SEQUENCE LISTING

<110> National University of Singapore
Tan, Hong Ji Adrian
Campana, Dario

<120> Neutralization of Human Cytokines with Membrane-Bound Anti-Cytokine Non-Signaling Binders Expressed in Immune Cells

<130> 4459.1149-001

<150> 62/651,311
<151> 2018-04-02

<160> 40

<170> PatentIn version 3.5

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ccc 63

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1 5 10 15

His Ala Ala Arg Pro
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ctgagctgct ccgcctctat cagcgtgtcc tacatgtatt ggtaccagca gaagccagga 120

caggcaccta ggctgctgat ctacgacatg tctaacctgg caagcggcat ccccgcacgc 180

ttctctggaa gcggatccgg cacagacttt acactgacca tcagctccct ggagcctgag 240

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accaaggtgg agatcaag 318

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<220>
<223> mb-aIL6 variable light chain amino acid sequence of anti IL-6

<400> 4

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

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ile Ser Val Ser Tyr Met
20 25 30

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

Asp Met Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

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

Asp Phe Ala Val Tyr Tyr Cys Met Gln Trp Ser Gly Tyr Pro Tyr Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

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<220>
<223> mb-aIL6 GSG linker nucleotide sequence

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ggcggcggcg gctctggagg aggaggaagc ggaggaggag gatcc 45

<210> 6
<211> 15
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<220>
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<400> 6

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

<210> 7
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<220>
<223> mb-aIL6 Variable heavy chain nucleotide sequence of anti IL-6

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tcttgtgccg ccagcggctt cacctttttct ccattcgcca tgagctgggt gagacaggca 120

ccaggcaagg gcctggagtg ggtggccaag atctcccctg gcggctcttg gacatactat 180

tccgacacag tgaccggccg gtttaccatc tccagagata acgccaagaa cagcctgtat 240

ctgcagatga atagcctgcg ggccgaggac acagccgtgt actattgtgc cagacagctg 300

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<210> 8

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<220>
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Phe
20 25 30

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

Ala Lys Ile Ser Pro Gly Gly Ser Trp Thr Tyr Tyr Ser Asp Thr Val
50 55 60

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

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

Ala Arg Gln Leu Trp Gly Tyr Tyr Ala Leu Asp Ile Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

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ccactgtccc tgaggcccga ggcatgcagg cctgcagcag gaggcgccgt gcacacccgc 120

ggcctggact tcgcctgtga tatctacatc tgggcacccc tggctggaac ctgcggagtc 180

ctgctgctgt cactggtcat taccctgtat tgc 213

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<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aIL6 CD8alpha hinge and transmembrane domain amino acid sequence

<400> 10

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

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

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

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

Leu Val Ile Thr Leu Tyr Cys
65 70

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cccgaaatcg tcctgaccca gtcccctgcc acactgtccc tgtctccagg agagagggcc 120

accctgagct gctccgcctc tatcagcgtg tcctacatgt attggtacca gcagaagcca 180

ggacaggcac ctaggctgct gatctacgac atgtctaacc tggcaagcgg catccccgca 240

cgcttctctg gaagcggatc cggcacagac tttacactga ccatcagctc cctggagcct 300

gaggatttcg ccgtgtacta ttgcatgcag tggtccggct atccatacac atttggcggc 360

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cggctgtctt gtgccgccag cggcttcacc ttttctccat tcgccatgag ctgggtgaga 540

caggcaccag gcaagggcct ggagtgggtg gccaagatct cccctggcgg ctcttggaca 600

tactattccg acacagtgac cggccggttt accatctcca gagataacgc caagaacagc 660

ctgtatctgc agatgaatag cctgcgggcc gaggacacag ccgtgtacta ttgtgccaga 720

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agc 783

<210> 12
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<213> ARTIFICIAL SEQUENCE

<220>
<223> sec-aIL6 amino acid sequence

<400> 12

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 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu
20 25 30

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

Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Asp Met Ser Asn Leu Ala Ser Gly Ile Pro Ala
65 70 75 80

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

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

Gly Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
    130                 135                 140

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
145                 150                 155                 160

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Phe Ala Met
                165                 170                 175

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Lys
            180                 185                 190

Ile Ser Pro Gly Gly Ser Trp Thr Tyr Tyr Ser Asp Thr Val Thr Gly
        195                 200                 205

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
    210                 215                 220

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
225                 230                 235                 240

Gln Leu Trp Gly Tyr Tyr Ala Leu Asp Ile Trp Gly Gln Gly Thr Thr
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Val Thr Val Ser Ser
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<220>
<223> aIL6BBz CD8alpha signal peptide nucleotide sequence

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ccc 63

<210> 14
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<213> ARTIFICIAL SEQUENCE

<220>
<223> aIL6BBz CD8alpha signal peptide amino acid sequence

<400> 14

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> 15
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<220>
<223> aIL6BBz aIL6 scFv nucleotide sequence

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ctgagctgct ccgcctctat cagcgtgtcc tacatgtatt ggtaccagca gaagccagga 120

caggcaccta ggctgctgat ctacgacatg tctaacctgg caagcggcat ccccgcacgc 180

ttctctggaa gcggatccgg cacagacttt acactgacca tcagctccct ggagcctgag 240

gatttcgccg tgtactattg catgcagtgg tccggctatc catacacatt tggcggcggc 300

accaaggtgg agatcaaggg cggcggcggc tctggaggag gaggaagcgg aggaggagga 360

tccgaggtgc agctggtgga gagcggcggc ggcctggtgc agcccggcgg ctccctgcgg 420

ctgtcttgtg ccgccagcgg cttcaccttt tctccattcg ccatgagctg ggtgagacag 480

gcaccaggca agggcctgga gtgggtggcc aagatctccc ctggcggctc ttggacatac 540

tattccgaca cagtgaccgg ccggtttacc atctccagag ataacgccaa gaacagcctg 600

tatctgcaga tgaatagcct gcgggccgag gacacagccg tgtactattg tgccagacag 660

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<400> 16

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

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ile Ser Val Ser Tyr Met
20 25 30

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

Asp Met Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

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

Asp Phe Ala Val Tyr Tyr Cys Met Gln Trp Ser Gly Tyr Pro Tyr Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
115 120 125

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
130 135 140

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Ala Ser Gly Phe Thr Phe Ser Pro Phe Ala Met Ser Trp Val Arg Gln
145                 150                 155                 160


Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Lys Ile Ser Pro Gly Gly
                165                 170                 175


Ser Trp Thr Tyr Tyr Ser Asp Thr Val Thr Gly Arg Phe Thr Ile Ser
            180                 185                 190


Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
        195                 200                 205


Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gln Leu Trp Gly Tyr
    210                 215                 220


Tyr Ala Leu Asp Ile Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225                 230                 235                 240


<210>  17
<211>  207
<212>  DNA
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<223>  aIL6BBz CD8alpha hinge and transmembrane domain nucleotide
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tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg cagtgcacac gagggggctg      120

gacttcgcct gtgatatcta catctgggcg cccttggccg ggacttgtgg ggtccttctc      180

ctgtcactgg ttatcaccct ttactgc                                          207


<210>  18
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<220>
<223>  aIL6BBz CD8alpha hinge and transmembrane domain amino acid
       sequence
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<400> 18

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 Ile Tyr Ile
35 40 45

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

Ile Thr Leu Tyr Cys
65

<210> 19
<211> 126
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<223> aIL6BBz 41BB domain nucleotide sequence

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actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg 126

<210> 20
<211> 42
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> aIL6BBz 41BB domain amino acid sequence

<400> 20

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> 21
<211> 336
<212> DNA
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<220>
<223> aIL6BBz CD3zeta domain nucleotide sequence

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agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

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<211> 112
<212> PRT
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<220>
<223> aIL6BBz CD3zeta domain amino acid sequence

<400> 22

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

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

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

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

<210> 23
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acaggcgaac tgctggatcc ttgcgggtac atctctccag agagccccgt ggtgcagctg 120

cactccaact tcaccgccgt gtgcgtgctg aaggagaagt gtatggacta ctttcacgtg 180

aacgccaatt atatcgtgtg gaagacaaac cacttcacca tccctaagga gcagtacaca 240

atcatcaata gaaccgccag ctccgtgacc ttcaccgata tcgccagcct gaacatccag 300

ctgacatgca atatcctgac cttcggccag ctggagcaga acgtgtatgg catcaccatc 360

atctccggcc tgcccctga gaagccaaag aacctgtctt gcatcgtgaa tgagggcaag 420

aagatgaggt gtgagtggga ccggggcaga gagacacacc tggagacaaa tttcaccctg 480

aagtccgagt gggccaccca caagtttgcc gactgcaagg ccaagaggga tacacccacc 540

agctgtacag tggattactc caccgtgtat tttgtgaaca tcgaagtgtg ggtggaggcc 600

gagaatgccc tgggcaaggt gaccagcgac cacatcaact tcgatcccgt gtacaaggtg 660

aagcctaacc caccccacaa tctgtctgtg atcaatagcg aggagctgtc tagcatcctg 720

aagctgacat ggaccaaccc ctccatcaag tctgtgatca tcctgaagta caatatccag 780

tatagaacaa aggacgccag cacctggtcc cagatccctc cagaggatac agcctccacc 840

aggtcctctt ttacagtgca ggacctgaag cctttcaccg agtacgtgtt ccggatccgg 900

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acctatgagg acaggcca 978

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<211> 326
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-gp130-IL6R gp130 domain amino acid sequence

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

Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
20 25 30

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
35 40 45

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
50 55 60

Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65 70 75 80

Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
85 90 95

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
100 105 110

Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
115 120 125

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

Glu Trp Asp Arg Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145 150 155 160

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Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
                165                 170                 175

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
            180                 185                 190

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
        195                 200                 205

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
    210                 215                 220

Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225                 230                 235                 240

Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
                245                 250                 255

Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
            260                 265                 270

Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
        275                 280                 285

Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
    290                 295                 300

Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305                 310                 315                 320

Thr Tyr Glu Asp Arg Pro
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<220>
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<400> 25
ggaggaggag gaagcggagg aggaggctcc ggcggcggcg gctct 45

<210> 26
<211> 15
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-gp130-IL6R GSG linker amino acid sequence

<400> 26

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

<210> 27
<211> 663
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-gp130-IL6R IL-6R domain nucleotide sequence

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gtggtgtgcg agtggggacc tcgcagcacc ccatccctga ccacaaaggc cgtgctgctg 120

gtgcggaagt tccagaatag ccctgccgag gactttcagg agccatgcca gtactctcag 180

gagagccaga agttcagctg tcagctggca gtgccagagg gcgatagctc cttttatatc 240

gtgtccatgt gcgtggcctc tagcgtgggc tccaagttct ctaagacaca gacctttcag 300

ggctgtggca tcctgcagcc tgacccaccc gccaacatca cagtgaccgc cgtggcccgg 360

aatccaagat ggctgtctgt gacatggcag gatccccaca gctggaactc ctctttctac 420

cggctgagat ttgagctgag gtatcgcgcc gagcggagca agacctttac cacatggatg 480

gtgaaggacc tgcagcacca ctgcgtgatc cacgatgcat ggagcggcct gaggcacgtg 540

gtgcagctga gagcacagga ggagttcgga cagggagagt ggagcgagtg gtccccagag 600

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cca 663

<210> 28
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<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-gp130-IL6R IL-6R domain amino acid sequence

<400> 28

Val Asp Val Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser
1 5 10 15

Pro Leu Ser Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser
20 25 30

Leu Thr Thr Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro
35 40 45

Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys
50 55 60

Phe Ser Cys Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile
65 70 75 80

Val Ser Met Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr
85 90 95

Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn
100 105 110

Ile Thr Val Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr
115 120 125

Trp Gln Asp Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe
130 135 140

Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met
145 150 155 160

Val Lys Asp Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly
165 170 175

Leu Arg His Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly
180 185 190

Glu Trp Ser Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu
195 200 205

Ser Arg Ser Pro Pro Ala Glu Asn Glu Val Ser Thr Pro
210 215 220

<210> 29
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<223> mb-gp130-IL6R CD8alpha hinge and transmembrane domain nucleotide sequence

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ccactgtctc tgaggcctga ggcatgcagg ccagcagcag gaggagcagt gcacacccgg 120

ggcctggact tcgcctgtga tatctacatc tgggccccac tggctggcac ttgcggggtc 180

ctgctgctgt ccctggtcat cactctgtat tgc 213

<210> 30
<211> 71
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-gp130-IL6R CD8alpha hinge and transmembrane domain amino acid sequence

<400> 30

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

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

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

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

Leu Val Ile Thr Leu Tyr Cys
65 70

<210> 31
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<213> ARTIFICIAL SEQUENCE

<220>
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ccc 63

<210> 32
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<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aTNFalpha CD8alpha signal peptide amino acid sequence

<400> 32

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> 33
<211> 330
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aTNFalpha Variable light chain nucleotide sequence of anti TNFalpha

<400> 33
gaaatcgtcc tgacccagtc ccccgccaca ctgtctctga gcccaggaga gagggccacc 60

ctgagctgca gagcctccca gtctgtgagc tcctacctgg cctggtatca gcagaagcca 120

ggacaggcac caaggctgct gatctacgac gcatccaaca gggcaacagg catccccgca 180

cgcttcagcg gatccggatc tggcagcggc accgacttta cactgaccat ctctagcctg 240

gagcctgagg atttcgccgt gtactattgc cagcagcgca gcaattggcc ccctttcaca 300

tttggcccag gcaccaaggt ggatatcaag 330

<210> 34
<211> 110
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aTNFalpha variable light chain amino acid sequence of anti TNFalpha

<400> 34

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

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

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

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

Pro Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 35
<211> 45

<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aTNFalpha GSG linker nucleotide sequence

<400> 35
ggaggaggag gatccggagg aggaggatct ggcggcggcg gcagc 45

<210> 36
<211> 15
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aTNFalpha GSG linker amino acid sequence

<400> 36

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

<210> 37
<211> 378
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aTNFalpha Variable heavy chain nucleotide sequence of anti TNFalpha

<400> 37
caggtgcagc tggtggagtc cggcggcggc gtggtgcagc caggcaggtc cctgaggctg 60

tcttgtgcag caagcggctt catcttttcc tcttacgcaa tgcactgggt gcggcaggca 120

cctggaaacg gcctggagtg ggtggccttc atgtcctacg acggctctaa taagaagtat 180

gccgattccg tgaagggccg gtttacaatc agcagagaca actccaagaa taccctgtat 240

ctgcagatga actctctgag ggccgaggac acagccgtgt actattgtgc ccgggataga 300

ggaatcgcag caggaggaaa ttactattac tatggcatgg acgtgtgggg ccagggcacc 360

acagtgaccg tgagctcc 378

<210> 38
<211> 126
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aTNFalpha Variable heavy chain amino acid sequence of anti TNFalpha

<400> 38

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
20 25 30

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

Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 39
<211> 216
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aTNFalpha CD8alpha hinge and transmembrane domain nucleotide sequence

<400> 39
aagcctacca caacccctgc accacggcca ccaacaccag cacctaccat cgcctctcag 60

cctctgagcc tgaggccaga ggcatgcagg ccagcagcag gaggagcagt gcacaccaga 120

ggcctggact ttgcctgtga tatctacatc tgggcccctc tggctgggac ttgcggggtg 180

ctgctgctgt cactggtcat cacactgtat tgttga 216

<210> 40
<211> 71
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> mb-aTNFalpha CD8alpha hinge and transmembrane domain amino acid sequence

<400> 40

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

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

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

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

Leu Val Ile Thr Leu Tyr Cys
65 70