 110

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

Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
    130                 135                 140

Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145                 150                 155                 160

Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
                165                 170                 175

Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
            180                 185                 190

Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
        195                 200                 205

Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
    210                 215                 220

Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225                 230                 235                 240

Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
                245                 250                 255
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Lys His Asp Tyr Val
260

<210> 24
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse4-1BB°ûÄÚÓò¹ËËáÐòÁÐ

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gcagctcaag aggaagatgc ttgtagctgc cgatgtccac aggaagaaga aggaggagga 120

ggaggctatg agctg 135

<210> 25
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse4-1BB°ûÄÚÓò°±»ùËáÐòÁÐ

<400> 25

Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln Pro Phe Lys
1 5 10 15

Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser Cys Arg Cys
20 25 30

Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu Leu
35 40 45

<210> 26
<211> 473
<212> PRT
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<220>
<223> Hu8E5-28ZCAR°±»ùËáÐòÁÐ£¨human£©

<400> 26

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Ile Lys Pro Ser Gln

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1               5                   10                  15

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

Tyr Asn Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Tyr Ile His Tyr Thr Gly Ser Thr Asn Tyr Asn Pro Ala Leu
    50                  55                  60

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Arg Ile Tyr Asn Gly Asn Ser Phe Pro Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
    130                 135                 140

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
145                 150                 155                 160

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

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

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
    210                 215                 220
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```
Tyr Tyr Cys Gln Asn Ala Tyr Ser Phe Pro Tyr Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Leu Glu Ile Lys Arg Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
    290                 295                 300

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
305                 310                 315                 320

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
                325                 330                 335

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
            340                 345                 350

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
        355                 360                 365

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
    370                 375                 380

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
385                 390                 395                 400

Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln
                405                 410                 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
            420                 425                 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
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        435                 440                 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
    450                 455                 460

Leu His Met Gln Ala Leu Pro Pro Arg
465                 470

<210>  27
<211>  471
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Hu8E5-BBZCAR°±»ùËáÐòÁÐ£¨human£©

<400>  27

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

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

Tyr Asn Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Tyr Ile His Tyr Thr Gly Ser Thr Asn Tyr Asn Pro Ala Leu
    50                  55                  60

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Arg Ile Tyr Asn Gly Asn Ser Phe Pro Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
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    130                 135                 140

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
145                 150                 155                 160

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

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

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
    210                 215                 220

Tyr Tyr Cys Gln Asn Ala Tyr Ser Phe Pro Tyr Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Leu Glu Ile Lys Arg Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
    290                 295                 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
305                 310                 315                 320

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
                325                 330                 335

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
            340                 345                 350
```

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

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
370 375 380

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
385 390 395 400

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
405 410 415

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
420 425 430

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
435 440 445

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
450 455 460

Met Gln Ala Leu Pro Pro Arg
465 470

<210> 28
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> humanCD8¦ÁÐÅºÅëÄ°±»ùËáÐòÁÐ

<400> 28

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

His Ala Ala Arg Pro
20

<210> 29
<211> 45
<212> PRT

<213> Artificial Sequence

<220>
<223> humanCD8½ÂÁ´Çø°±»ùËáÐòÁÐ

<400> 29

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1   5   10   15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20   25   30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        35   40   45

<210> 30
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> humanCD28¿çÄ¤Çø°±»ùËáÐòÁÐ

<400> 30

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

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

<210> 31
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> humanCD28°ûÄÚÓò°±»ùËáÐòÁÐ

<400> 31

Arg Ser Lys Arg Ser Arg Leu Leu 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

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 32
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> human4-1BB°ûÄÚÓò°±»ùËáÐòÁÐ

<400> 32

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

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

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

<210> 33
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> humanCD3µÄ°ûÄÚ¶ÎCD3¦Î°±»ùËáÐòÁÐ

<400> 33

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

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

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

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

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu

65 70 75 80

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

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

Arg

<210> 34
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse CCL19ºËËáÐòÁÐ

<400> 34
atggcccccc gtgtgacccc actcctggcc ttcagcctgc tggttctctg gaccttccca 60

gccccaactc tgggggggtgc taatgatgcg gaagactgct gcctgtctgt gacccagcgc 120

cccatccctg ggaacatcgt gaaagccttc cgctaccttc ttaatgaaga tggctgcagg 180

gtgcctgctg ttgtgttcac cacactaagg ggctatcagc tctgtgcacc tccagaccag 240

ccctgggtgg atcgcatcat ccgaagactg aagaagtctt ctgccaagaa caaaggcaac 300

agcaccagaa ggagccctgt gtct 324

<210> 35
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> 28BBZº±»ùËáÐòÁÐ

<400> 35

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

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

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Tyr Asn Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Tyr Ile His Tyr Thr Gly Ser Thr Asn Tyr Asn Pro Ala Leu
    50                  55                  60

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Arg Ile Tyr Asn Gly Asn Ser Phe Pro Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
    130                 135                 140

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
145                 150                 155                 160

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

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

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
    210                 215                 220

Tyr Tyr Cys Gln Asn Ala Tyr Ser Phe Pro Tyr Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Leu Glu Ile Lys Arg Thr Thr Thr Pro Ala Pro Arg Pro Pro
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               245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
    290                 295                 300

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
305                 310                 315                 320

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
                325                 330                 335

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
            340                 345                 350

Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu
        355                 360                 365

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
    370                 375                 380

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
385                 390                 395                 400

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
                405                 410                 415

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
            420                 425                 430

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
        435                 440                 445

Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
    450                 455                 460
```

```
Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
465                 470                 475                 480


Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
                485                 490                 495


Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
            500                 505                 510


Pro Pro Arg
        515
```